

932

```

1  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRG
51 DTEWCLAPIP LGGYVKMVDI REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTIAARAGF QSGDKIQSVN
151 GTPVADWGSQ QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLNYER AGQHTADIR PDTVEQSDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFGALMML LMMVAFFND VTRLLG*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m591 / g591 97.3% identity in 446 aa overlap

	10	20	30	40	50	60
m591.pep	LHTLLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFFFTRKRG	DTEWCLAPIP
g591	LQTLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFFFTRKRG	DTEWCLAPIP
	10	20	30	40	50	60
m591.pep	LGGYVKMVDI	REGEVSEADL	PYAFDKQHPA	KRIAIVAAGP	LTNLALAVLL	YGLSFSFGVT
g591	LGGYVKMVDI	REGEVSEADL	PYAFDKQHPA	KRIAIVAAGP	LTNLALAVLL	YGLSFSFGVT
	70	80	90	100	110	120
m591.pep	ELRPYVGTVE	PDTIAARAGF	QSGDKIQSVN	GTPVADWGSQ	QTEIVLNLEA	GKVAVGVQTA
g591	ELRPYVGTVE	PDTIAARAGF	QSGDKIQSVN	GTPVADWGSQ	QTEIVLNLEA	GKVAVGVQTA
	130	140	150	160	170	180
m591.pep	SGAQTVRTID	AAGTPEAGKI	AKNQGYIGLM	PFKITTVAGG	VEKGSPEAKA	GLKPGDRLTA
g591	SGAQTVRTID	AAGTPEAGKI	AKNQGYIGLM	PFKITTVAGG	VEKGSPEAKA	GLKPGDRLTA
	190	200	210	220	230	240
m591.pep	ADGKPIASWQ	EWANLTRQSP	GKKITLNYER	AGQHTADIR	PDTVEQSDHT	LIGRVGLRPQ
g591	ADGKPIASWQ	EWANLTRQSP	GKKITLNYER	AGQHTADIR	PDTVEQSDHT	LIGRVGLRPQ
	250	260	270	280	290	300
m591.pep	PDRAWDAQIR	RSYRPSVVRA	FGMGWEKTVS	HSWTTLKFFG	KLISGNASVS	HISGPLTIAD
g591	PDRAWDAQIR	RSYRPSVVRA	FGMGWEKTVS	HSWTTLKFFG	KLISGNASVS	HISGPLTIAD
	310	320	330	340	350	360
m591.pep	IAGQSAELGL	QSYLEFLALV	SISLGVNLNL	PVPVLDGGHL	VFYTAEWIRG	KPLGERVQNI
g591	IAGQSAELGL	QSYLEFLALV	SISLGVNLNL	PVPVLDGGHL	VFYTAEWIRG	KPLGERVQNI
	370	380	390	400	410	420
m591.pep	GLRFGALMML	LMMVAFFND	VTRLLGX			
g591	GLRFGALMML	LMMVAFFND	VTRLLGX			
	430	440				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1845>:

a591.seq

```

1   TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG ATTGTGCGGC GTCAAGGTTG
101 TCGTTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTGACACAG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCCG
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTTACC GAACTGCGCC CCTATGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGCGGCG GTGGA AAAAG GCAGCCCCCG CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAC
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGCC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCCTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGCG AAATAATCA GCGGCAACGC CTCCTCAGC
1051 CATATTTCG GTCCGCTGAC CATTGCCGAT ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTT GGCACCTGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGCCACCTC
1201 GTGTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAAACATC GGTTTGCGCT TCGGGCTTGC CCTCATGATG CTGATGATG
1301 CGGTCGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1846; ORF 591.a>:

```

a591.pep
1   LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRG
51  DTEWCLAPIP LGGYVKMVD T REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV E PDTIARAGF QSGDKIQSVN
151 GTPVADWGSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLYER AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFLALMM LMMAVAFEND VTRLIG*

```

m591/a591 99.6% identity in 446 aa overlap

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          10      20      30      40      50      60
m591.pep  LHTLLAFIFAILILVSLHEFGHYIVARLCGVKVVRFSGVFGKPFFFTRKRGDTEWCLAPIP
          |||
a591       LHTLLAFIFAILILVSLHEFGHYIVARLCGVKVVRFSGVFGKPFFFTRKRGDTEWCLAPIP
          10      20      30      40      50      60

          70      80      90      100     110     120
m591.pep  LGGYVKMVDTREGEVSEADLPYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT
          |||
a591       LGGYVKMVDTREGEVSEADLPYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT
          70      80      90      100     110     120

          130     140     150     160     170     180
m591.pep  ELRPYVGTV EPDTIARAGFQSGDKIQSVNGTPVADWGSAQTEIVLNLEAGKVAVGVQTA
          |||
a591       ELRPYVGTV EPDTIARAGFQSGDKIQSVNGTPVADWGSAQTEIVLNLEAGKVAVGVQTA
          130     140     150     160     170     180

          190     200     210     220     230     240
m591.pep  SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGRDLTA
          |||
a591       SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGRDLTA
          190     200     210     220     230     240

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934

	250	260	270	280	290	300
m591.pep	ADGKPIASWQEWANLTRQSPGKKITLNYERAGQHTADIRPDTVEQSDHTLIGRVGLRPQ					
a591	ADGKPIASWQEWANLTRQSPGKKITLTYERAGQHTADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m591.pep	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
a591	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m591.pep	IAGQSAELGLQSYLEFLALVVISLGVNLNLLPVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
a591	IAGQSAELGLQSYLEFLALVVISLGVNLNLLPVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
	370	380	390	400	410	420
	430	440				
m591.pep	GLRFGALMMLMMAVAFFNDVTRLLGX					
a591	GLRFGALMMLMMAVAFFNDVTRLLGX					
	430	440				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1847>:

g592.seq..

```

1  atgattccgg acgtgttcgg tcagattttt tcgggcgcgt tcaaattcga
51  cgcggcagca ggcggcttac tcggcggtct gatttcgcaa acgatgatga
101 tgggcatcaa acgcggcctg tattccaacg aggcgggtat gggttccgcg
151 ccgaacgccg ccgccgccgc cgaagtgaac caccctgttt cgcaaggtat
201 gattcaaatg ctgggcgtgt ttgtcgatac catcatcggt tgttcttgca
251 ccgccttcac catcttgatt taccaacagc cttatggcga tttgagcggg
301 cgcggcgtga cgcaggcggc gattgtcagc caagtggggc aatggggcgc
351 gggtttcctc gccgtcatcc tgtttatgtt tgccttttcc accgttatcg
401 gcaactatgc ctatgccgag tccaacgtcc aattcatcaa aagccattgg
451 ctgattaccg ccgttttccg tatgctgggt ttggcgtggg tctatttcgg
501 cgcgggttgc aatgtgcctt tggctcggga tatggcggat atggcgatgg
551 gcatcatggc gtggatcaac ctgcgcgcca tcctgctgct ctgcgcattg
601 gcgtttatgc tgctgcgcga ttacaccgcc aagctgaaaa tgggcaaaaga
651 ccccgagttc aaactttccg aacatccggg cctgaaacgc cgcacaaat
701 ccgatgtttg gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1848; ORF 592.ng>:

g592.pep ..

```

1  MIPDVFGQIF SGAFKFDAAA GGLGGLISQ TMMGIKRL YSNEAGMGS
51  PNAAAAAEVK HPVSQGMQM LGVFVDIIV CSCTAFILI YQPYGDL
101 AALTQAAIVS QVQWAGAGFL AVILFMFAPS TVIGNYAYAE SNVQFIKSHW
151 LITAVFRMLV LAWVYFGAVA NVPLVDMAD MAMGIMAWIN LVAILLLSPL
201 AFMLLRDYTA KLKMGKDEP KLSEHPGLKR RIKSDVW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1849>:

m592.seq ..

```

1  ATGATTCCGG ACGTGTTCGG TCAGATTTT TCGGGCGCGT TCAAATTCTGA
51  CGCGGCAGCA GCGGCGTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
101 TGGGCATCAA ACGCGGCCTG TATTTCAAAC AGGCGGGTAT GGGTTCCGCG
151 CCGAACGCCG CCGCCGCCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
201 GATTCAAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTTGCA
251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
301 CCGGCGCTGA CGCAGGCGGC GATTGTCAGC CAAGTGGGGC AATGGGGCGC
351 GGGCTTCCTC GCCGTCATCC TGTTTATGTT TGCCTTTTCC ACCGTTATCG
401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCATCAA AAGCCATTGG
451 CTGATTACCG CCGTTTTCGG TATGCTGGTT TTGGCGTGGG TCTATTTCCG
501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG

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935

601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA  
 651 CCCCAGATTG AAACCTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT  
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1850; ORF 592>:

m592.pep ..  
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGSA  
 51 PNAAAAAEVK HPVSQGMQM LGVFVDIIIV CSCTAFIILI YQPPYGDLSG  
 101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW  
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL  
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW\*

m592 / g592 100.0% identity in 237 aa overlap

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRLYSNEAGMGSA PNAAAAAEVK					
g592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRLYSNEAGMGSA PNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQIMLGVFVDIIIVCSCTAFIILIYQPPYGDLSGAALTQAAIVSQVGQWGAGFL					
g592	HPVSQGMQIMLGVFVDIIIVCSCTAFIILIYQPPYGDLSGAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFS TVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
g592	AVILFMFAFS TVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPLAFMLLRDYTA KLKMGKDPEF KLSEHPGLKRRIKSDVW*					
g592	MAMGIMAWINLVAILLLSPLAFMLLRDYTA KLKMGKDPEF KLSEHPGLKRRIKSDVW*					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1851>:

a592.seq  
 1 ATGATTCCGG ACGTGTTCGG TCAGATTTTT TCGGGCGCGT TCAAATTCGA  
 51 CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA  
 101 TGGGCATCAA ACGCGGCTG TATTCCAACG AGGCGGGTAT GGGTTCCGCG  
 151 CCGAACGCCG CCGCCGCCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT  
 201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTTGCA  
 251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT  
 301 GCGGCGCTGA CGCAGCGGC GATTGTCAGC CAAGTGGGGC AATGGGGCGC  
 351 GGGCTTCCTC GCCGTCATCC TGTTTATGTT TGCCTTTTCC ACCGTTATCG  
 401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTATCAA AAGCCATTGG  
 451 CTGATTACCG CCGTTTCCG TATGCTGGTT TTGGCGTGGG TCTATTTCCG  
 501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG  
 551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG  
 601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA  
 651 CCCCAGATTG AAACCTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT  
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1852; ORF 592.a>:

a592.pep  
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGSA  
 51 PNAAAAAEVK HPVSQGMQM LGVFVDIIIV CSCTAFIILI YQPPYGDLSG  
 101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW  
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL  
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW\*

m592/a592 100.0% identity in 237 aa overlap

936

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMGMGIKRGLYSNEAGMGSAPNAAAAAEVK					
a592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMGMGIKRGLYSNEAGMGSAPNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQMLGVFVDTIIVCSCTAFIILIYQQPYGDLGSAALTQAAIVSQVGQWGAGFL					
a592	HPVSQGMQMLGVFVDTIIVCSCTAFIILIYQQPYGDLGSAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
a592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX					
a592	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1853>:

g593.seq..

```

1  atgcttgaac tgaacggact ctgcaaatgc ttcggcggca aaacggtcgc
51  cgacaacatc tgcctgactg tcgggcggcg caaaatactc gccgtactgg
101 ggcggtcggg ctgctggcaa tccaccctgc tgaatatgat tgcgggcatc
151 gtccggccgg acggcggcga aattcggctg aacggggaaa acattacctg
201 tatgccgcct gaaaaacgcc gtatctcgct gatgtttcaa gattacgcgc
251 tgtttcccca tatgagtgcg ctggaaaata cggcattcgg tttgaaaatg
301 caaaaaatgc cgaaagccga agccgaacgc ctgccttgtg cggcacttgc
351 cgaagtccgg ctggaaaacg aggcgcaccg caagcctgaa aaactttccg
401 gaggcgagaa gcaacggttg gcaactggcg gcgctttggt tgtccgcctt
451 tccctgctgt tgcctgatga atcgttttcc agtttggaac cgcatttgcg
501 cgaccggctg cgccgtatga ccgccgaacg catccgcaag ggcgggcatc
551 ctgccgtttt ggtaacgcat tcgcccgaag aggcctgcac ggcgggcgac
601 gaaatcgccg tcatgcacga ggggaaaatc cttcaatgcg gtacgcccga
651 aaccttgatt caaacgcctg ccggcgctga ggtcgcccggt ctgatggggc
701 tgcccaatac cgacgatgac cgccatattc cgcaaaatgc cgtgtgcttg
751 gacaatcatg gaacggaatg ccgtctgctg tccctcgtcc gcctgcccga
801 ctgcgtccgg ctttccgcgg tccatcccga acacggcgag ctgaccttaa
851 acctgactgt cggacaacat acggacggtg tttccgaaa cggtagcggtc
901 cgcattccgc tcgatgaagg gcgtatcgtc cgtttccgat ga

```

This corresponds to the amino acid sequence <SEQ ID 1854; ORF 593.ng>:

g593.pep..

```

1  MLELNLCKC FGGKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIRL NGENITCMPP EKRRISLMFQ DYALFPHMSA LENTAFGLKM
101 QKMPKAEAEER LALSALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLI QTPAGVQVAR LMGLPNTDDD RHIPQNAVCL
251 DNHGTECRLL SLVRLPDSLR LSAVHPEHGE LTLNLTVGQH TDGISGNGTV
301 RIRVDEGRIV RFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1855>:

m593.seq

```

1  ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGCAATA AAACCGTCGC
51  CGACAACATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTTGG
101 GGCGGTCGGG CTGCGGAAAA TCCACCCTGC TGAATATAAT TGCGGGGATT
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AACGGAGAAA ACATTACCCG

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201 TATGCCGCCC GAAAAACGCC GTATCTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCCA TATGAGTGCG CTGGAAAATG CGGCATTTCG TTTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAACGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAAAACG AGGCGCACCG CAAGCCTGAA AAACCTTTCCG
401 GAGGCGAGAA GCAACGGCTG GCGTTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTGGACGA ATCGTTTTCC AGTTTGGACA CGCATTTGCG
501 CGGCACGCTG CGCCGTATGA CTGCCGAACG TATCCGAAAC GCGGCATCC
551 CTGCCGTTTT GGTAACGCAT TCGCCGAAG AAGCCTGTAC GACGGCAGAC
601 GAAATCGCCG TGATGCATAA AGGGAGGATT CTACAATACG GTACGCCCGA
651 AACATTGGTC AAAACACCAT CCGCGTGCA GGTCCGCCGA CTGATGGGTT
701 TGCCCAATAC CGACGATAAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
801 ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCGGCACGCC GGGGCGGTAT CGGGCAAGGA TACGGTACGC
901 ATCCATATCG AAGAACGGGA AATCGTCCGC TTCCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1856; ORF 593>:

```

m593.pep ..
  1 MLELNLCKR FGKNTVADNI CLTVGRGKIL AVLGRSGCGK STLLNIIAGI
 51 VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAAGFLKM
101 QKMPKAEAEER LAMAALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTLRLGTL RRMTAERIRN GGIPAVLVTH SPEEACTTAD
201 EIAVMHKGRI LQYGTPELTV KTPSCVQVAR LMGLPNTDDN RHIPQHAVRF
251 DQDGMCECVL SRTCLPESFS LSVLHPEHGI LWNLDMRHA GAVSGKDTVR
301 IHIEEREIVR FR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m593 / g593 83.4% identity in 313 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGKNTVADNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGGEIWL					
g593	MLELNLCKCFGGKTVADNICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGGEIRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAGFLKMQKMPKAEAEERLAMAALAEVG					
g593	NGENITCMPPEKRRISLMFQDYALFPHMSALENTAFGLKMQKMPKAEAEERLALSALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTLRLGTLRRMTAERIRN					
g593	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTLRLDRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTTADEIAVMHKGRI LQYGTPELTVKTPSCVQVARLMGLPNTDDN					
g593	GGIPAVLVTHSPEEACTTADEIAVMHEGKILQCGTPELTIQTPAGVQVARLMGLPNTDDD					
	190	200	210	220	230	240

938

	250	260	270	280	290	299
m593.pep	RHIPQHAVRFDQDGM	ECRVL	SRTCLPESF	SLSVLHPEHGIL	WLNLD	-RHAGAVSGKDTV
	:	:		:	:	
g593	RHIPQNAVCLDNHGT	ECRLLSL	VLRLPDSLRL	SAVHPEHGELT	LNLT	VGQHTDGISGNGTV
	250	260	270	280	290	300
	300	310				
m593.pep	RIHIEEREIVRFRX					
	::	:				
g593	RIRVDEGRIVRFRX					
		310				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1857>:

```

a593.seq
1  ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGCGGCA AAACGGTTGC
51  CGACGATATC TGCCTGACTG TCGGGCGCGG CAAATACTC GCCGTTTTGG
101 GCGGTCGGG CTGCGGCAAA TCCACCCTGC TGAATATGAT TGCGGGCATC
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AATGGGGAAA ACATTACCCG
201 TATGCCGCCG GAAAAACGCC GTATTTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCCA TATGAGTGCA CTGGAAAATG CGGCATTTCG TTTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAAAGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAAAACG AGGCGCACCG CAAGCCTGAN AAACCTTCCG
401 GAGGCGAAAA GCAACGGTTG GCACTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTGGACGA ATCGTTTTCC AGTTTGGACA CGCATTTCGG
501 CGACCGGCTG CGCCGCATGA CTGCCGAACG TATCCGCAAG GCGGCGATCC
551 CTGCCGTTTT GGTAACGCAT TCGCCGAAG AGGCCTGCAC GGCGGCAGAC
601 GAAATCGCCG TCATGCACGA GGGGAAAATC CTTCAATGCG GTACGCCCGA
651 AACCTTGTTT CAAACGCCTG CCGGCGTGCA GGTCGCCCAT CTGATGGGGC
701 TGCCCAATAC CGACGATGAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
801 ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCCGCACGCC GGTGAAATAT CGGGAAACGA TACGGTACGC
901 ATCCATATCG AAGACAGGGA AATCGTCCGC TTCCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1858; ORF 593.a>:

```

a593.pep
1  MLELNLCKR FGGKTVADDI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAFLGLKM
101 QKMPKAEAES LAMAALAEVG LENEHRKPX KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLV QTPAGVQVAH LMGLPNTDDD RHIPQHAVRF
251 DQDGMCECVL SRTCLPESFS LSVLHPEHGI LWLNLDMPHA GEISGNDTVR
301 IHIEDREIVR FR*

```

m593/a593 92.9% identity in 312 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFRGNKT	VADNICL	TVGRGKIL	AVLGRSGCGK	STLLNMIAGI	VRPDGGEIWL
a593	MLELNLCKRFRGGKT	VADDICL	TVGRGKIL	AVLGRSGCGK	STLLNMIAGI	VRPDGGEIWL
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPEKRR	ISLMFQDY	ALFPHMSA	LENAFLGLKM	QKMPKAEAE	RLAMAAAEVG
a593	NGENITRMPPEKRR	ISLMFQDY	ALFPHMSA	LENAFLGLKM	QKMPKAEAE	SLAMAALAEVG
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEHRKPEKLSG	GGEKQRLA	LARALVVRP	SLLLLDESFS	SLDTHLRGT	LRMTAERIRN
a593	LENEHRKPKLSG	GGEKQRLA	LARALVVRP	SLLLLDESFS	SLDTHLRDL	RRMTAERIRK
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEE	ACTTADEI	AVMHKGRIL	QYGTPEL	VKTPSCVQ	VARLMGLPNTDDN

939

```

|||||:|||||:|:| |||||:|:| |||||:|||||:
a593  GGIPAVLVTHSPEEACTAADEIAVMHEGKILQCGTPETLVQTPAGVQVAHLMGLPNTDDD
      190      200      210      220      230      240

      250      260      270      280      290      300
m593.pep RHIPQHAVRFDQDGMCECRVLSRTCLPESFSLSVLHPEHGILWLNLDMRHAGAVSGKDTV
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a593  RHIPQHAVRFDQDGMCECRVLSRTCLPESFSLSVLHPEHGILWLNLDMPHAGEISGNDTVR
      250      260      270      280      290      300

      310
m593.pep IHIEEREIVRFRX
||||:|||||
a593  IHIEDREIVRFRX
      310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1859>:

g594.seq..

```

1  atgggtgcag ataccgatgg cgacaaggat gttcggctta atcgaacggg
51  tctcgttttt agcatactcc ggctgctggt ccgcacgga attgggatcg
101 gtaagttcgc cgttcaggcc ttccaggctc ttaagctgct gatctgtacg
151 gttgagcacc caaatcggtt tgccttgcca ctccgcggtc agcagctgac
201 ccgcttcgat ttactgaca tccacctcga cggcagcacc ggaggccttg
251 gctttttccg aagggaaaaa actggccaca aacggcggtg ccacacccaa
301 tgctgccact ccgcccgcgc cgcaggtcgc aagtgtcagg aaacggcggc
351 ggccgttggt gatttcttga ttatccatta ttcagtcgtc ctaatatattt
401 gggaatgccg agccattaaa cattgcaatt ttacccagtt tgcagtgata
451 ctcaaagcat tattaataat aaggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1860; ORF 594.ng>:

g594.pep

```

1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR KCQETAAAVV DFLIIHYSV LIFWECRAIK HCNFTQFAVI
151 LKALFKIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1861>:

m594.seq

```

1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTTCG CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAGCTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GCGCGCCTTG
251 GCTTTTTCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCGCGC CGCAGGTCGC GAGTGTGAGG AAACGGCGGC
351 GGCCGTTGTT GATTTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGAATACCG AGCCATTAAA CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTTAAAAT AAGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1862; ORF 594>:

m594.pep

```

1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIIHYSV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m594 / g594 98.1% identity in 158 aa overlap

940

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
g594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
g594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRCQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
g594	DFLIHYSVVLIFWECRAIKHCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1863>:

```
a594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAACTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GCGGGCCTTG
251 GCTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCGCGC CGCAGGTGCG GAGTGTCAAG AAACGGCGGC
351 GGCGTTGTT GATTTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGAATACCG AGCCATTAAG CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTTAAAT AAGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1864; ORF 594.a>:

```
a594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIHYSVV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*
```

m594/a594 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
a594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
a594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
a594	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1865>:

```
g595.seq..
1  atgagaaaat tcaatttgac cgcattgtcc gtgatgcttg ccttggtttt
51  gaccgcgtgc cagccgccgg aggcggagaa agccgcgccg gccgcgtccg
101 gtgagacca atccgccaac gaaggcggtt cggtcggtat cgccgtcaac
```

```
151 gacaatgcct gcgaaccgat gaatctgacc gtgccgagcg gacaggttgt
201 gttcaatatt aaaaacaaca gcggccgcaa gtcgaatgg gaaatcctga
251 agggcgatgat ggtggtggac gaacgcgaaa atatcgcccc ggggctttcc
301 gacaaaatga accgtaacct gctgccgggc gaatacgaaa tgacctgcgg
351 ccttttgacc aatccgcgcg gcaagctggt ggtagccgac agcggcttta
401 aagacaccgc caacgaagcg gatttgaaa aactgccccca accgctcgcc
451 gactataaag cctacgttca aggcgaggtt aaagagctgg cggcgaaaac
501 caaaaccttt accgaagccg tcaaagcagg cgacattgaa aaggcgaaat
551 ccctgtttgc cgccaccgcg gtccattacg aacgcacgca accgattgcc
601 gagctttttca gcgaactcga ccccgtcacg gatgcgtgtg aagacgactt
651 caaagacggg gcgaaagatg ccgggtttac cggcttccac cgtatcgaa
701 acgccctttg ggtggaaaaa gacgtatccg gcgtgaagga aaccgcggcc
751 aaactgatga ccgatgtcga agccctgcaa aaagaaatcg acgattggc
801 gttccctccg ggcaaagtgg tcggcggcgc gtccgaactg attgaagaag
851 cggcgggcag taaaatcagc ggcgagaag accgttacag ccacaccgat
901 ttgagcgact tccaagctaa tgcggacgga tctaaaaaaa tcgtcgattt
951 gttccgtccg ttgattgagg ccaaaaacaa agccttggtg gaaaaaacg
1001 ataccaactt caaacaggtc aacgaaattc tggcgaaata ccgcaccaa
```



942

1051 gacgggttttg aaacctacga caagctgagc gaagccgacc gcaaagcatt  
 1101 acaggctcct attaacgcgc ttgccgaaga ccttgcccaa cttcgcgga  
 1151 tactcggctt gaaataa

This corresponds to the amino acid sequence <SEQ ID 1866; ORF 595.ng>:

g595.pep ..  
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGI AVN  
 51 DNACEPMNLT VPSGQVFN I KNNSGRKLEW EILKGMVVD ERENIAPGLS  
 101 DKMNRNLLPG EYEMTCGLLT NPRGKLVAD SGFKDTANEA DLEKLPQPLA  
 151 DYKAYVQGEV KELA AKTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA  
 201 ELFSELDPVI DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA  
 251 KLMTDVEALQ KEIDALAFPP GKVVGGA SEL IEAAAGSKIS GEEDRYSHTD  
 301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTD TNFKQV NEILAKYRTK  
 351 DGFETYDKLS EADRKALQAP INALAE DLAQ LRGILGLK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1867>:

m595.seq  
 1 ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT  
 51 GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG  
 101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTAGTAT CGCCGTCAAC  
 151 GACAATGCCT GCGAACC GAT GGA ACTGACC GTGCCGAGCG GACAGTTGT  
 201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA  
 251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC  
 301 GATAAAATGA CCGTCAACCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG  
 351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAAACGAC AGCGGCTTTA  
 401 AAGACACCGC CAACGAAGCG GATTTGGAAA AACTGTCCCA ACCGCTCGCC  
 451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAAC  
 501 CAAAAC TTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGCGGAAAT  
 551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC  
 601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT  
 651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTTTAC CGTATCGAAT  
 701 ACGCCCTTTG GGTGGA AAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG  
 751 AAAC TGATGA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC  
 801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAAC TG ATTGAAGAAG  
 851 TGGCGGGCAG TAAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT  
 901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT  
 951 GTTCCGTCCG CTGATCGAGG CCAAAAACAA AGCCTTGT TG GAAAAACCG  
 1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA  
 1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT  
 1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CTTGCCCAA CTTGCGGGCA  
 1151 TACTCGGCTT GAAATAA

This corresponds to the amino acid sequence <SEQ ID 1868; ORF 595>:

m595.pep  
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSI AVN  
 51 DNACEPMELT VPSGQVFN I KNNSGRKLEW EILKGMVVD ERENIAPGLS  
 101 DKMTVTLLPG EYEMTCGLLT NPRGKLVTD SGFKDTANEA DLEKLSQPLA  
 151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA  
 201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA  
 251 KLMTDVEALQ KEIDALAFPP GKVVGGA SEL IEEVAGSKIS GEEDRYSHTD  
 301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTD TNFKQV NEILAKYRTK  
 351 DGFETYDKLG EADRKALQAS INALAE DLAQ LRGILGLK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m595 / g595 95.4% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLALS	SVMLALGLTAC	QPPEAEKAAP	AASGEAQTAN	EGGSVSI	AVNDNACEPMELT
g595	MRKFNLALS	SVMLALGLTAC	QPPEAEKAAP	AASGETQSAN	EGGSVGI	AVNDNACEPMNLT
	10	20	30	40	50	60
	70	80	90	100	110	120

943

m595.pep	VPSGQVVFN	KNNSGRKLEWEIL	KGVMVVD	ERENIAPGL	SDKMTVTLL	PGEYEMTCGLLT
g595	VPSGQVVFN	KNNSGRKLEWEIL	KGVMVVD	ERENIAPGL	SDKMNRNLL	PGEYEMTCGLLT
	70	80	90	100	110	120
m595.pep	NPRGKLVV	TDSGFKDTANEAD	LEKLSQPLADY	KAYVQGEVKEL	VAKTKTFT	EAVKAGDIE
g595	NPRGKLVV	ADSGFKDTANEAD	LEKLPQLADY	KAYVQGEVKEL	AAKTKTFT	EAVKAGDIE
	130	140	150	160	170	180
m595.pep	KA	KS	LFADTRVHYERIE	PIAELFSELD	PVIDAREDD	FKDGAKDAGFTGFHRIEYALWVEK
g595	KA	KS	LFAATRVHYERIE	PIAELFSELD	PVIDACEDD	FKDGAKDAGFTGFHRIEHALWVEK
	190	200	210	220	230	240
m595.pep	DV	SGVKEIAAKLMTD	VEALQKEIDAL	AFPPGKVVG	GASELIEEV	AGSKISGEEDRYSHTD
g595	DV	SGVKETAAKLMTD	VEALQKEIDAL	AFPPGKVVG	GASELIEEA	AGSKISGEEDRYSHTD
	250	260	270	280	290	300
m595.pep	LS	DFQANVDGSKKIV	DLFRPLIEAKN	KALLEKTD	TNFKQVNEI	LAKYRTKDGFTYDKLG
g595	LS	DFQANADGSKKIV	DLFRPLIEAKN	KALLEKTD	TNFKQVNEI	LAKYRTKDGFTYDKLS
	310	320	330	340	350	360
m595.pep	EAD	RKALQASINALA	EDLAQLRGIL	GLKX		
g595	EAD	RKALQAPINALA	EDLAQLRGIL	GLKX		
	370	380	389			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1869>:

```

a595.seq
1  ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51  GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTACGTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCAGT GGAACGTACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTCCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTTGGAAG AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTATGTTCA AGGCGAAGTC AAAGAGCTGG TGGCGAAAAC
501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTCCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAGTATGTA CCGATGTGTA AGCCCTGCAA AAAGAAATCG ACGCATTTGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGGCG GTCCGAACTG ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCGAAAAAAA TCGTCGATTT
951 GTTCCGTCCG TTGATCGAGA CAAAAACAA AGCCTTGTGT GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTGCGGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1870; ORF 595.a>:

```

a595.pep
1  MRKENLTALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIAVN
51  DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAAPGLS

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944

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101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

```

m595/a595 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLTALSVM LALGLTACQPPEAEKAAPAASGEAQTANEGGSVSI AVNDNACEPMELT					
a595	MRKFNLTALSVM LALGLTACQPPEAEKAAPAASGEAQTANEGGSVSI AVNDNACEPMELT					
	10	20	30	40	50	60
m595.pep	70	80	90	100	110	120
	VPSGQVVFNIK NNSGRKLEWEILKGVMVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
a595	VPSGQVVFNIK NNSGRKLEWEILKGVMVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
m595.pep	130	140	150	160	170	180
	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
a595	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
m595.pep	190	200	210	220	230	240
	KAKSLFADTRVHYERIEPIAE L FSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
a595	KAKSLFADTRVHYERIEPIAE L FSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
	190	200	210	220	230	240
m595.pep	250	260	270	280	290	300
	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD					
a595	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
m595.pep	310	320	330	340	350	360
	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTK DGFETYDKLG					
a595	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTK DGFETYDKLG					
	310	320	330	340	350	360
m595.pep	370	380	389			
	EADRKALQASINALAEDLAQLRGILGLKX					
a595	EADRKALQASINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1871>:

g596.seq. (partial).

```

1  ..atgctgctct tggacgagcc gaccaaccac ttggatgcgg aatcggtgga
51  atggctggag caattcctcg tgcgcttccc cggcacagtg gtcgcggtaa
101 cgcacgaccg ctacttcctc gacaacgccg ccgaatggat tttggaactc
151 gaccgcggac acggcattcc gtggaaaggc aattactcgt cttggctgga
201 gcagaaagaa aaacgcttgg aaaacgaggc gaaatccgaa gccgcgcgcg
251 tgaaggcgat gaagcaggaa ttggaatggg tgcgccaaaa tgccaaaggc
301 cgccaagcca agcccaaaagc gcgtttggcg cgttttgaag aaatgagcaa
351 ctacgaatac caaaaacgca acgaaaactca ggaaatcttt atccctgttg
401 ccgagcggtt gggtaacgaa gtgattgaat ttgtgaatgt ttccaaatcg

```

945

```

451   ttccggcgata aagtgcctgat tgacgggtttg agcttcaaag tgccggcgagg
501   cgcgattgtc ggcatcatcg gcccgaaacgg cgcgggttaa tcgacgctgt
551   tcaaaatgat tgccgggcaaa gagcagcccg attcgggcca agtgaaaatc
601   gggcaaaccg tgaaaatgag cttgattgac caaagccgag aaggttttgc
651   aaacgacaaa accgtgttcg acaacattgc cgaagggtcg gatattttgc
701   aggtcggaca gtttgaaatc cccgcccggc aatatattgg acgcttcaac
751   tttaaaggca gcgaccaaag caaaatcgca aggcagcttt ccggcgcgga
801   acgcgccgct ctgcacttgg caaaaacctt gttggcgagg ggcaatgtgt
851   tgctgctgga cgaaccgtcc aacgatctcg acgtggaaac cctgcgcgag
901   ttggaagacg cattgttggg atttgccggc agcgtgatgg tgatttcgca
951   cgaccgctgg tttctcgacc gcatagccac gcatatcttg gcgtgtgaag
1001  gcgactccaa atgggtgttc ttcgacggca actatcaaga atacgaagcc
1051  gacaagaaac gccgactcgg caaagaaggc gcgaaaccga aacgcatcaa
1101  atacaaaccg gtaacgcgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 1872; ORF 596.ng>:

g596.pep (partial).

```

1   ..MLLLDEPTNH LDAESVEWLE QFLVRFPGTV VAVTHDRYFL DNAAEWILEL
51  DRGHGIPWKG NYSSWLEQKE KRLNEAKSE AARVKAMKQE LEWVRQNAKG
101 RQAKPKARLA RFEEMSNEYE QKRNETQEIF IPVAERLGNE VIEFVNVSKS
151 FGDKVLIDGL SFKVPAGAIV GIIGPNGAGK STLFKMIAGK EQPDSGEVKI
201 GQTVKMSLID QSREGLQNDK TVFDNIAEGR DILQVGQFEI PARQYLGRFN
251 FKGSQSKIA RQLSGGERGR LHLAKTLLGG GNVLLLDDEPS NDLDVETLRA
301 LEDALLEFAG SVMVISHDRW FLDRIATHIL ACEGDSKWVF FDGNYQEYEA
351 DKRRRLGKEG AKPKRIKYKP VTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1873>:

m596.seq..

```

1   ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATTG AAGATATTTT CCTTTCTTTC TTCCCCGGCG
101 CGAAATATCGG CCTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGA TAAGGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGCATC AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGCGAGGAA GTGGAAAGCG GTTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAAGA AGTGTATGCC GAGTACGCCA ATCCTGATGC
351 GGATTTTGAC GCGTTGGCAG AAGAGCAGGG CCGCTTGGA GCGATTATTG
401 CCGCAGGTTC GTCCACGGGC GCGGTGCGG AACACGAATT GGAAATCGCC
451 GCCGACGCGC TCGCCTGCC GGAATGGGAT GCCAAAATCG ATAATTTGTC
501 CCGCGGTGAA AAACGCGCGC TTGCCTTGTG CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGGG TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCCGCA CAGTCGTTGC
651 GGTAACGCAC GACCCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGCCATGGT ATTCCGTGGA AAGGCAATTA CTCGCTTGG
751 CTGGAGCAGA AAGAAAAACG CTTGGAAAAC GAGGCAAAAT CCGAAGCCGC
801 GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCCGCCA AGCCAAGTCC AAAGCGCGTT TGGCTCGTTT TGAAGAAATG
901 AGCAACTACG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTTATTCC
951 CGTTGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTA AATGTTTCCA
1001 AATCGTTTCG CGATAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051 GCGGGCGCGA TTGTCGGCAT CATCGGCCCG AACGGCGCGG GTAAATCTAC
1101 GCTGTTCAAA ATGATTTCGG GCAAAGAGCA GCCTGATTCC GGCGAGGTGA
1151 AAATCGGACA AACCCTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAAG GCCCGACAT
1251 TTTGCAGGTT GGTCAAGTTT AAATTCCCGC CCGCCAATAT TTGGGGCGTT
1301 TCAACTTCAA AGGCAGCGAC CAAAGCAAAA TTGCAGGTCA ATTGTCTGGC
1351 GGCGAACGCG GTCGTCTGCA CTTGGCAAAA ACCTTGTGTA GCGGCGGCAA
1401 TGTATTGCTG CTGGATGAAC CGTCTAACGA CCTTGACGTG GAAACCTGTC
1451 GCGGTTTGGG AGACGCATTG TTGGAATTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GTTGGTTTCT CGACCGCATC GCCACGCATA TCTTGGCGTG
1551 TGAAGGCGAC TCTAAATGGG TGTTCTTCTG CCGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGT TTGGGCGAAG AAGGCGCGAA ACCGAAACGC
1651 ATCAAATACA AACCAGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1874; ORF 596>:

m596.pep..

946

```

1  MSQQYVYSML RVSKVVPQK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEPE LPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADF ALAEEQGRLE AIIAAGSSTG GGAEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAAE WILELDRGHG IPWKGNYSW
251 LEQKEKRLN EAKSEAARVK AMKQELWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNIEVIEFV NVSKSFGDKV LIDDLSEKVP
351 AGAIVGIIGP NGAGKSTLFK MISGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKIAGQLSG
451 GERGRHLAK TLLSGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNV QEYADKKRR LGEEGAKPKR
551 IKYKPVTR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m596 g596 98.4% identity in 373 aa overlap

```

          160      170      180      190      200      210
m596.pep  LPEWDAKIDNLSGGEKRRVALCKLLSKPDMLLDEPTNHLDAESVEWLEQFLVRFPGTV
          |||||||||||||||||||||||||||||||||||||||||||||||||||
g596      MLLDEPTNHLDAESVEWLEQFLVRFPGTV
              10      20      30

          220      230      240      250      260      270
m596.pep  VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQE
          |||||||||||||||||||||||||||||||||||||||||||||||||||
g596      VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQE
              40      50      60      70      80      90

          280      290      300      310      320      330
m596.pep  LEWVRQNAKGRQAKSKARLARFEEMSNEYEQKRNETQEIFIPVAERLGNEVIEFVNVSKS
          ||||||||||||||| |||||||||||||||||||||||||||||||||||
g596      LEWVRQNAKGRQAKPKARLARFEEMSNEYEQKRNETQEIFIPVAERLGNEVIEFVNVSKS
              100     110     120     130     140     150

          340      350      360      370      380      390
m596.pep  FGDKVLIDDLSEFKVPAGAIVGIIGPNGAGKSTLFKMIAGKEQPDGGEVKIGQTVKMSLID
          ||||||| |||||||||||||||||||||||||:|||||||||||||||||
g596      FGDKVLIDGLSEFKVPAGAIVGIIGPNGAGKSTLFKMIAGKEQPDGGEVKIGQTVKMSLID
              160     170     180     190     200     210

          400      410      420      430      440      450
m596.pep  QSREGLQNDKTVFDNIAEGRDILQVQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGR
          |||||||||||||||||||||||||||||||||||||||||||||||||||
g596      QSREGLQNDKTVFDNIAEGRDILQVQFEIPARQYLGRFNFKGSDQSKIARQLSGGERGR
              220     230     240     250     260     270

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947

	460	470	480	490	500	510
m596.pep	LHLAKTLLSGGNVLLLDPEPSNDLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL					
g596	LHLAKTLLGGGNVLLLDPEPSNDLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL					
	280	290	300	310	320	330

	520	530	540	550	559
m596.pep	ACEGDSKWVFFDGNVQEYADKKRRLGEEGAKPKRIKYKPVTRX				
g596	ACEGDSKWVFFDGNVQEYADKKRRLGKEGAKPKRIKYKPVTRX				
	340	350	360	370	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1875>:

```

a596.seq
1  ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATTA AAGATATTTT CCTTCTTTT TCCCCGCGC
101 CGAAAAATCGG TTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGA TAAAGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGTATT AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGTGAGGAA GTGGAAAGCG GTTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAGGA AGTGTATGCC GAGTACGCCA ATCCCGATGC
351 GGATTTTGAC GCGTTGGCGG AAGAGCAGGG GCGTTTGAA GCGATTATTG
401 CGGCGGGTTC GTCCACGGGC GGCGGTGCGG AACACGAATT GGAATCGCT
451 GCCGACGCGC TCGCCTGCC GGAATGGGAT GCCAAAATCG ATAATTTGTC
501 CGGCGGTGAA AAACGCCGCG TCGCTTTGTG CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGGA TCGGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGC GC TCCCCGTA CAGTCGTTGC
651 CGTAACACAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGGCACGGT ATTCCGTGGA AAGGAAATTA CTCGTCTTGG
751 TTGAGCAGA AAGAAAAACG TTTGGAAAAC GAGGCGAAAT CCGAAGCCGC
801 GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCCGTCA AGCCAAGTCC AAAGCGCGTT TGGCGCGTT TGAAGAAATG
901 AGCAACTATG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTCATTCC
951 CGTCGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTG AATGTTTCCA
1001 AATCGTTCGG CGACAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051 GCGGGCGCGA TTGTCGGCAT CATCGGTCCG AACGGCGCGG GTAAATCGAC
1101 ACTGTTTAAA ATGATTGCGG GCAAAGAGCA GCCCGATTCC GGTGAAGTGA
1151 AAATCGGGCA AACCCTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAAG GTCGCGATAT
1251 TTTACAGGTC GGGCAGTTTG AAATCCCCGC CCGCAATAT TTGGGACGCT
1301 TCAATTTCAA AGGCAGCGAC CAAAGCAAAA TCACGGGGCA GCTTTCGGC
1351 GGCGAACGCG GACGTTTGCA CTTGGCAAAA ACCTTGTTGG GCGGTGGCAA
1401 TGTGTTGCTG CTGGACGAAC CGTCCAACGA CCTCGACGTG GAAACCCTGC
1451 GCGCGTTGGA AGACGCATTG CTGGAATTTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GCTGGTTTCT CGACCGTATT GCTACGCATA TCTTGGCTTG
1551 CGAAGCGGAC TCCAAATGGG TGTTCTTTGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGA CTCGGCGAAG AAGGCACGAA ACCGAAACGC
1651 ATCAAATACA AACCAGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1876; ORF 596.a>:

```

a596.pep
1  MSQQYVYSML RVSKVVPQK TIIKDISLSF FPAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEPE LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADF ALAEEQGRLE AIIAAGSSTG GGAHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAEE WILELDRGHG IPWKGNYSW
251 LEQKEKRLN EAKSEAARVK AMKQELEWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNEVIEFV NVSKSFGDKV LIDDLSEFKVP
351 AGAIVGIIIGP NGAGKSTLFK MIAGKEQPDS GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKITGQLSG
451 GERGLHLAK TLLGGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNV QEYADKKRR LGEEGTPKPR
551 IKYKPVTR*

```

m596/a596 99.3% identity in 558 aa overlap

948

m596.pep	10	20	30	40	50	60
	MSQQYVYSMLRVSKVVPQKTIKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
a596	MSQQYVYSMLRVSKVVPQKTIKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
	10	20	30	40	50	60
m596.pep	70	80	90	100	110	120
	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
a596	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
	70	80	90	100	110	120
m596.pep	130	140	150	160	170	180
	ALAEEQGRLEAIIAAGSSTGGGAHEHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
a596	ALAEEQGRLEAIIAAGSSTGGGAHEHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
	130	140	150	160	170	180
m596.pep	190	200	210	220	230	240
	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
a596	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
	190	200	210	220	230	240
m596.pep	250	260	270	280	290	300
	IPWKGNYSWLEQKEKRLNEAKSEAAARVKAMKQELEWVRQNAKGRQAKSKARLARFEEM					
a596	IPWKGNYSWLEQKEKRLNEAKSEAAARVKAMKQELEWVRQNAKGRQAKSKARLARFEEM					
	250	260	270	280	290	300
m596.pep	310	320	330	340	350	360
	SNYEYQKRNETQEIFIPVAERLGNIEVFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIGP					
a596	SNYEYQKRNETQEIFIPVAERLGNIEVFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIGP					
	310	320	330	340	350	360
m596.pep	370	380	390	400	410	420
	NGAGKSTLFKMISGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
a596	NGAGKSTLFKMIAGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
	370	380	390	400	410	420
m596.pep	430	440	450	460	470	480
	GQFEIPARQYLGRFNFKGSQSKIAGQLSGGERGRHLAKTLLSGGNVLLDEPSNDLDV					
a596	GQFEIPARQYLGRFNFKGSQSKITGQLSGGERGRHLAKTLLSGGNVLLDEPSNDLDV					
	430	440	450	460	470	480
m596.pep	490	500	510	520	530	540
	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYEQYEADKKRR					
a596	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYEQYEADKKRR					
	490	500	510	520	530	540
m596.pep	550	559				
	LGEEGAKPKRIKYKPVTRX					
a596	LGEEGAKPKRIKYKPVTRX					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1877>

g597.seq

```

1  ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51  CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACGCAAAA CAGCGCGAGG CTTGGGACAA ATTCCAAAAA

```

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151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTCG CGTTTTCGTAT CGGGGAACTA TAAAAACAGC CGGCCGAATG
251 CGGTTGCCCT GTTCTTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCCTCC AATCGGGAAG TTGTCAAGGA
351 TTTGGAAAAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TCGCGCGGAA CAGACGGAAA GCCGCAGACA
501 GAATGCCAAA ATCTCCAAAG ATGCCCCGAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAAGCA GCTGAACAAG CTCTTGAGCA ATTTGgagaa aaAAAAagcc
601 gaacaccgCA TtcaggAtgc ggAagcaaAA agaAAATTGG CTGAagcCaa
651 actGgcggca gccgAAAAAG CCAGAAAAGA AGCGGCGCAG CAGAAGGCTG
701 AAGCGCGACG TCGGGAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGgTT TCAGCCGCAT
801 GCAGGGACGT TTGAAAAAAC CGGTTGACGG TGTGCCGACC GGGCTTTTCG
851 GGCAGAACCG GAGCGGcggc GATGTTTGGA AAGGCGTGT CTATTCCACT
901 CGCGCTGCAA CGGTTGAAAG CATTGCGCcg gGAACggtaa GCTATGCGGA
951 cgaGTTGGAC GGCTACGGCA AAGTGGTGT GATCGATCAC GGCGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCCGCCGG CAAGGGTTAT
1051 ACGGTCCGGG CAGGAAGCAA AATCGGCACG AGCGGGTCGC TCGCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCGAGGTCAG GTGTTGAACC
1151 CTTGCGGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1878; ORF 597>:

g597.pep

```

1 MLLHVSNSLK QLQEERIRQE RIRQERIRQA RGNLASVNRK QREAWDKFQK
51 LNTLNLRLKT EVAATKAQIS RFVSGNYKNS RPNVALFLK NAEPEGQKNRF
101 LRYTRYVNAS NREVVKDLEK QQKALAVQEQ KINNELARLK KIQANVQSLL
151 KKQGVTDAAE QTESRRQNAK ISKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEAKLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QPFSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVIDH GENYISIIYAG LSEISAGKGY
351 TVAAGSKIGT SGSLPDGEEG LYLQIRYRQ VLNPSGWIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1879>:

m597.seq

```

1 ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51 CCGCCAAGAG CGTATCCGTC AGGCGCGCGG CAACCTTGCT TCCGTCAACC
101 GCAAACAGCG CGAGGCTTGG GACAAGTTCC AAAAAGTCAA TACCGAGCTG
151 AACCGTTTGA AAACGGAAGT CGCCGCTACG AAAGCGCAGA TTTCCTGTTT
201 CGTATCGGGG AACTATAAAA ACAGCCAGCC GAATGCGGTT GCCCTGTTCC
251 TGAAAAACGC CGAACCAGGT CAGAAAAACC GCTTTTTCGC TTATACGCGT
301 TATGTAAACG CTCCAATCG GGAAGTTGTC AAGGATTTGG AAAAACAGCA
351 GAAGGCTTTG GCGGTACAAG AGCAGAAAAT CAACAATGAG CTTGCCCGTT
401 TGAAGAAAAA TCAGGCAAAAC GTGCAATCTC TGCTGAAAAA ACAGGGTGTA
451 ACCGATGCGG CGGAACAGAC GGAAGCCGC AGACAGAATG CCAAATCGC
501 CAAAGATGCC CGAAAAGTGC TGAACAGAA AGGGAACGAG CAGCAGCTGA
551 ACAAGCTCTT GAGCAATTG GAGAAGAAA AGGCCGAACA CCGCATTGAG
601 GATGCGGAAG CAAAAAGAAA ATTGGCTGAA GCCAGACTGG CGGCAGCCGA
651 AAAAGCCAGA AAAGAAGCGG CGCAGCAGAA GGCTGAAGCA CGACGTGCGG
701 AAATGTCCAA CTTGACCGCC GAAGACAGGA ACATCCAAGC GCCTTCGGTT
751 ATGGGTATCG GCAGTGCCGA CGGTTTCAGC CGCATGCAAG GACGTTTGAA
801 AAAACCGGTT GACGGTGTGC CGACCGGACT TTTCGGGCAG AACCGGAGCG
851 GCGGCGATAT TTGGAAGGC GTGTTCTATT CCACTGCACC GGCAACGGTT
901 GAAAGCATTG CGCCGGGAAC GGTAAGCTAT GCGGACGAGT TGGACGGCTA
951 CGGCAAAGTG GTCGTGGTCG ATCACGGCGA GAACTACATC AGCATCTATG
1001 CCGGTTTGAG CGAAATTTCC GTCGGCAAGG GTTATATGGT CGCGGCAGGA
1051 AGCAAAATCG GTCGAGCGG GTCGCTGCCG GACGGGGAAG AGGGGCTTTA
1101 CCTGCAATA CGTTATCAAG GTCAGGTATT GAACCTTCG AGCTGGATAC
1151 GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1880; ORF 597>:

m597.pep

```

1 MLLHVSNSLK QLQEERIRQE RIRQARGNLA SVNRKQREAW DKFQKLNTL
51 NLRKTEVAAT KAQISRFVSG NYKNSQPNVA ALFLKNAEPG QKNRFLRYTR
101 YVNASNREV V KLEKQKAL AVQEQKINNE LARLKKIQAN VQSLLKKQGV
151 TDAAEQTESR RQNAKIAKDA RKLLEQKQNE QQLNKLNSL EKKKAEHRIQ
201 DAEAKRKLAE ARLAAAEKAR KEAAQQAEEA RRAEMSNLTA EDRNIQAPSV
251 MGIGSADGFS RMQRLKKPV DGVPTGLFGQ NRSGGDIWKG VFYSTAPATV
301 ESIAPGTVSY ADEL DGYGKV VVDHGENYI SIYAGLSEIS VGKGYMVAAG
351 SKIGSSGSLP DGEEGLYLQI RYQGQVLNPS SWIR*

```



Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 597 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. gonorrhoeae*:

m597/g597 96.1% identity in 389 aa overlap

	10	20	30	40	50	60
g597.pep	MLLHVSNSLKQLQEERIRQERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNLRLKT					
m597	MLLHVSNSLKQLQEERIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNLRLKT					
	10	20	30	40	50	
	70	80	90	100	110	120
g597.pep	EVAATKAQISRFSVSGNYKNSRPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFSVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
	130	140	150	160	170	180
g597.pep	QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKISKDARKLLE					
m597	QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
	120	130	140	150	160	170
	190	200	210	220	230	240
g597.pep	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEAKLAAAEKARKEAAQKAEARRAEM					
m597	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
	180	190	200	210	220	230
	250	260	270	280	290	300
g597.pep	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
	310	320	330	340	350	360
g597.pep	APATVESIAPGTVSYADELDGYGKVVDHGENYISYAGLSEISAGKGYTVAAGSKI GT					
m597	APATVESIAPGTVSYADELDGYGKVVDHGENYISYAGLSEISVKGGMVAAGSKIGS					
	300	310	320	330	340	350
	370	380	390			
g597.pep	SGSLPDGEEGLYLQIRYRGQVLNPSGWIRX					
m597	SGSLPDGEEGLYLQIRYQGQVLNPSWIRX					
	360	370	380			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1881>

a597.seq

```

1  ATGCTGCTTC ATGTCAGCAA TTCCCTCAAG CAGCTTCAGG AAGAGCGTAT
51  CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACCGCAAA CAGCGCGAGG CTGGGACAA GTTCCAAAAA
151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTCG CGTTTCGTAT CGGGGAACTA TAAAAACAGC CAGCCGAATG
251 CGGTTGCCCT GTTCTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCCTC AATCGGGGAG TTGTCAAGGA
351 TTTGGAAAAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TCGGGCGGAA CAGACGGAAA GCCGCAGACA
501 GAATGCCAAA ATCGCCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGGAGAA GAAAAAGGCC
601 GAACACCGCA TTCAGGATGC GGAAGCAAAA AGAAAATTGG CTGAAGCCAG
651 ACTGGCGGCA GCCGAAAAAG CCAGAAAAGA AGCGGCGCAG CAGAAGGCTG
701 AAGCACGACG TGCGGAAATG TCCAACCTGA CGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGGTT TCAGCCGCAT
801 GCAAGGACGT TTGAAAAAAC CGGTTGACGG TGTGCCGACC GGACTTTTCG
851 GGCAGAACCG GAGCGGCGGC GATGTTTGGA AAGGCGTGT CTATTCCACT
901 GCACCGGCAA CGGTTGAAAG CATTGCGCCG GGAACGGTAA GCTATGCGGA

```

951

```

951 CGAGTTGGAC GGCTACGGCA AAGTGGTCGT GGTCGATCAC GGCGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTCCGTCGG CAAGGGTTAT
1051 ATGGTCGCGG CAGGAAGCAA AATCGGCTCG AGCGGGTCGC TGCCGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTGA TCAAGGTCAG GTATTGAACC
1151 CTTGAGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1882; ORF 597.a>:

## a597.pep

```

1  MLLHVSNSLK QLQEEIRQE RIRQERIRQA RGNLASVNRK QREAWDKFQK
51  LNTELNRKLT EVAATKAQIS RFVSGNYKNS QPNAVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QQKALAVQEQ KINNELARLK KIQANVQSL
151 KKQGVTDAAE QTESRRQNAK IAKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEARLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVDH GENYISIIYAG LSEISVGKGY
351 MVAAGSKIGS SGSLPDGEEG LYLQIRYQGQ VLNPSWIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 597 shows 98.5% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. meningitidis*

m597/a597 98.5% identity in 389 aa overlap

	10	20	30	40	50	60
a597.pep	MLLHVSNSLKQLQEEIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNRKLT					
m597	MLLHVSNSLKQLQEEIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNRKLT					
	10	20	30	40	50	
	70	80	90	100	110	120
a597.pep	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
	130	140	150	160	170	180
a597.pep	QQKALAVQEQKINNELARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
m597	QQKALAVQEQKINNELARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
	120	130	140	150	160	170
	190	200	210	220	230	240
a597.pep	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
m597	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
	180	190	200	210	220	230
	250	260	270	280	290	300
a597.pep	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
	310	320	330	340	350	360
a597.pep	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS					
m597	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS					
	300	310	320	330	340	350
	370	380	390			
a597.pep	SGSLPDGEEGLYLQIRYQGQVLNPSWIRX					
m597	SGSLPDGEEGLYLQIRYQGQVLNPSWIRX					
	360	370	380			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1883>:

g601.seq

```

1  ATGTTCCCAA CCGGCAATTT GGTGACGAA ATTGATGTGC CGAATATAGG
51  TCGTCTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ACGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAGGA CGACATCAAC
151 AACGATGCCG CCGCGCTGGA AAAATTTGAA ACCATCCGCG CATATGGCGC
201 GCTGAAAATG GGTTCGATCA GCGACGTATC CGAAGCCGCC GCCCGCGCGC
251 GCACGCCGAA ACCCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGCGGCAAAA CCGTAAACGC CGCCGACATC GATTTGCCGG TACGCGCCCT
351 GAGCATGGGC AACTGCACC ACGCTATGAT GGGCATCGCC TCGGTCGCCA
401 TCGCCGCCGC CGTGCTCGGT ACGCTGGTCA ACCTTGCCGC AGGCGGCGGA
451 ACGCGTAAAG AAGTGCCTT CGGGCATCCG TCAGGTACGC TCGTGTCTGG
501 TGCTGCCGCC GAATGTCAGG ACGGACAATG GACGGCCGCC aaagcggtca
551 tgaGCCGCAG CGCACgcgtg attatggaaa gttgGGTGCg cgttcccgat
601 gattGTTTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 1884; ORF 601.ng>:

g601.pep

```

1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE TIRAYGALKM GLISDVSEAA ARARTPKPAF VAPAADYTAS
101 SGKTVNAADI DLPVRALSMG KLHHAMMGIA SVAIAAAVLG TLVNLAAGGG
151 TRKEVRFGHP SGTLRVGAAA ECQDGQWTAA KAVMSRSARV IMESWVRVPD
201 DCF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1885>:

m601.seq

```

1  ATGTTCCCAA CCGGCAATTT GGTGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC ACAGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CGGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCTCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAACGC CGCCGACATC GATTTGCTGG TACGCGCCCT
351 GAGCATGGGC AACTGCACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTA CCCGGTACGC TGGTCAACCT TGCCGCAGGC
451 GGCGGAACGC GTAAAGAAAGT GCGCTTCGGG CATCCTTCCG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTATGAG CCGTAGCGCA CGCGTGATGA TGGAAGGTTG GGTCAGGGTG
601 CCTGAGGATT GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1886; ORF 601>:

m601.pep

```

1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GGTRKEVRFV HPSGTLRVGA AAECQDGQWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 601 shows 94.1% identity over a 205 aa overlap with a predicted ORF (ORF 601.ng) from *N. gonorrhoeae*:

m601/g601

	10	20	30	40	50	60
m601.pep	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
g601	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m601.pep	KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG					

953

```

g601      |||||:|||||
          TIRAYGALKMGLISDVSEAAARARTPKPAFVAPAADYTASSGKTVNAADIDLPVRALSMG
          70      80      90      100     110     120

          130     140     150     160     170     180
m601.pep  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAECQDGQWT
          |||||:|||||
g601      KLHHAMMGIA SVAI--AAAVLGTLVNLAAGGGTRKEVRFHPSGTLRVGAAECQDGQWT
          130     140     150     160     170

          190     200
m601.pep  ATKAVMSRSARVMMEGWVRVPEDCFX
          |:|||||:|:|:|:|:|:|
g601      AAKAVMSRSARVIMESWVRVPDDCFX
          180     190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1887>:

```

a601.seq
1  ATGTTCCCAA CCGGCAATTT GGTCTGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC  ACGGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CAGCTTTGGA  AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGTCTGATCA  GCGACGTATC CGAAGCTGCC GCCCGCGCGC
251 ACACGCCGAA AGTCGCCTTC  GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAATGC  CGCCGACATC GATTTGCTGG TACGCGCCCT
351 GAGCATGGGC AAATTGCACC  ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTG  CCCGTACGCG TGGTCAACCT TGCCGAGGCG
451 GGCGGAACGC GTAAAGAAGT  GCGCTTCGGG CATCCTTCCG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT  GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTTATGAG CCGCAGCGCA  CGCGTGATGA TGGAAGGTTG GGTCAGGGTG
601 CCGGAAGATT GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1888; ORF 601.a>:

```

a601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GGTRKEVREG HPSGTLRVGA AAECQDGQWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*

```

m601/a601 100.0% identity in 205 aa overlap

```

          10      20      30      40      50      60
m601.pep  MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
          |||||
a601      MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
          10      20      30      40      50      60

          70      80      90      100     110     120
m601.pep  KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG
          |||||
a601      KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG
          70      80      90      100     110     120

          130     140     150     160     170     180
m601.pep  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAECQDGQWT
          |||||
a601      KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAECQDGQWT
          130     140     150     160     170     180

          190     200
m601.pep  ATKAVMSRSARVMMEGWVRVPEDCFX
          |||||
a601      ATKAVMSRSARVMMEGWVRVPEDCFX
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1889>:

```
g602.seq
  1 ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTC CCTTCTGCT
 51 CGGCGGGCAG ATAAACCGTC ATCGTCAGGC GAGCAACCGT GGATTGTGTT
101 CCTTCGGCGG TTTTCAGGGT AATCGGGAAG CGCAGGTCTT TAATGCCGAC
151 CTGATTGATC GGCAGGTTGC GCAAATCTCT GCTGGATTGC ACGTCTGCAA
201 TGGCGTTCAT GCGTTGTTTG TCCTTAATAT TCAGATAAAT ATTGAGATGT
251 GTGTATTGTA TGGCAGGcag atgccgtctg aAAAAacgct gtcggCCGCC
301 TGCCTGCAAA Tgcgagatta TATCACTTGC TTTtggcgGC TGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1890; ORF 602.ng>:

```
g602.pep
  1 MLLHQCDKAR HMRPFLGGQ INRHRQASNR GLCSFGGFQG NREAQVFNAD
 51 LIDRQVAQIS AGLHVCNGVH ALFVLNIQII IEMCVLYGRQ MPSEKLSAA
101 CLQMRDYITC FWRLH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1891>:

```
m602.seq
  1 ATGTTGCTCC ATCAATGCGA CAAAACGCGA CATATGCGTC CCCTTCTGCT
 51 CAGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAATGGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTCAT GAGTTGTTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC GCCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1892; ORF 602>:

```
m602.pep
  1 MLLHQCDKTR HMRPLLSRQ VNRHGQTGNG GLDAFCSLQG NRKAQVFDTD
 51 LIDRQIAQIS AGLHVCNSVH ELFFLNHVI VEMCAWYGVS AGEYTVNLQM
101 RDYITRF*QL H*
```

m602/g602 65.2% identity in 115 aa overlap

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLSRQVNRHGQTGNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	:    : :   ::     :  ::   :    :     :					
g602	MLLHQCDKARHMRPFLGGQINRHRQASNRGLCSFGGFQGNREAQVFNADLIDRQVAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSAGEYTVN---LQMRDYITRF*QLHX					
	:       : : :      :     :           :					
g602	AGLHVCNGVHALFVLNIQIIEMCVLYGRQMPSEKLSAACLQMRDYITCFWRLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1893>:

```
a602.seq
  1 ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTA CCCTTCTGCT
 51 CGGCGAGCAG GTAAACCGTC ATGGTCAGAC GGGCAACTGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTCAT GAGTTGTTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC ACCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1894; ORF 602.a>:

```
a602.pep
  1 MLLHQCDKAR HMRTLLGRQ VNRHGQTGNC GLDAFCSLQG NRKAQVFDTD
 51 LIDRQIAQIS AGLHVCNSVH ELFFLNHVI VEMCAWYGVS TGEYTVNLQM
101 RDYITRF*QL H*
```

m602/a602 95.5% identity in 111 aa overlap

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLLSRQVNRHGQTGNNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
a602	MLLHQCDKARHMRLLLLGRQVNRHGQTGNCGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSTGEYTVNLQMRDYITREFXQLHX					
a602	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSTGEYTVNLQMRDYITREFXQLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1895>:

g603.seq

```

1  ATGGATTCCC GCCTGCGTGG GAATGACGCT AGGAAATACG GCATACGCTT
51  TGCCCAAAGA GGCCGTCTGA AACACACTCC GCCCAACGCC CATCCTTTTT
101 CAGACGGCCC CGCACC AAAA AAACAACCAC AAAC TACAAG GAGAAACATC
151 ATGTCCGACC AACTCATTCT TGTCCTGAAC TGCGTCAGTT CATCGCTCAA
201 AGGCGCCGTT ATCGACCGCA AAAGCGGCAG CGTCGTCCTA AGCTGCCTCG
251 GGAACGCCT GACTACGCCC GAAGCCGTCA TTACCTTCAA CAAAGACGGC
301 AACAAACGCC AAGTTCCTCT GAGCGGCCGC AACTGGCACG CCGGCGCGGT
351 GGGTATGCTG TTGAACGAAC TGGAAAAACA CGGACTGCAC GACCGCATCA
401 AAGCCATCGG CCGCCGCATC GCCCACGGCG GCGAAAAATA TCACGAGTCC
451 GTCCTCATCG ACCAAGACGT CCTTGACGAA CTGAAAGCCT GCATCCCGTT
501 CGCCCCGCTG CACAACCCCG CCAACATCAG CGGCATCCTC GCCGCGCAGG
551 AACACTTTCC CGGCCTGCCC AACGTCGCGG TGATGGACAC CTCGTTCCAC
601 CAAACCATGC CGGAGCGGGC CTACACTTAT GCCGTGCCGC GCGAATTGCG
651 CAAAAAATAC GCCTTCCGCC GCTACGTTT CCACGGTACC GGTATGCGTT
701 ACGTCGCCCC TGAAGCCGCA CGCATCTTGG GCAAACCTct ggaaGACATC
751 CGCATGATTA TTGCCCACTT AGGCAACGGC GCATCTATTA CCGCCGTCAA
801 AAACGGCAAA TCCGTCGATA CCGGTATGGG TTTCACGCCG ATCGAAGGTT
851 TGGTAATGGG TACACGTTGC GGCACACCG ATCCGGGCGT ATACAGCTAT
901 CCGACTTTCC ACGCAGGGAT GGATGTTGCC CAAGTTGATG AAATGCTGAA
951 CGAAAAATCA GGTTCCTCCG GTATTTCCgA actTCCCAAC GACTGCCGCA
1001 CCCTCGAAAT CGCCGCCGAC GAAGGCCGCG AAGGCGCGCG CCTCGCCCTc
1051 gaAGTCATGA CCTGCCGCT CGCCAAATAC ATCGCTTCGA TGGCTGTGGC
1101 CTGCGGCAGT GTTGACGCAC TCGTGTTTAC CGGCGGTATC GGCAGAAACT
1151 CGCGTAATAT CCGTGCCAAA ACCGTTTCTT ATCTTGATT CTGCGGTCTG
1201 CACATCGACA CCAAAGCCAA TATGGA AAAA CGTACGGCA ATTGCGGCAT
1251 TATCAGCCCG ACCGATTCTT CTCCGGCTGT TTTGGTCGTC CCGACCAATG
1301 AAGAACTGAT GATTGCCTGC GACACTGCCG AACTTGCCGG CATCTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1896; ORF 603.ng>:

g603.pep

```

1  MDSRLRGNDA RKYGIRFAQR GRLKHTPPNA HPFSDGPAPK KQPQTTRRNI
51  MSDQLILVLN CVSSSLKGAV IDRKSGSVVL SCLGERLTP EAVITFNKDG
101 NKRQVPLSGR NCHAGAVGML LNELEKHGLH DRIKAIGRRI AHGGEKYHES
151 VLIDQDVLDE LKACIPFAPL HNPNANISGIL AAQEHFPGLP NVGVMDTSFH
201 QTMPEAYTY AVPRELRKKY AFRRYGFHGT GMRYVAPEAA RILGKPLEDI
251 RMIIAHLGNG ASITAVKNGK SVDTGMGFTP IEGLVMGTRC GDTDPGVYSY
301 PTFHAGMDVA QVDEMLNEKS GFPGISELPN DCRTLEIAAD EGREGARLAL
351 EVMTCRLAKY IASMAVACGS VDALVFTGGI GENSRNIRAK TVSYLDLFLGL
401 HIDTKANMEK RYGNNGIISP TDSSPAVLV PTNEELMIAC DTAELAGIL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1897>:

m603.seq

```

1  CTGTCCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACCT TGCGCTGAT GTCTGC.CTT
101 TTTCAGACGA CCCCACTA AAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT CCTCGTTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGCGCC GTTATCGACC GAMAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG cCtGACCAG CCCGAAGCCG TCATTACGTT CAACAAAGAC

```

m603 . pep

Computer analysis of this amino acid sequence gave the following results:

ORF 603 shows 91.6% identity over a 450 aa overlap with a predicted ORF (ORF 603.ng) from *N. gonorrhoeae*:

		10	20	30	40	50	60
m603 . pep		LSSRRRGRNND	RCKGIRFAQ	RGLKHLAPD	VCXFSDDP	TLKKQPQT	TRRNIMSDQLILVL
		::	:		:		:
g603		MDSRLRG-ND	ARKYGIRFAQ	RGLKHTPPNA	HPFSDGPA	PKKQPQT	TRRNIMSDQLILVL
		10	20	30	40	50	
		70	80	90	100	110	120
m603 . pep		NCGSSSLKGA	VIDRXSGSV	VLSCLGERL	TTPEAVIT	FNKDGNGR	QVPLSGRNCHAGAVGM
g603		NCVSSSLKGA	VIDRKSGSV	VLSCLGERL	TTPEAVIT	FNKDGNGR	QVPLSGRNCHAGAVGM
	60	70	80	90	100	110	
		130	140	150	160	170	180
m603 . pep		LLNELEKHGL	HDRIKAIGH	RIAHGGEKY	SESVLIDQ	AVMDELNAC	IPLAPLHN PANISGI
				:			:
g603		LLNELEKHGL	HDRIKAIGR	RIAHGGEKY	HESVLIDQ	DVDELKAC	IPFAPLHN PANISGI
	120	130	140	150	160	170	
		190	200	210	220	230	240
m603 . pep		LAAQEHFPGL	PNVGVMDS	FSHQTMPER	AYTYAVPRE	LRKKYAFR	RYGFHGTS MRYVAPEA
							:

957

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g603      LAAQEHFPGLPNVGVMDSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTGMRYVAPEA
          180      190      200      210      220      230

          250      260      270      280      290      300
m603.pep  ARILGKPLEDIRMIIAHLGNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS
          |||||:|||||:|||||:|||||:|||||:|||||
g603      ARILGKPLEDIRMIIAHLGNGASITAVKNGKSVDTGMGFTPIEGLVMGTRCGDIDPGVYS
          240      250      260      270      280      290

          310      320      330      340      350      360
m603.pep  YLTSHAGMDVAQVDEMLNKKSGLLGISELSND CRTLEIAADEGHEGARLAL EVM TYRLAK
          |||||:|||||:|||||:|||||:|||||:|||||
g603      YPTFHAGMDVAQVDEMLNEKSGFPGISELPND CRTLEIAADEGREGARLAL EVM TCRLAK
          300      310      320      330      340      350

          370      380      390      400      410      420
m603.pep  YIASMAVCGGVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          |||||:|||||:|||||:|||||:|||||:|||||
g603      YIASMAVACGSVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          360      370      380      390      400      410

          430      440      450
m603.pep  PTDSSPAVLVVPTNEELMIACDTAELAGILX
          |||||:|||||:|||||:|||||:|||||
g603      PTDSSPAVLVVPTNEELMIACDTAELAGILX
          420      430      440      450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1899>:

```

a603.seq
1   CTGTCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACAC TCCGCCCAAC GCCCATCCTT
101 TTTCAGACGA CCCACACC. AAAAAACAAC CACAAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT TCTGTCTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGTGCC GTTATCGACC GCAAAGCGG CAGCGTCGTC CTAAGTGCC
251 TCGGCGAACG CCTGACCACG CCCGAAGCCG TCATTACGTT CAGCAAAGAC
301 GGCAACAAAC GCCAAGTTCC CCTGAGCGGC CGGAATGCC ACGCCGGCGC
351 GGTGGGTATG CTGTTGAACG AACTGGAAAA ACACGAACTG CACGACCGCA
401 TTCAAGCCGT CGGCCACCGC ATCGCCACG GCGGCGAAAA ATACAGCGAG
451 TCTGTTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTCGCCGCAC
551 AGGAACATTT CCCCAGTCTG CCAATGTCTG GCGTGATGGA TACTTCGTTT
601 CACCAAACCA TGCCGAGCG TGCCTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTCC GCCGTACGG TTTCCACGGC ACCAGTATGC
701 GTTACGTTGC CCCTGAAGCC GCATGCATCT TGGGCAACC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCA CTTAGGCAAC GGCGCATCCA TTACCGCCAT
801 CAAAAACGGC AAATCCGTCG ATACCAGTAT GGGTTTCACG CCGATCGAAG
851 GTTTGGTAAT GGTACGCGC TGCGGCGATA TCGACCCGGG CGTATACAGC
901 TATCTGACTT CACACGCCGG TTTGGATGTT GCACAAGTTG ATGAAATGCT
951 GAATAAAAAA TCAGGCTTGC TCGGTATTTC CGAACTCTCC AACGACTGCC
1001 GCACCCTCGA AATCGCCGCC GACGAAGGCC ACGAAGGCCG GCGCCTCGCC
1051 CTCGAAGTTA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGGTGC GCGG GCGTTGACG CACTCGTGTT CACCGGCGGT ATCGGCGAAA
1151 ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTTGA TTTCTTGGGT
1201 CTCGACATCG ACACCAAAGC CAATATGGAA AAACGCTACG GCAATTCGGG
1251 TATTATCAGC CCGACCGATT CTTCTCCGGC TGTTTTGGTT GTCCCGACCA
1301 ATGAAGAACT GATGATTGCC TGCGACACTG CCGAACTTGT CGGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1900; ORF 603.a>:

```

a603.pep
1   LSSRRRGRNN DRKCGIRFAQ RRLKHTPPN AHPFSDPTX KKQPQTTRRN
51  IMSDQILVL NCGSSSLKGA VIDRKSGSVV LSCLGERLTT PEAVITFSKD
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHEL HDRIQAVGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LHPANISGI LAAQEHFPGP PNVGVMDSF

```



958

201 HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ACILGKPLED  
 251 IRMIIAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS  
 301 YLTSHAGLDV AQVDEMLNKK SLLGISELS NDCRTLEIAA DEGHEGARLA  
 351 LEVM TYRLAK YIASMAVGCG GVDALVFTGG IGENS RNIRA KTVSYLDFLG  
 401 LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELVGIL  
 451 \*

## m603/a603 96.7% identity in 450 aa overlap

	10	20	30	40	50	60
m603.pep	LSSRRRGRNDRKCGIRFAQRGR	LKHLAPDVCXFSD	DDLKQKQPQTTRRN	IMSDQLILVL		
a603	LSSRRRGRNDRKCGIRFAQRGR	LKHTPPNAHPFSDD	PXTKKQKQPQTTRRN	IMSDQLILVL		
	10	20	30	40	50	60
	70	80	90	100	110	120
m603.pep	NCGSSSLKGAVIDRXSGSVVLS	SCLGERLTTPEAVITFN	KDGNKRQVPLSGRN	CHAGAVGM		
a603	NCGSSSLKGAVIDRKSGSVVLS	SCLGERLTTPEAVITFS	KDGNKRQVPLSGRN	CHAGAVGM		
	70	80	90	100	110	120
	130	140	150	160	170	180
m603.pep	LLNELEKHGLHDRIKAIGHRIA	HGGEKYS	ESVLIDQAVMDELNACI	PLAPLHN	PANISGI	
a603	LLNELEKHELHDRIQAVGHRIA	HGGEKYS	ESVLIDQAVMDELNACI	PLAPLHN	PANISGI	
	130	140	150	160	170	180
	190	200	210	220	230	240
m603.pep	LAAQEHFPGLPNVGVMDTSF	HQTMPERAYTYAVPRELR	KKYAFRRYGFHG	TSMRYVAPEA		
a603	LAAQEHFPGLPNVGVMDTSF	HQTMPERAYTYAVPRELR	KKYAFRRYGFHG	TSMRYVAPEA		
	190	200	210	220	230	240
	250	260	270	280	290	300
m603.pep	ARILGKPLEDIRMIIAHLNG	SITAIKNGKSVDTSMGFT	PIEGLVMGTRCGDID	PGVYS		
a603	ACILGKPLEDIRMIIAHLNG	SITAIKNGKSVDTSMGFT	PIEGLVMGTRCGDID	PGVYS		
	250	260	270	280	290	300
	310	320	330	340	350	360
m603.pep	YLTSHAGMDVAQVDEMLNKK	SGLLGISELSNDCRTLEIA	ADGHEGARLALEVMT	YRLAK		
a603	YLTSHAGLDVAQVDEMLNKK	SGLLGISELSNDCRTLEIA	ADGHEGARLALEVMT	YRLAK		
	310	320	330	340	350	360
	370	380	390	400	410	420
m603.pep	YIASMAVGCGGVDALVFTGG	IGENS RNIRAKTVSYLDF	FLGLHIDTKANME	KRYGNSGIIS		
a603	YIASMAVGCGGVDALVFTGG	IGENS RNIRAKTVSYLDF	FLGLHIDTKANME	KRYGNSGIIS		
	370	380	390	400	410	420
	430	440	450			
m603.pep	PTDSSPAVLVPTNEELMIAC	DTAELAGILX				
a603	PTDSSPAVLVPTNEELMIAC	DTAELVGILX				
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1901>:

g604.seq

1 ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA  
 51 CCAGCGTACC GAGCACGGCG GCGGCGATGG CGACCGAGGC GATGCCCATC  
 101 ATAGCGTGGT GCAGTTTGCC CATGCTCAGG GCGCGTACCG GCAAATCGAT  
 151 GTCGGCGGCG TTTACGGTTT TGCCGCTGGA GGCGGTGTAA TCGGCGGCGG  
 201 GCGCGACGAA GCGGGTTTC GCGGTGCGCG CGCGGCGGC GGCTTCGGAT

959

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251 ACGTCGCTGA TCAAACCCAT TTTCAGCGCG CCATATGCGC GGATGGTTTC
301 AAATTTTTC AGCGCGGCGG CATCGTTGTT GATGTCGTCC TGCAACTCTT
351 TGCCCGTGTA GCCCAAGTCG GCGGCGTTCA GGAAAACGGT CGGAATGCCC
401 GCGTTGATGA GCGTGGCTTT CAGACGACCT ATATTCGGCA CATCAATTTT
451 GTCGACCAA TTGCCGTTG GGAACATACT GCCTTcgCG TCGGCTGGAT
501 CTA

```

This corresponds to the amino acid sequence <SEQ ID 1902; ORF 604.ng>:

g604.pep

```

1 MPEAHFFTRS AACGKVDQRT EHGGGDGDRG DAHHSVVQFA HAQGAYRQID
51 VGGVYGFAAG GGVIGGRDE GGFRRARAGG GFGYVADQTH FQRAICADGF
101 KFFQRGGIVV DVVLQLFARV AQVGGVQENG RNARVDERGF QTTYIRHINF
151 VDQIAGWEHT AFAVGWI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1903>:

m604.seq

```

1 ATGCCCCAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA
51 CCAGCGTACC GGGTACGGCG GCGGCGGTTC CAATGGCAAC AGAGGCGGTA
101 CCCATCATCG CGTGGTGCA TTTGCCCATG CTCAGGGCGC GTACCAGCAA
151 ATCGATGTCG GCGGCGTTCA CGGTTTGGC ACTGGAGGCG GTGTAATCGG
201 CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG AGCGGCAGCT
251 TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
301 TTTCTCGAAT TTTTCCAAAG CCGCGGCATC GTTGTGATG TCGTCTTGCA
351 ACTCTTTGCC TGTGTAGCCC AAGTCGGCGG CATTCAAGAA AACGGTCGGA
401 ATGCCCCGCT TGATGAGCGT GGCTTTCAA CGGCCTATAT TCGGCACATC
451 AATTTTCATG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
501 CTGGATC

```

This corresponds to the amino acid sequence <SEQ ID 1904; ORF 604>:

m604.pep

```

1 MPEAHFFTRS AACGKVDQRT GYGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
51 IDVGGVHGFA TGGGVIGGGR DEGDFFRRVRA SGSGFYVADQ THFQRTVSAD
101 FLEFFQSRGI VVDVVLQLFA CVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFAVGWI

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 604 shows 83.4% identity over a 169 aa overlap with a predicted ORF (ORF 604.ng) from *N. gonorrhoeae*:

m604/g604

```

              10      20      30      40      50      60
m604.pep    MPEAHFFTRSAACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGFA
              ||||| :|| :|| :|| ||||| :||| :|||
g604         MPEAHFFTRSAACGKVDQRTGEGG--DGDRGDAHHSVVQFAHAQGAYRQIDVGGVYGFA
              10      20      30      40      50

              70      80      90      100     110     120
m604.pep    TGGGVIGGGRDEGDFFRRVRASGSFGYVADQTHFQRTVSADFLEFFQSRGIVVDVVLQLFA
              :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
g604         AGGGVIGGGRDEGGFRRARAGGGFGYVADQTHFQRAICADGFKFFQRGGIVVDVVLQLFA
              60      70      80      90      100     110

              130     140     150     160     169
m604.pep    CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWI
              ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
g604         RVAQVGGVQENGRNARVDERGFQTTYIRHINFVDQIAGWEHTAFAVGWIX
              120     130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1905>:

a604.seq

```

1 ATGCCCCAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA
51 CCAGCGTACC GGGCACGGCG GCGGCGGTTC CAATGGCAAC AGAGGCGGTA
101 CCCATCATCG CGTGGTGCAA TTTGCCCATG CTCAGGGCGC GTACCAGCAA
151 ATCGATGTCG GCGCATTC ACGGTTTGGC ACTGGAGGCG GTGTAATCGG

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960

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201 CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG GGCGGCAGCT
251 TCGGATACGT CGCTGATCAG ACCCATTTC AGCGCACCGT AAGCGCGGAT
301 TTTCTCGAAT TTTTCCAAAG CTGCGGCATC GTTGTGTGATG TCGTCTTGCA
351 ACTCTTTGCC CGTGTAGCCC AAGTCGGCGG CATTTCAGGAA AACGGTCGGA
401 ATGCCCGCGT TGATGAGCGT GGCTTTCAAA CGGCCTATAT TCGGCACATC
451 AATTTTCATCG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
501 CTGGATCAAG AAATTCGATT TGTACTTCGG CTGCCGGGAA CGTTACGCCG
551 TCGAGCTCAA AATCGCCTGT TTCCAAACT GCGCCGTTTT GCATCGGTAC
601 ATGGGCAATA ATGGTTTTGC CGATGTTTTT CTGCCAGATT TTGACTGTGC
651 AGATGCCGTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1906; ORF 604.a>:

```

a604.pep
1  MPEAHFFTRS AACGKVDQRT GHGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
51  IDVGGIHGFA TGGGVIGGGR DEGDFRRVRA GGSFGYVADQ THFQRTVSAD
101 FLEFFQSCGI VVDVVLQLFA RVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFAVGWI KFDLYFGCRE RYAVELKIAF QNCAVLHRY
201 MGNNGFADV FLPDFCDAVX *

```

m604/a604 97.0% identity in 169 aa overlap

```

              10      20      30      40      50      60
m604.pep      MPEAHFFTRSAACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGFA
a604           MPEAHFFTRSAACGKVDQRTGHGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGIHGFA
              10      20      30      40      50      60

              70      80      90      100     110     120
m604.pep      TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFFLEFFQSRGIVVDVVLQLFA
a604           TGGGVIGGGRDEGDFRRVRAGGSFGYVADQTHFQRTVSADFFLEFFQSCGIVVDVVLQLFA
              70      80      90      100     110     120

              130     140     150     160     169
m604.pep      CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVAGWI
a604           RVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVAGWIKKFDLYFGCRE
              130     140     150     160     170     180

a604           RYAVELKIAFQNCAVLHRYMGNNGFADVFLPDFCDAVX
              190     200     210     220

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1907>:

```

g605.seq
1  ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51  AATCGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCCGAC
151 TATATGCAGG CCGGCGACAG CAGCATTGAT TACGCCGCTa tGCCGGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATgc cgtcaaagtc aaAGGCTATT
251 TCATCtacCc cgGCCAGCTT TTTTgcaata ttgccgccga agcCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA atCTTTACCG CGATTGAAAG
351 CTCCGCCTCC GGCTAcccgT CCGAACAAGG CATCAAAGGC TTGTTTGACG
401 ACTTCgACAC CACCAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAAAAC
451 AAACGCCTTG CCGCCGTCCT TAAAGGCGTG GCGGAACTCG ATTTGCGCAA
501 TTTTGAAGAC CACCGCATCG ACCTTTTCGG TGATGCCTAC GAATACCTGA
551 TTTCCAACTA CGCcgCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TCTCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGGCAGGA
651 GAAAGTCAAC AAAATCTACG ACCCGCCTG CGGCTCGGGC AGCCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAACACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCAGCA TGAATATGTT
801 TCTGCACAAC GTCAATTACA ACAAATTCCA CATCGAATTG GGCGACACGC
851 TGACCAACCC CAAACTCAAA GACAGCAAAC CCTTTGATGC CGTCGTCTCC
901 AATCCGCCCT ATTCCATCGA CTGGATAGGC AGCGACGACC CCACCTtgaT

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961

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951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTCGCACCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCTA TCGTCTCATT CCCC GGCGATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATc CGCCAATATC TGGTGGAGGG CAACTATGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCTGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTTCGCCG ACAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACCCGCGAG GTCATCGACA
1451 TCAGACAGCT CAACGCCGAA ATCAGCGAAA CCgtcgCcaa AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAA CCTAG

```

This corresponds to the amino acid sequence <SEQ ID 1908; ORF 605.ng>:

g605.pep

```

1 MMTEMQQRAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNKLKE IFTAIESSAS GYPSEQGIKG LFDDFDTTSS RLGSTVADKN
151 KRLAAVLKGV AELDFGNFED HRIDLFDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLQAKKQF DEHIIIEGFF
251 GQEIHNHTYN LARMNMFHNL VNYNKFHIEL GDTLTNPKLK DSKPFDVVS
301 NPPYSIDPW SDDPTLINDD RFAPAGVLAP KSKADFALIL HALNYLSGRG
351 RAATVSPFGI FYRGGAEQKI RQYLVGNYV ETVIALAPNL FYGTCLAVNI
401 LVLKHKDNT DIQFIDASGF FKKETNNNVL TEEHIAEIVK LFADKADVPH
451 IAQNAAQQTV KDNGYNLAVS SYVEAEDTRE VIDIRQLNAE ISETVAKIER
501 LRREIDEVIA EIET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1909>:

m605.seq

```

1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51 AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTC TACCGCTTTA TCAGCGAAAA CTTACCGAC
151 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCCGCTA TGCCGGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATGC CGTCAAAGTT AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCCGA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACCG CGATTGAAAG
351 CTCCGCCTCC GGCTATCCGT CCGAACAGGA CATCAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACTGTTGC CGACAAGAAC
451 AAACGCCTTG CCGCCGTCCT CAAAGGCGTG GCGGAACTCG ATTTGCGCAA
501 TTTTGAAAAC CACCACATCG ACCTTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCAACTA CGCTGCCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TATCAAAGCT GATTGCGCGG CTGGCGGTGC ACGGACAGGA
651 GAAAGTCAAC AAAATCTACG ACCCAGCTTG CGGCTCGGGC AGTCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCCGA TGAACATGTT
801 CCTGCACAAC GTCAATTACA ACCAATTCCA CATCGAATTG GGCGACACAC
851 TGACCAACCC AAAGCTCAAA GACAGCAAAC CCTTTGATGC CATCGTTTCC
901 AATCCGCCTT ATTCCATCAA CTGGATAGGC AGCGACGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTTGCCCCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCCA TCGTCTCATT CCCC GGCGATT TTCTATCGCG GCGGCGCAGA
1101 ACAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ATCGAAGAAC
1301 ACATTGCTGA AATCGTCAAA CTCTTCGCCG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGTGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACACGCGAA ATTATCGACA
1451 TCAAACAGCT CAACGCCGAA ATCGGCGAAA CCGTCGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1910; ORF 605>:

m605.pep

```

1 MMTEMQQRAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ

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962

101 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDDFDTTSS RLGSTVADKN  
 151 KRLAAVLKGV AELDFGNFEN HHIDLFGBAY EYLISNYAAN AGKSGGEFFT  
 201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLQAKKQF DEHIEEGFF  
 251 GQEINHHTTYN LARMNMFHVN VYNYQFHIEL GDTLTNPKLK DSKPFDAIVS  
 301 NPPYSINWIG SDDPTLINDR RFAPAGVLAP KSKADFAFIL HALNYLSGRG  
 351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI  
 401 LVLSKHKDNT DIQFIDASGF FKKETNNNVL IEEHIAEIVK LFADKADVP  
 451 IAQNAAQQTVD KNGYNLAVS SYVEAEDTRE IIDIKQLNAE IGETVAKIER  
 501 LRREIDEVIA EIEA\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 605 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 605.ng) from *N. gonorrhoeae*:

m605/g605

	10	20	30	40	50	60
m605.pep	MMTEMQRAQLHRQIWKIADEVRGAVDGVDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
g605	MMTEMQRAQLHRQIWKIADEVRGAVDGVDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
g605	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m605.pep	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGV AELDFGNFENHHIDLFGBAY					
g605	GYPSEQGIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGV AELDFGNFEDHRIDLFGBAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m605.pep	EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLQAKKQF					
g605	EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLQAKKQF					
	190	200	210	220	230	240
	250	260	270	280	290	300
m605.pep	DEHIEEGFFGQEINHHTTYNLARMNMFHNVNYNQFHIELGDTLTNPKLKDSKPFDAIVS					
g605	DEHIEEGFFGQEINHHTTYNLARMNMFHNVNYNKFHIELGDTLTNPKLKDSKPFDAVVS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m605.pep	NPPYSINWIGSDDPTLINDR RFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI					
g605	NPPYSIDWIGSDDPTLINDR RFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m605.pep	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
g605	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m605.pep	FKKETNNNVLIEEHIAEIVKLFADKADVP HIAQNAAQQTVDKNGYNLAVSSYVEAEDTRE					
g605	FKKETNNNVLTEEHIAEIVKLFADKADVP HIAQNAAQQTVDKNGYNLAVSSYVEAEDTRE					

963

	430	440	450	460	470	480
	490	500	510			
m605 . pep	IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX					
	:     :         :                             :					
g605	VIDIRQLNAEISETVAKIERLRREIDEVIAEIEIX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1911>:

```
a605 . seq
1   ATGATGACCG AAATACAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51  AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTCAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTTACCGAC
151 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCCGCTA TGCCGGACAG
201 CATCATCACG CCGGAAATCA AAGACGATGC CGTCAAAGTC AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCCGA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACCAG CGATTGAAAG
351 CTCCGCCTCC GGCTATCCGT CCGAACAAGA CATTAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAGAAC
451 AAACGCCCTG CCGCCGTCTT AAAAGGCGTG GCGGAACTCG ATTTCCGGCAG
501 TTTTGAAGAC CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCAAC TA CGCTGCCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGGCAGGA
651 GAAAGTAAAC AAAATCTACG ACCCAGCTTG CGGCTCGGGC AGCCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAATATGTT
801 TCTGCACAAC GTCAATTACA ACAAATTCCA CATCGAATTG GGCGACACAC
851 TGACCAATCC CAAACTCAAA GACAGCAAAC CCTTTGATGC CGTCGTTTCC
901 AATCCGCCCT ATTCCATCAA CTGGATAGGC AGCGGCGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCCC CTGCAGGCGT ACTCGCCCCG AAATCCAAAG
1001 CCGATTTTGC CTTCAATTCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCCA TCGTCTCATT CCCCAGCATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTCA
1151 TCGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATA
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AGGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTTCGCCG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTTG AACCCGAAGA CACCCGCGAA ATTATCGACA
1451 TCAAACAGCT TAACGCCGAA ATCAGCGAAA CCGTTGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA
```

This corresponds to the amino acid sequence <SEQ ID 1912; ORF 605.a>:

```
a605 . pep
1   MMTEIQQRAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51  YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDDFDTTSS RLGSTVADKN
151 KRLAAVLKGV AELDFGSFED HHIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLQAKKQF DEHIIIEGFF
251 GQEINHHTYN LARMNMFELHN VYNKFHIEL GDTLTNPCLK DSKPFDVAVS
301 NPPYSINWIG SGDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI
401 LVLSKHKDNT DIQFIDAGGF FKKETNNNVL TEEHIAEIVK LFADKADVPH
451 IAQNAAQQTV KDNNGYNLAVS SYVEPEDTRE IIDIKQLNAE ISETVAKIER
501 LRREIDEVIA EIEA*
```

m605/a605 98.1% identity in 514 aa overlap

	10	20	30	40	50	60
m605 . pep	MMTEMQRAQLHRQIWKIADEVGAVDGDWDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
	:     :     :     :     :     :     :					
a605	MMTEIQQRAQLHRQIWKIADEVGAVDGDWDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
	10	20	30	40	50	60
	70	80	90	100	110	120
m605 . pep	YAAMPDSIITPEIKDDAVKVKGFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					

g606.seq

1	ATGTCCAAAT	TTATCGCCAA	ACAATCGGTC	GGTGCGAAG	TCATCGACAC
51	GCCGcgCACC	GAAGAGAAG	CCTGGCTTCT	GAACACTGTC	GAAGCCCAAg
101	gcgGGCAATG	GAATCTGAA	ACGCGAGAAG	TCGCCATCTA	CCACTCCCCC
151	GAACCCAAATG	CCTTTGCCAC	GGGCGCATCG	AGAAACAGT	CCCTGATCGC
201	CGTCAGCacc	ggtttgctcg	accatATgac	GCGCGACgaa	gtggaagccg
251	tgTTGGCGCA	CGAAATGGCG	CACGTCGGCA	ACGGCGACAT	GGTTACGCTG
301	ACGCTGatTC	AAGGCGTGGT	CAATACCTTT	GTCGTGTTCC	TGTCGCGCAT
351	TATTGCCAAC	CTGATTGCC	GAACACAACG	CGGCAGCCAG	TCCCAGGGAA
401	CTTATTTCCT	AGTCAGCATG	GTAATCCAAA	TCTGTGTCGG	CTTCTTGCC
451	AGCCTGATTG	TCATGTGGTT	CAGCCGCCAA	CGCGAATACC	GCGCCGAcgc
501	gggCGcggCA	AAACTGGTCG	GCGCACCgAA	AATGATTTC	GCCCTGCAAA
551	GGCTTAAAGG	CAACCCGGTC	GATTTGCCCG	AAGAAATGAA	CGCAATGGGC
601	ATCCGCGGAG	ATACGCGCGA	CTCCCTGCTC	AGCACCACC	CTTCGCTGGA
651	CAACCCGAATC	GCCCCCTCA	AATCGCTTTA	A	

This corresponds to the amino acid sequence <SEQ ID 1914; ORF606.ng>:

g606.pep

```

1  MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRDE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1915>:

m606.seq

```

1  ATGTCCAAAT TTATCGCCAA ACAATCGGTC GCGCGGAAG TTATCGACAC
51  GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTTCGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTACGCTG
301 ACGTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCG GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCTT GGTTCAGCAT GTATTCCAAA TCCTGTTTCG CTTCCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGGAATACC GCGCCGATGC
501 GGGCGCGGCA AAACCTGGTC GCGCGCCGAA AATGATTTCG GCCCTGCAAA
551 GGCTCAAAGG CAACCCGGTC GATTTGCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCTGCTC AGCACCCACC CTTGCTGGA
651 CAACCGTATC GCCCGCCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1916; ORF 606>:

m606.pep

```

1  MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRDE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 606 shows 100.0% identity over a 225 aa overlap with a predicted ORF (ORF 606.ng) from *N. gonorrhoeae*:

m606/g606

m606.pep	10	20	30	40	50	60
	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
g606	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
	10	20	30	40	50	60
m606.pep	70	80	90	100	110	120
	RNSSLIAVSTGLLDHMTRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
g606	RNSSLIAVSTGLLDHMTRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
	70	80	90	100	110	120
m606.pep	130	140	150	160	170	180
	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
g606	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
m606.pep	190	200	210	220		
	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
g606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1917>:

a606.seq



966

```

1  ATGTCCAAAT TCATCGCCAA ACAATCGGTC GCGCGGGAAG TTATCGACAC
51  GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTTTGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTTACGCTG
301 ACGCTGATTG AAGGCGTGGT CAATACCTTT GTCGTGTTC TGTGCGGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTTCT GGTCAGCATG GTATTCCAAA TCCTGTTCGG CTTCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGACGC
501 GGGCGCGGCA AACTGGTCG GCGCGCCGAA AATGATTTC GCCCTGCAA
551 GGCTTAAAGG CAACCCGGTC GATTTGCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCCACC CTTGCTGGA
651 CAACCGAATC GCCCGCCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1918; ORF 606.a>:

```

a606.pep
1  MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRDE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*

```

m606/a606 100.0% identity in 226 aa overlap

	10	20	30	40	50	60
m606.pep	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSP	EPNAFATGAS				
a606	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSP	EPNAFATGAS				
	10	20	30	40	50	60
	70	80	90	100	110	120
m606.pep	RNSSLIAVSTGLLDHMTRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
a606	RNSSLIAVSTGLLDHMTRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m606.pep	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
a606	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
	190	200	210	220		
m606.pep	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
a606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1919>:

```

g607.seq
1  ATGCTGCTCG accTcgaCCG CTTTTCTTt tccGTCTTCC TGAAAGAAAT
51  CCGCTGCTG ACCGCCCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTCGTC GATACCGTGA TGGCGGGCGG TGCGGGCAAG
151 GAAGATTGGG CGGCGGTGGC TTTGGGCAGC AGCGGTTT CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAACC GgtgAAGCAG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTTC GGCTGATTTT GGGGATTTTC GGCATGATT TGATGTGGGC
351 GGCGATTACG CCGTCCGCA ACTGGCTGAC TTTGAGCGAT TATGTGGAAG
401 gcacAAtggc gcAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGTACACC GCGCACTGCA CGCCTACGCT TCCAGCTGA ACCGCCGCGC
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCCGTA TGCCCGCTTT GGGTGGCGCA

```

```

601 GGTTCGGGCG TGGCGACAAT GGCGGTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAAATTCTT CCGCCCGTTC GGACTGACAG
701 CGAAATTCGg caaACCGGat tGGgcGGTGT TCAAACAGAT TtGGAAAATC
751 gGgcgcGCCA TCGGGCTGTC TTATTTTTTG GAAgccaGcg cGTTTTCGTT
801 TATCGTGTTC TTGATTGCGC CTtccggCGA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTCG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCAG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CAGGAGTGTC GCTGGTGTCG GGCTGGGTGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCGGTTC GCCGCTGGCA
1051 AGCATGTACA ACGATGaTCC GGCAGTTTTA AGCATCGCCT CCACCGTCCT
1101 GCTGTTCGCC GGCCTGTtcc aACCGGCAGA CTTCACCCAA TGTATCGCGT
1151 CCTATGCCCT GCGCGGCTAC AAAGTCACCA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TCTGGGGCTG CCGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC AGCCGTCGCC TTGGTGTGGT GCTTGAAAA ATACAGTATG
1351 GAGTTGGTCA AATCACACAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1920; ORF 607.ng>:

g607.pep

```

1 MLLDLDRFSF SVFLKEIRLL TALALPMLLA QVAQVGIGFV DTMAGGAGK
51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT GEAGETGRQG
101 IWFLGILGIF GMILMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRLAHAYA SSLNRPRILM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGVATMAVF WFSALALWIY IAKEKFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMIPQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWVLAVITVL SLVLFRSPLA
351 SMYNDPAVL SIASTVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMFIH
401 AAFAWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAVA LVWCLEKYSM
451 ELVKSHKAV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1921>:

m607.seq

```

1 ATGCTGCTCG ACCTCAACCG CTTTTCTTTT CCCGTCTTCC TGAAAGAAGT
51 CCGCCTGCTG ACCACTCTTG CCCTGCCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTTGTC GATACTGTGA TGGCGGGCGG TGCGGGCAAG
151 GAAGACTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAACC GACGAAGTGG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTCG GGCTGTTTTT GGGCGTGTTC GGCATGGTCT TGATGTGGGC
351 GGCGATTACG CCGTTCGCA ACTGGCTGAC CTTGAGCGAT TATGTGGAAG
401 GCACGATGGC GCAGTATATG TTGTTACCA GCTTGGCGAT GCCGCGGCA
451 ATGTTACACC GCGCGCTGCA CGCCTACACT TCCAGCCTGA ACCGCCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCCGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GCGGTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAATTTCTT CCGCCCATTC GGACTGACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGAAAAATC
751 GGCGCACCCA TCGGGCTGTC TTATTTTTTG GAAGCCAGCG CGTTTTCGTT
801 TATCGTGTTC TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTCG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTTA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCGGTTC GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGTTTTA AGCATCGCCG CCACCGTCTT
1101 ACTGTTTCGCC GGCTTGTTCC AACCAGCAGA CTTACCCAA TGTATCGCCT
1151 CCTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TTTGGGGCTG CCGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCAAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGATAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1922; ORF 607>:

m607.pep

```

1 MLLDLNRFSF PVFLKEVRLL TTLALPMLLA QVAQVGIGFV DTMAGGAGK
51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG

```

Homology with a predicted ORF from *N.gonorrhoeae*

m607/g607

	10	20	30	40	50	60
m607.pep	MLLDLNRFSPFVFLKEVRLTLTALPMLLAQVAQVIGIFVDTVMAGGAGKEDLAAVALGS					
	:     :     :     :     :     :     :     :     :     :					
g607	MLLDLDRFSFSVFLKEIRLLTALALPMLLAQVAQVIGIFVDTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m607.pep	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGLFLGVFGMVLMWAAIT					
	:     :     :     :     :     :     :     :     :					
g607	SAFATVYITFMGIMAALNPMIAQLYGAGKTGEAGETGRQGIWFGLLILGIFGMILMWAAIT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAMVHRAHAYTSSLNRPRLLIMLVSFAAFVLN					
	:     :     :     :     :     :     :     :     :					
g607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAMVHRAHAYASSLNRPRLLIMLVSFAAFVLN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m607.pep	VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD					
	:     :     :     :     :     :     :     :     :					
g607	VPLNYIFVYGKFGMPALGGAGCGVATMAVFWFSALALWIYIAKEKFFRPFGLTAKFGKPD					
	190	200	210	220	230	240
	250	260	270	280	290	300
m607.pep	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIQSV					
	:     :     :     :     :     :     :     :     :					
g607	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIQSV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m607.pep	GSAGTVRIGFSLGRREFSRARYISGVSLVLVGWMLAVITVLSLVLFRSPLVSMYNNDDPAVL					
	:     :     :     :     :     :     :     :     :					
g607	GSAGTVRIGFSLGRREFSRARYISGVSLVSGWVLAVITVLSLVLFRSPLASMYNDDPAVL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m607.pep	SIAATVLLFAGLFGPADFTQCIASYALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFN					
	:     :     :     :     :     :     :     :     :					
g607	SIAS TVLLFAGLFGPADFTQCIASYALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFD					
	370	380	390	400	410	420
	430	440	450	460		
m607.pep	MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX					
	:     :     :     :     :     :     :     :     :					
g607	MGIYGFWTALIASLTIAAVALVWCLEKYSMEVLVKSHKAVX					
	430	440	450	460		

This corresponds to the amino acid sequence <SEQ ID 1924; ORF 607.a>:

m607/a607 98.9% identity in 459 aa overlap

	10	20	30	40	50	60
m607.pep	MLLDLNRFSFPVFLKEVRLLTTLALPMLLAQVAQVGIGFVDVTVMAGGAGKEDLAAVALGS					
a607						
	10	20	30	40	50	60
m607.pep	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGLFLGVFGMVLMWAAIT					
a607						
	70	80	90	100	110	120
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAMVHRLHAYTSSLNRPRLIMLVSFAAFVLN					
a607						
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAMVHRLHAYASSLNRPRLIMLVSFAAFVLN					
a607						
	190	200	210	220	230	240

970

```

m607.pep      VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
a607          VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
              190      200      210      220      230      240

              250      260      270      280      290      300
m607.pep      WAVFKQIWKIGAPIGLSYFLEASAFSFIIVFLIAPFGEDYVAAQQVGISLSGILYMI PQSV
a607          WAVFKQIWKIGAPIGLSYFLEASAFSFIIVFLIAPFGEDYVAAQQVGISLSGILYMI PQSV
              250      260      270      280      290      300

              310      320      330      340      350      360
m607.pep      GSAGTVRIGFSLGRREFSRARYISGVSLVLGWMLAVITVLSLVLFRSPLVSMYNN DPAVL
a607          GSAGTVRIGFSLGRREFSRARYISGVSLVSGWMLAVITVLSLVLFRSPLVSMYNN DPAVL
              310      320      330      340      350      360

              370      380      390      400      410      420
m607.pep      SIAATVLLFAGLFQPADFTQCIASALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFN
a607          SIAATVLLFAGLFQPADFTQCIASALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFD
              370      380      390      400      410      420

              430      440      450      460
m607.pep      MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSRKAVX
a607          MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSRKAVX
              430      440      450      460

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1925>:

g608.seq

```

1  ATGTCCGCCC TCCTCCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTACCT CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAAACTGGCG GGACGCATCA CAGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAATT ACCTTCCGCA ACAGCGCGAT
201 ACGGAAAATC CTCCAAGGCG GCGAACCCGG GGCTGGCGAC ATCAGGCTCG
251 AAGGCGACCT CATCCTCGGC ATcGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCTCGC CATCGGacgA ATTGGCACGG ATTTTCGGCA CGCAGGCAGg
351 catcggcagc CGTGCCACCG ACATCGGACA CGGCatCaaa cAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGCGAACC CGAGTCcgCa
451 aacaccggca acgaagccct tgccgactgc ctCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACAGG CTCGAACGCG
551 ACATTGGAT AGACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1926; ORF 608.ng>:

g608.pep

```

1  MSALLPIINR LILQSPDSRS ELTSFAGKTL TLNIAGLKLA GRITEDGLLS
51  AGNGFADTEI TFRNSAIRKI LQGEPGAGD IRLEGLDILG IAVLSLLGSL
101 RSRASDELAR IFGTQAGIGS RATDIGHIK QIGRNIAEQI GGFSREPESA
151 NTGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1927>:

m608.seq

```

1  ATGTCCGCCC TCCTCCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTGCAG CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAATT ACCTTCCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGAG GCGAACCCGG GGCGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCTCGC CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
351 CATCGGACG CGTGCCGCGG ACATCGGACA CGGCATCAAA CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGCGAATC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT

```

971

501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG  
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1928; ORF 608>:

m608.pep  
1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS  
51 AGNGFADTEI TFRNSAVQKI LQGGEPEGAGD IGLEGDILG IAVLSLLGSL  
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GGFSRESESA  
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 608 shows 95.2% identity over a 188 aa overlap with a predicted ORF (ORF 608.ng) from *N. gonorrhoeae*:

m608/g608

	10	20	30	40	50	60
m608.pep	MSALLPIINRLILQSPDSRS ELAAFAGKTL TLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	:					
g608	MSALLPIINRLILQSPDSRS ELTSFAGKTL TLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m608.pep	TFRNSAVQKILQGGEPEGAGDIGLEGDILG IAVLSLLGSLRSRASDELARIFGTQADIGS					
	:					
g608	TFRNSAIRKILQGGEPEGAGDIRLEGDILG IAVLSLLGSLRSRASDELARIFGTQAGIGS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m608.pep	RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR					
	:					
g608	RATDIGHGIKQIGRNIAEQIGGFSREPESANTGNEALADCLDEISRLRDGVERLNERLDR					
	130	140	150	160	170	180
	189					
m608.pep	LERDIWIDX					
g608	LERDIWIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1929>:

a608.seq  
1 ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCCTGA  
51 CAGCCGCTCG GAACTGCGC CCTTCGCAGG CAAAACACTG ACCCTGAACA  
101 TTGCGGGTT GAACTGCGC GGACGCATCA CGGAAGACGG TTTGCTCTCG  
151 GCGGAAACG GCTTGCAGA CACCGAAATC ACCTTCCGCA ACAGCGCGGT  
201 ACAGAAATC CTCCAAGGCG GCGAACCGG GCGGGGCGAC ATCGGGCTCG  
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG  
301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA  
351 CATCGGCAGC CGTGCCGCG ACATCGGACA CGGCATCAA CAAATCGGCA  
401 GGAACATCGC CGAACAAATC GGCAGATTTT CCCGCGAACC CGAGTCCGCA  
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT  
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG  
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1930; ORF 608.a>:

a608.pep  
1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS  
51 AGNGFADTEI TFRNSAVQKI LQGGEPEGAGD IGLEGDILG IAVLSLLGSL  
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GRFSREPESA  
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID\*

m608/a608 98.9% identity in 188 aa overlap

10 20 30 40 50 60

972

```

m608.pep      MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
a608           MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
                10      20      30      40      50      60
                70      80      90     100     110     120
m608.pep      TFRNSAVQKILQGGEPGAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
a608           TFRNSAVQKILQGGEPGAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
                70      80      90     100     110     120
                130     140     150     160     170     180
m608.pep      RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR
a608           RAADIGHGIKQIGRNIAEQIGRFSREPESANIGNEALADCLDEISRLRDGVERLNERLDR
                130     140     150     160     170     180
                189
m608.pep      LERDIWIDX
a608           LERDIWIDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1931>:

```

g609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTTGA
51 TCGGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTCG GGTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGTT TCCACATAAT
201 CGATAACTTC CTCGATACCG ACTTCGGCAT CGGAAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGATTATG CGCGCCATAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCATACTG TGGCCGTATG
351 CCCCCTCTTT CATTCACCC GTGAGGCTGA CATCATAATC CAGtaa

```

This corresponds to the amino acid sequence <SEQ ID 1932; ORF 609.ng>:

```

g609.pep
1  MVVDRLEILA LDETLDFAV GNQRSSDIAH HIFHEFRVFV GLFGNVFFIG
51 AFEQAVELAA RLRFHIDNF LDTDFGIGSQ ADGNVRTILM RAILGNFFGT
101 RAKRGYGNHD LHTVAVCPVF HFTREADIII Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1933>:

```

m609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTTGA
51 TCGGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTCG GGTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGTTTGTG CGCGCCGTAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCATACTG TGGCCGTATG
351 CCCCCTCTTT GATTCGCCC GTGAGACAGA CATCATAATC CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1934; ORF 609>:

```

m609.pep
1  MVVDRLEILA LDETLDFAV GNQRSSDIAH HIFHEFRVFV GFFGNVFFIG
51 AFEQAVELAA RLRLHIIDDF LDTDFGIGSQ ADGNVRTLVV RAVLGNFFGT
101 RAKRGYGNHD LHTVAVCPVF DFARETDIII Q*

```

m609/g609 93.1% identity in 131 aa overlap

```

                10      20      30      40      50      60
m609.pep      MVVDRLEILALDDETLDFAVGNQRSSDIAHHIFHEFRVFVGFFGNVFFIGAFEQAVELAA
a609           MVVDRLEILALDDETLDFAVGNQRSSDIAHHIFHEFRVFVGLFGNVFFIGAFEQAVELAA
                10      20      30      40      50      60
                70      80      90     100     110     120
m609.pep      RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAVLGNFFGTAKRGYGNHDLHTVAVCPVF
a609           RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAVLGNFFGTAKRGYGNHDLHTVAVCPVF

```

```
a609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAATCTTTGA
51  TCGCTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTCG GGTTCCTGTA GGCTTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGGTTGTG CGGCCCATAT TGGGAAATTT CTTTGGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCACTACT TGGCCGTATG
351 CACCGTCTTT CATTCGCCCC GTGAGGCTGA CATCATAATC CAGTAA
```

```
a609.pep
  1  MVVDRLEILA LDDETLDAFV GNQRSSDIAH HIFHEFRVFEV GFFGNVFFIG
 51  AFEQAVELAA RLRLHIIDDF LDTDFGIGSQ ADGNVRTLVV RAILGNFFGT
101  RAKRGYGNHD LHTVAVCTVF HFAREADIII Q*
```

		10	20	30	40	50	60
m609.pep		MVVDRLLEILALDDETLD	AFVGNQRSSDIAHHIF	HEFRVFVGVFFGNVFF	IGAFEQAVELAA		
a609		MVVDRLLEILALDDETLD	AFVGNQRSSDIAHHIF	HEFRVFVGVFFGNVFF	IGAFEQAVELAA		
		10	20	30	40	50	60
		70	80	90	100	110	120
m609.pep		RLRLHIIDDFLDTDFG	IGSQADGNVRTLVVRA	VLGNFFGTRAKRGYGN	HDLHTVAVCPVF		
a609		RLRLHIIDDFLDTDFG	IGSQADGNVRTLVVRA	ILGNFFGTRAKRGYGN	HDLHTVAVCTVF		
		70	80	90	100	110	120
		130					
m609.pep		DFARETDIIIQX					
		:					
a609		HFAREADIIIQX					
		130					

```

g610.seq
1  ATGATTGGAG  GGCTTATGCA  ATTTCCCTTAC  CGCAATGTTC  CGGCTTCGCG
51  TATGCGCCGT  ATGCGCAGGG  TTGATTTTTC  ACGCGCGCTG  ATTCGCGGAG
101  ATATGCTGAC  CGCCGATGAT  ATGATTTTAT  CGGTGTTCGT  ATTGGAGGGG
151  GCGGCGCGCG  AGGAGGATGT  GCCTTCTATC  CCGGCGGTGA  AGCGTCAAGG
201  TTTGGACAGG  CTGCTGTTTA  CGCGCGGAAG  GCGCGTGAAG  CTCGGTATTC
251  CGATGTTGGC  ACTCTTTCCC  TGGTGTTACG  CAAACAAACG  CGCGCGTGC
301  CAGGAGGCGT  ACAATCCCGA  AGGACTCGTG  CCGTCAACTG  tccgagccTT
351  GCGCGAGAGG  TttcCggaac  tggggattat  gcaggtatgc  gcgctcgAtc
401  cttatacggt  gcacGGTCAG  GACGCAGTGA  CGGACgaaaa  cggttaCGTG
451  ATGaatgATg  aaaCCGTAGA  AGTCTTGGTG  AAACAGGCTT  TATGTCATGC
501  AGAGGCGGGC  ACGCAGGTCG  TTGCTCCTTC  CGATATGATG  GACGGGCGTA
551  TCGGCGCCAT  CCGCGAGGCT  TTGAGGATG  CCGGACATAT  CCATACGCGG
601  ATTATGGCAT  ATTCGCGCAA  ATATGCTTCT  CGATTCTACG  GCGCTTTCGG
651  TGATGCGGTA  GGCAGTTCGG  GCAATTGGG  AAAGCGAGAT  AAAAAGACTC
701  ATCAGATGGA  TCCTGCAAAAT  ACCGATGAGG  CGTGCATGA  AGTGGCGGCT
751  GATATTACAG  AAGGTGCGGA  TATGGTGATG  GTGAAGCCCG  GTTTGCCGTA

```



974

```
801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTA CCGACTTATG
851 CCTATCAGGT TTCGGGCGAA TATGCGATGT TGCAGGCGGC GGTGCGCAAC
901 GCGTGGCTGG ACGGCGGCAA AGTGGTTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGACGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1938; ORF 610.ng>:

**g610.pep**

```
1 MIGGLMQFPY RNVPASRMRR MRRDDFSRRL MREHMLTADD LIYPVFLVLE
51 AAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTGRA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG TQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLAQAVAN
301 GWLDGGKVVL ESLLAFKRAG ADGILTYYAI EAAKMLKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1939>:

**m610.seq**

```
1 ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTC CGGCTTCGCG
51 TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCTG ATGCGCGAAC
101 ACACGCTGAC CGCCGATGAT TTGATTTATC CGGTGTTTCT ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGTGTGA AGCGTCAAAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GCGGGTAAAG CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCCTTCGATC
401 CTTATACGGT TCACGGTCAG GACGGGCTGA CGGACGAAA CGGTTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTGGTTC AAGCAGGCTT TGTGCCACGC
501 TGAAGCGGGC GCGCAGGTGG TTGCCCTTTC CGATATGATG GACGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
651 TGATGCGGTA GCGAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTCAAG AAGGTGCGGA TATGGTAATG GTCAAGCCCG GTTTGCCGTA
801 TTTGGACGTT GTCCGCCGCG TAAAGGACGA GTTCGGTGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGT TGCAGGCAGC GATTGCCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGACGGGA TTTTGACCTA TTACGCTATT GAGGCGGCAA
1001 AGATGTTGAA GCGTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1940; ORF 610>:

**m610.pep**

```
1 MIGGLMQFPY RNVPASRMRR MRRDDFSRRL MREHMLTADD LIYPVFLVLE
51 SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLAQAIAN
301 GWLDGGKVVL ESLLAFKRAG ADGILTYYAI EAAKMLKR*
```

**m610/g610** 98.5% identity in 338 aa overlap

	10	20	30	40	50	60
m610.pep	MIGGLMQFPYRNV	PASRMRRMRDD	FSRRLMREHT	LTADDLIYPV	FVLEGSAREE	DVPSM
g610	MIGGLMQFPYRNV	PASRMRRMRDD	FSRRLMREH	MLTADDLIYP	VFVLEGAAREE	DVPSM
	10	20	30	40	50	60
	70	80	90	100	110	120
m610.pep	PGVKRQSLDRLL	FTAEEAVKLG	IPMLALFPV	VTANKTERAQ	EAYNPEGLV	PSTVRALRER
g610	PGVKRQSLDRLL	FTAEEAVKLG	IPMLALFPV	VTANKTGRAQ	EAYNPEGLV	PSTVRALRER
	70	80	90	100	110	120
	130	140	150	160	170	180
m610.pep	FPELGIMTDV	ALDPYTVHGQ	DGLTDENGYV	MNDETVEVLV	KQALCHAEAG	AQVVAPSDMM
g610	FPELGIMTDV	ALDPYTVHGQ	DGLTDENGYV	MNDETVEVLV	KQALCHAEAG	TQVVAPSDMM
	130	140	150	160	170	180
	190	200	210	220	230	240
m610.pep	DGRIGAIREA	LEDAGHIHTR	IMAYSAKYAS	AFYGPFRDAV	GSSGNLGKAD	KKTYQMDPAN

975

```

g610      DGRIGAIAREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
           190      200      210      220      230      240

           250      260      270      280      290      300
m610.pep  TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTYAYQVSGEYAMLQAAIAN
           |||||
g610      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTYAYQVSGEYAMLQAAVAN
           250      260      270      280      290      300

           310      320      330      339
m610.pep  GWLDGGKVVLESLLAFKragADGILTYAIEAAKMLKRX
           |||||
g610      GWLDGGKVVLESLLAFKragADGILTYAIEAAKMLKRX
           310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1941>:

```

a610.seq
1   ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CGGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCCGT ATGCGCGAGC
101 ATACGCTGAC TGCCGATGAT TTGATTATC CGGTGTTCGT ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GGCGGTAAAG CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT GCACGGTCAG GACGGGCTGA CGGACGAAAA CGGTTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTGGTTC AAGCAGGCTT TGTGTCATGC
501 AGAGGCAGGC GCACAGGTCG TTGCTCCTTC CGATATGATG GATGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCGCCCAA ATATGCTTCT GCATTTTACG GCCCTTTCGG
651 TGATGCGGTA GGCAGTTCGG GCAATTGTTG CAAGGCAGAT AAAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTCAGG AAGGTGCGGA TATGGTGATG GTCAAGCCCG GTTTGCCGTA
801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGCGGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGC TGCAGGCGGC GGTGCGCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTTC GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGATGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1942; ORF 610.a>:

```

a610.pep
1   MIGGLMQFPY RNVSASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIARE LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLQAAVAN
301 GWLDGGKVVLE SLLAFKrag ADGILTYYAI EAAKMLKR*

```

m610/a610 99.4% identity in 338 aa overlap

```

           10      20      30      40      50      60
m610.pep  MIGGLMQFPYRNVPASRMRRMRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           |||||
a610      MIGGLMQFPYRNVSASRMRRMRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           10      20      30      40      50      60

           70      80      90      100     110     120
m610.pep  PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           |||||
a610      PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120

           130     140     150     160     170     180

```

976

```

m610.pep    FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
             |||||
a610         FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
             130      140      150      160      170      180

             190      200      210      220      230      240
m610.pep    DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
             |||||
a610         DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
             190      200      210      220      230      240

             250      260      270      280      290      300
m610.pep    TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAIAN
             |||||
a610         TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAVAN
             250      260      270      280      290      300

             310      320      330      339
m610.pep    GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
             |||||
a610         GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
             310      320      330

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1943>:

```

g611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCCCGGA CTCTGTCGAG
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TTTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCGCGCG CGTCCGCATT Ctcgcgcagg ttgtGGCtgt
201 tatcctTGGG CGGGCTGggt tgtttgcccg ccataaTTtc cagtacctgA
251 TcgcgGTCta tggtttcCCa ttCcatcagg gctttgcaca TCGTTTCCAT
301 cttgTCGCGG TTTTcatcga ggaTTTGTa ggcaacCTGA TACTgctcgt
351 ccaaaaAtccg Gcggatttcc gcgtcgAtgt cctgctgggt tTTCTCGGAA
401 ATGTTTTCGCG AACGGgttac gctGCGCCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTtc gTCATgccc TAGCGCGTTA
501 CCATTTTCGCG TGCCATTTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1944; ORF 611.ng>:

```

g611.pep
1  MPSENGMKR QLAGCRLFGK LSLVFRLLPG LCRGGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVILG RAGLFARHNF QYLIAYVGFP FHQGFARHFH
101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRGTG AAPQEDFAFV
151 FRINHHAHFV AHAVARYHFA CHLGCAFKVV *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1945>:

```

m611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCGCGCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTTGCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCTGA TGGTTTCCCA TTCCATCAGG GCTTTCGACA TCGTTTCCAT
301 CTGTGTCGCG TTTTCATCGA GGATTTGTa GGCAACCTGA TATTGCTCGT
351 CCAAAAATCCG GCGGATTTC GCGTCGATGT CCGTCTGGGT TTTCTCGGAA
401 ATGTTTTCGCG AACGGGTTAC GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTc GCTCATGCCG TAGCGCGTTA
501 CCATTTTCGCG CGCCATTTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1946; ORF 611>:

```

m611.pep
1  MPSENGMKR QLAGCRLFGK LSLVFRLLG LCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGFQ FHQGFARHFH
101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/g611 96.1% identity in 180 aa overlap

10 20 30 40 50 60

977

```

m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
g611          MPSENGMGKRQLAGCRLFGKLSLVFRLLPGLCRGGVCRGRCFGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60

              70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
g611          LAQVVAVILGRAGLFARHNFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRRTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
g611          ADFRVDVLLGFLGNVLRRTGYAAPQEDFAFVFRINHHAHFVAHAVARYHFACHLGCAFKVV
              130     140     150     160     170     180

m611.pep      X
g611          |
g611          X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1947>:

```

a611.seq
1   ATGCCGTCTG AAAACAGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTGCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCCTTTGGG CGGGCTGGGT TGTTTGCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCTGA TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTGTGTCGGG TTTTCATCGA GGATTTTGTA GGCAACCTGA TACTGCTCGT
351 CCAAAATCCG GCGGATTTCC GCATCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTGCG AACGGGTTAC GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCGCATAA ACCATCACGC CCATTTTGTC GTCATGCCG TAGCGCGTTA
501 CCATTTTCGG CGCCATTTGG GTTGC GCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1948; ORF 611.a>:

```

a611.pep
1   MPSENRMGKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGF FHQGFARHFH
101 LVAVFIEDFV GNLILLVQNP ADFRIDVLLG FLGNVLRRTGY AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

m611/a611    98.9% identity in 180 aa overlap

              10      20      30      40      50      60
m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
a611          MPSENRMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60

              70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
a611          LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRRTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
a611          ADFRIDVLLGFLGNVLRRTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
              130     140     150     160     170     180

m611.pep      X

```

a611                    I  
                          X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1949>:

```
g612.seq
  1 ATGGGctttcg gcggaatat tgcAAAAAAG CTGGCcgGg taGATGAAAT
  51 AGCCTttgac tttgacggca TCGTCTTTGA TTTCGGGCGT GATGATGCTG
 101 TCCGGCataG CGGCGTAATC AATGCTGCTG TCGCCGGCCT GCATATAGTC
 151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
 201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCGATTTTC
 251 CAAATTTGGC GGTGCAGTTG GGC GCGTTGT TGCATTTCGG TCATCATCGA
 301 AATCCATATA TAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
 351 ATTTTTTTAC GGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1950; ORF 612.ng>:

```
g612.pep
  1 MGFGGNIAKK LAGVDEIAFD FDGIVDFGR DDAVRHSGVI NAAVAGLHIV
  51 GEVFADKAVE KCAENVLFKV PAIHRAAYFV GDFPNLAVQL GALLHFGHHR
 101 NPYIKLNKSK SPDIFRRFFY GHSN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1951>:

```
m612.seq
  1 ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
  51 AGCCTTTAAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
 101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
 151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
 201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
 251 CAAATTTGGC GGTGCAGTTG GGC GCGTTGT TGCATTTCGG TCATCATCGA
 301 AATCCATATA .AAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
 351 ATTTTTTTAC GGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1952; ORF 612>:

```
m612.pep
  1 MGFGGNIAKK LAGVDEIAFN FDGIVDFGR DDAVRHSGVI NTAVACLHIV
  51 GEVFADKAVE KCAENVLFKV PAIHRAAYFV GNFPNLAVQL GALLHFGHHR
 101 NPYXKLNKSK SPDIFRRFFY GHSN*
```

m612/g612 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m612.pep	MGFGGNIAKKLAGVDEIAFNFDGIVDFGRDDAVRHSGVINTAVACLHIVGEVFADKAVE					
g612	MGFGGNIAKKLAGVDEIAFDGIVDFGRDDAVRHSGVINAAVAGLHIVGEVFADKAVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m612.pep	KCAENVLFKVP AIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRRFFY					
g612	KCAENVLFKVP AIHRAAYFVGDFPNLAVQLGALLHFGHHRNPYIKLNKSKSPDIFRRFFY					
	70	80	90	100	110	120
m612.pep	GHSNX					
g612	GHSNX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1953>:

```
a612.seq
  1 ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
  51 AGCCTTTGAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
 101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
 151 GGTAAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
 201 GTTTGAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
 251 CAAATTTGGC GGTGCAGTTG GGC GCGTTGT TGTATTTCGG TCATCATCGA
 301 AATCCATAT. AAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
 351 ATTTTTT.AC GGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1954; ORF 612.a>:

```

a612.pep
  1  MGFGGNIAKK LAGVDEIAFD FDGIVDFDGR DDAVRHSGVI NTAVACLHIV
 51  GKVFADKAVE KCAENVLFEV PAIHRAAYFV GNFPNLAVQL GALLYFGHHR
101  NPYXKLNSK SPDIFRRFFX GHSN*

m612/a612    96.0% identity in 124 aa overlap

              10      20      30      40      50      60
m612.pep     MGFGGNIAKKLAGVDEIAFNFDGIVDFDGRDDAVRHSGVINTAVACLHIVGEVFADKAVE
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a612          MGFGGNIAKKLAGVDEIAFDGIVDFDGRDDAVRHSGVINTAVACLHIVGKVFADKAVE
              10      20      30      40      50      60

              70      80      90     100     110     120
m612.pep     KCAENVLFKVPAlHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNSKSPDIFRRFFY
              |||||:|||||:|||||:|||||:|||||:|||||:|||||
a612          KCAENVLFEPAlHRAAYFVGNFPNLAVQLGALLYFGHHRNPYXKLNSKSPDIFRRFFX
              70      80      90     100     110     120

m612.pep     GHSNX
              ||||
a612          GHSNX
  
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1955>:

```

g613.seq
  1  ATGTCGCGTT CGAGCCTGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCGT CGaggcagtc ggcaagggct tcgttgccgg
101  tgtttGcgGA CTCGGGTTCG CGGGAAAATC CGCCGATTG TTCGGCGATG
151  TTCCTGCCGA TTTgtttGat GCCGTGTCCG ATGTCGGTGG CACGgtgccc
201  gatgcCTGCC TGCCTGCCGA AAATCCGTGC CAATTcgtCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CgATGCCGAG GATGAGGTCC
301  CCTTCGAGCC TGATGTCGCC AGCCCCGGGT TCGCCGCTT GGAGGATTTT
351  CCGTATCGCG CTGTTGCGGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
401  CCGCCGAGAG CAAACCGTCT TCTGTGATGC GTCCCGCCAG TTTCAGCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGAGGTAA GTTCCGAGCG
501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATTGGGGC GGAGAATGCC TGTTGTTGCT GTTGCCGCTT
601  ATTTTACAGG CTAA
  
```

This corresponds to the amino acid sequence <SEQ ID 1956; ORF 613.ng>:

```

g613.pep
  1  MSRSSLRRS LRRSTPSRSL LISSRQSARA SLPVFADSGS RENPPICSAM
 51  FLPICLMPCP MSVARLPMPA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101  PSSLMSPAPG SPPWRIFRIA LLRKVISVSA KPFPAESKPS SVMRPASFSP
151  AMFRVSVLPA KEVSSERLSG LCRIRRLMMG RRADIFSDWG GECLLLLLPL
201  ILQA*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1957>:

```

m613.seq
  1  ATGTCGCGTT CGAGCCGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCGT CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101  TGTTTGCGGA CTCGGATTTC CGGGAAAATC CGCCGATTG TTCGGCGATG
151  TTCCTGCCGA TTTGTTTGAT GCCGTGTCCG ATGTCGGCGG CACGGCTGCC
201  GATGTCTGCC TGCCTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCC
301  CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCTCCTT GGAGGATTTT
351  CTGTACCGCG CTGTTGCGGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
401  CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAGCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGCGGCAA GTTCCGAGCG
501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATCGGGGC GGAGAATGCC TGTTGTTGCT GTTGCCGCTT
  
```

601 ATTTTACAGG CTAA

This corresponds to the amino acid sequence <SEQ ID 1958; ORF 613>:

```
m613.pep
  1 MSRSSRSRRS LRRSTPSRSL LISSRQSARA SLPMFADSDS RENPPICSAM
 51 FLPICLMPCP MSAARLPMsa CVPKIRANSS DARERRLPSR DSTAMPRMRS
101 PSSPMSPAPG SPPWRIFCTA LLRKVISVSA KPFFAESKPS SVMRPASFSP
151 AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLLPL
201 ILQA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m613/g613 94.6% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
g613	MSRSSLSRRSLRRSTPSRSLLISSRQSARASLPVFADSGSRENPPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVVKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPWRIFCTA					
	:					
g613	MSVARLPMPACVVKIRANSSDARERRLPSRDSTAMPRMRSPSSLMSPAPGSPPWRIFRIA					
	70	80	90	100	110	120

981

	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFSFAMFRVSVLPAAASSERLSGLCRIRRLMMG					
g613	LLRKVISVSAKPFPAESKPSSVMRPASFSFAMFRVSVLPAAKEVSSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
g613	RRADIFSDWGGECLLLLLPLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1959>:

```
a613.seq
1  ATGTCGCGTT  CGAGCCGGTC  GAGGCGTTCG  TTGAGGCGTT  CCACGCCGTC
51  GCGCAGTCTG  CTTATTTTCG  CGAGGCAGTC  GGCAAGGGCT  TCGTTGCCGA
101  TGTTTGCGGA  CTCGGGTTTC  CGGGAAAATC  TGCCGATTTC  TTCGGCGATG
151  TTCCTGCCGA  TTTGTTTGAT  GCCGTGTCCG  ATGTCGGCGG  CACGGCTGCC
201  GATGTCTGCC  TCGGTGCCGA  AAATCCGTGC  CAATTCGTCC  GATGCGCGGG
251  AACGCAGGCT  GCCGAGCAGG  GACAGTACCG  CGATGCCGAG  GATGAGGTTC
301  CCTTCGAGCC  CGATGTCGCC  CGCCCCGGGT  TCGCCGCCCT  GGAGGATTTT
351  CTGTACCGCG  CTGTTGCCGA  AGGTGATTTC  GGTGTCTGCA  AAGCCGTTTC
401  CCGCCGAGAG  CAAACCGTCT  TCCGTGATGC  GTCCCGCCAG  TTTCAACCCG
451  GCAATGTTCA  GGGTCAGTGT  TTTGCCTGCG  AAGGCGGCAA  GTTCCGAGCG
501  GCTGTCCGGG  CTTTGCAGAA  TCAGGCGGTT  GATGATGGGG  AGGAGGGCGG
551  ACATATTTTC  TGATCGGGGC  GGAGAATGCC  TGTGTGTTCT  GTTGACGCTT
601  ATTTTACAGG  CTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1960; ORF 613.a>:

```
a613.pep
1  MSRSSRSRRS  LRRSTPSRSL  LISSRQSARA  SLPMFADSGS  RENLPICSAM
51  FLPICLMPCP  MSAARLPMSA  CVPKIRANSS  DARERRLPSR  DSTAMPRMRS
101  PSSPMSPAPG  SPPWRIFCTA  LLRKVISVSA  KFFPAESKPS  SVMRPASFPN
151  AMFRVSVLPA  KAASSERLSG  LCRIRRLMMG  RRADIFSDRG  GECLLLLLTL
201  ILQA*
```

m613/a613 98.0% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
a613	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSGSRENLPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVPKIRANSSDARERRLPSPRDSTAMPRMRSPSSPMSPAPGSPWRIFCTA					
a613	MSAARLPMSACVPKIRANSSDARERRLPSPRDSTAMPRMRSPSSPMSPAPGSPWRIFCTA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFSFAMFRVSVLPAAASSERLSGLCRIRRLMMG					
a613	LLRKVISVSAKPFPAESKPSSVMRPASFPAMFRVSVLPAAASSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
a613	RRADIFSDRGGECLLLLLTLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1961>:



982

```

g614.seq
1   AtggcTgcgt  tcAacgcttt  ggacggcaaa  aaagaagaca  acggggcaaat
51  cgaatATTCT  CAGTTCATCC  GACAGGTCAA  CAACGGCGAA  GTATCCGGCG
101 TCAACATCGA  AGGATCCGTC  GTCAGCGGTT  ACCTGATTAA  AGGCGAGCGC
151 ACCGACAAAA  GCACCTTCTT  CACCAACGCG  CCCTTGGATG  ACAACCTGAT
201 TCAAACCCCT  TTGAACAAAA  ACGTCCGCGT  AAAAGTAACG  CCGGAAGAAA
251 AACCGAGCGC  GCTGACTGCC  CTGTTTACA  GCCTGCTGCC  CGTCCTGCTG
301 CTGATTGGCG  CATGGTTCTA  CTTTATGCGT  ATGCAGGCGG  GCGGCGGCGG
351 AAAAGGCGGC  GCATTCTCCT  TCGGCAAAAG  CCGCGCCCGC  CTGCTGGACA
401 AAGATGCCAA  CAAAGTTACC  TTTGCCGATG  TCGCCGGCTG  CGACGAAGCC
451 AAAGAAGAAG  TGCAGGAAAT  CGTCGATTAC  CTCAAAGCAC  CGAACCCTa
501 tcaAAGcctc  ggcggccgtg  ttcCGCGCGG  CATCCTgCtg  gcgGgcagcc
551 CGGGAaccgg  taaAACACTC  TTGGCGAAAG  CCATTGCAGG  CGAGGCCGCG
601 GTGCCGTTCT  TCAGCATTTT  CGGTTCCGAT  TTTGTCGAAA  TGTTGCTCGG
651 TGTCGGTGCA  AGCCGCGTCC  GCGATATGTT  CGAGCAGGCA  AAGAAAAACG
701 CCCCATGCAT  TATCTTTATC  GACGAGATTG  ACGCGGTAGG  CCGCCAACGC
751 GCGCGAGgTT  TGGCGGCGCG  CAATGATGAG  CGCGAGCAAA  CATTAAACCA
801 ATTATTGGTT  GAAATGGACG  GTTTTGAGAG  CAATCAGACT  GTAATTGTGA
851 TTGCGGCAAC  CAACGCCCCC  GACGTAATCG  ATCCTGCGCT  GCAACGCCCC
901 GGCCGCTTCG  ACCGCCAAGT  CGTCGTCCCC  CTGCCGGACA  TCCGGGGGCG
951 CGAACAGatn  ttGAACGTCC  ATTCTaaAAA  AGTGCcttTG  gacgaATCTg
1001 tggatTTTATT  GTCCCTCGCG  CGCGGCACGC  cgggtttTTC  cggcgcggat
1051 tTggcgaaac  tgggtcaacga  agccccctg  tttgccggcc  gccgcaacaa
1101 agtgaaagtc  gatcaaagcg  attTGAAGAC  GCCAAAGACA  AAATCTATAT
1151 GGGTCCGGAA  CGCCGCAGTA  TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1962; ORF 614.ng>:

```

g614.pep
1   MAAFNALDGK  KEDNGQIEYS  QFIRQVNNGE  VSGVNIIEGSV  VSGYLIKGER
51  TDKSTFFFTNA  PLDDNLIQTL  LNKNVVRVKVT  PEEKPSALTA  LFYSLLPVLL
101 LIGAWFYFMR  MQAGGGGKGG  AFSFGKSRAR  LLDKDANKVT  FADVAGCDEA
151 KEEVQEIVDY  LKAPNRYQSL  GGRVPRGILL  AGSPGTGKTL  LAKAIAGEAG
201 VPFFSISGSD  FVEMFVGVA  SRVRDMFEQA  KKNAPCIIFI  DEIDAVGRQR
251 GAGLGGGNDE  REQTLNQLLV  EMDGFESNQT  VIVIAATNRP  DVLDPALQRP
301 GRFDRQVVVP  LPDIRGREQX  LNVHSHKKVPL  DESVDLLSLA  RGTGPGFSGAD
351 LAKLVNEAPL  FAGRRNKVKV  DQSDLKTPKT  KSIWVRNAAV  W*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1963>:

```

m614.seq
1   ATGGCTGCGT  TCAACGCTTT  AGACGGTAAA  AAAGAAGACA  ACGGGCAAAT
51  CGAATACTCT  CAGTTCATCC  AACAGGTCAA  CAACGGCGAA  GTATCCGGCG
101 TCAACATCGA  AGGATCCGTC  GTCAGCGGCT  ACCTGATTAA  GGGCGAGCGC
151 ACCGACAAAA  GCACTTTCTT  CACCAACGCG  CCTTTGGACG  ACAACCTAAT
201 TAAACACTG  CTCGACAAAA  ACGTCCGCGT  AAAAGTAACG  CCGGAAGAAA
251 AACCGAGCGC  GCTGGCTGCC  CTGTTTACA  GCCTGCTGCC  CGTCCTGCTG
301 CTGATTGGCG  CATGGTTCTA  CTTTATGCGT  ATGCAGACGG  GCGGCGGCGG
351 AAAAGGCGGC  GCATTCTCAT  TCGGTAAAAG  CCGCGCCCGC  CTGCTGGACA
401 AAGATGCCAA  CAAAGTGACC  TTTGCCGATG  TCGCCGGCTG  CGACGAAGCC
451 AAAGAAGAAG  TACAGGAAAT  CGTCGATTAC  CTCAAAGCGC  CGAACCCTa
501 TCAAAGCCTG  GGCGGGCGCG  TGCCGCGCGG  CATCCTGCTG  GCGGGCAGCC
551 CGGGTACGGG  TAAGACGCTT  TTGGCGAAAG  CGATTGCAGG  CGAAGCCGCG
601 GTGCCGTTCT  TCAGCATTTT  AGGTTCCGAC  TTTGTCGAAA  TGTTGCTCGG
651 TGTCGGTGCG  AGCCGCGTCC  GCGATATGTT  CGAGCAGGCG  AAGAAAAACG
701 CCCCTGCAT  CATCTTTATC  GACGAGATTG  ACGCAGTCGG  CCGCCAACGC
751 GGCGCAGGTT  TGGGCGGCGG  CAATGATGAG  CGCGAGCAAA  CATTAAACCA
801 ATTGTTGGTT  GAAATGGACG  GTTTTGAGAG  CAATCAGACT  GTAATTGTGA
851 TTGCGGCAAC  CAACGCCCCC  GACGTAATCG  ATCCTGCGCT  GCAACGCCCC
901 GGCCGTTTCT  ACCGCCAAGT  GGTGTGTCCT  CTGCCGGACA  TCCGAGGGCG
951 CGAACAGATT  TTGAACGTCC  ATTCTAAAAA  AGTGCCCTTG  GACGAATCTG
1001 TGGATTTTATT  GTCCCTCGCG  CGCGGCACGC  CGGGTTTTTC  CGGCGCGGAT
1051 TTGGCGAACT  TGGTCAACGA  AGCCGCCCTG  TTTGCCGGCC  GCCGAATAA
1101 AGTCAAAGTC  GATCAGAGCG  ATTTGAAGAC  GCCAAAGACA  AAATCTATAT
1151 GGGTCCGGAA  CGCCGCAGTA  TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1964; ORF 614>:

983

```

m614.pep
  1  MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIEGSV VSGYLIKGER
 51  TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101  LIGAWFYFMR MQTGGGKGGG AFSFGKSRR LLDKDANKVT FADVAGCDEA
151  KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAGEAG
201  VPFFSISGSD FVEMFVGUGA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251  GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301  GRFDRQVVVP LPDIRGREQI LNVHSHKVPL DESVDLLSLA RGTPGFSGAD
351  LANLVNEAAL FAGRRNKVKV QSDLKTPKT KSIWVRNAAV W*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m614/g614 98.0% identity in 391 aa overlap

m614.pep	10	20	30	40	50	60
	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVVSGYLIKERTDKSTFFTNA					
g614	MAAFNALDGKKEDNGQIEYSQFIRQVNNGEVSGVNIEGSVVSGYLIKERTDKSTFFTNA					
	10	20	30	40	50	60
m614.pep	70	80	90	100	110	120
	PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGKGG					
g614	PLDDNLIQTLLNKNVRVKVT PEEKPSALTALFYSLPVLL LIGAWFYFMR MQAGGGGKGG					
	70	80	90	100	110	120
m614.pep	130	140	150	160	170	180
	AFSFGKSRRLLDKDANKVTFADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL					
g614	AFSFGKSRRLLDKDANKVTFADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL					
	130	140	150	160	170	180
m614.pep	190	200	210	220	230	240
	AGSPGTGKTL LAKAIAGEAGVPFFSISGSD FVEMFVGUGASRVRDMFEQA KKNAPCIIFI					
g614	AGSPGTGKTL LAKAIAGEAGVPFFSISGSD FVEMFVGUGASRVRDMFEQA KKNAPCIIFI					
	190	200	210	220	230	240
m614.pep	250	260	270	280	290	300
	DEIDAVGRQRGAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP					
g614	DEIDAVGRQRGAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP					
	250	260	270	280	290	300
m614.pep	310	320	330	340	350	360
	GRFDRQVVVPLPDIRGREQILNVHSHKVPLDESVDLLSLARGTPGFSGADLANLVNEAAL					
g614	GRFDRQVVVPLPDIRGREQXNVHSHKVPLDESVDLLSLARGTPGFSGADLAKLVNEAPL					
	310	320	330	340	350	360
m614.pep	370	380	390			
	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
g614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1965>:

```

a614.seq
  1  ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
 51  CGAATATTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
101  TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
151  ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTTGGACG ACAACCTGAT
201  TAAACACTG CTCGACAAAA ACGTCCGTGT AAAAGTAACG CCGGAAGAAA
251  AACCAGAGCG GCTGGCTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG

```

984

```

301 CTGATTGGCG CGTGGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGCAAAAG CCGCGCCCGC CTACTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTA
501 TCAAAGCCTG GCGGGGCGCG TGCCGCGCGG CATCCTGCTG GCGGGCAGCC
551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCCGTTCT TCAGCATTTC AGGTTCCGAC TTTGTGCGAA TGTTCTGTCG
651 TGTCCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
701 CCCCTGTCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GCGCAGGTT TGGGCGGCGG TAATGATGAG CGCGAGCAA CATTAAACCA
801 ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCCGTTTCG ACCGCCAAGT GGTTGTCCCC CTGCCGGACA TCCGGGGGCG
951 CGAACAGATT TTGAACGTCC ACTCTAAAAA AGTGCCTTTG GACAAATCTG
1001 TGGATTTATT GTCCCTCGCG CGCGGCACGC CGGGTTTTTC CGGCGCGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGTCCGGAA CGCCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1966; ORF 614.a>:

```

a614.pep
1  MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIIEGSV VSGYLIKGER
51  TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101 LIGAWFYFMR MQTGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAGEAG
201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQI LNVHSHKKVPL DKSVDLLSLA RGTGPGFSGAD
351 LANLVNEAAL FAGRRNKKV DQSDLKTPKT KSIWVRNAAV W*

m614/a614 99.7% identity in 391 aa overlap

          10      20      30      40      50      60
m614.pep  MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKGERTDKSTFFTNA
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a614      MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKGERTDKSTFFTNA
          10      20      30      40      50      60

          70      80      90      100     110     120
m614.pep  PLDDNLIKTL LDKNVRVKVTPEEKPSALAA LFYSLLPVLL LIGAWFYFMRMQTGGGGKGG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a614      PLDDNLIKTL LDKNVRVKVTPEEKPSALAA LFYSLLPVLL LIGAWFYFMRMQTGGGGKGG
          70      80      90      100     110     120

          130     140     150     160     170     180
m614.pep  AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDY LKAPNRYQSLGGRVPRGILL
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a614      AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDY LKAPNRYQSLGGRVPRGILL
          130     140     150     160     170     180

          190     200     210     220     230     240
m614.pep  AGSPGTGKTLLAKAIAGEAGVPFFSISGSD FVEMFVGVGASRVRDMFEQA KKNAPCIIFI
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a614      AGSPGTGKTLLAKAIAGEAGVPFFSISGSD FVEMFVGVGASRVRDMFEQA KKNAPCIIFI
          190     200     210     220     230     240

          250     260     270     280     290     300
m614.pep  DEIDAVGRQRGAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a614      DEIDAVGRQRGAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
          250     260     270     280     290     300

          310     320     330     340     350     360
m614.pep  GRFDRQVVVPLPDIRGREQILNVHSHKKVPL DESVDLLSLARGT GPGFSGADLANLVNEAAL
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a614      GRFDRQVVVPLPDIRGREQILNVHSHKKVPL DKSVDLLSLARGT GPGFSGADLANLVNEAAL

```

985

	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
a614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1967>:

```

g615.seq
1   ATGTGGAAC  GGCGGCGGCG  CGGTGtcggC  AGCTTtgaag  agcagcGaAT
51  agatgCCGCC  GGCAAACCAC  AATGCGGAAa  gcaggCtgaa  gcGGTTgcgC
101 GGCagcTTca  tGCCGCCTCC  TcGTCCaGCC  ACGtttGgca  gattttggac
151 aggcgcAGGa  ATTTGCGcCc  gcgtgcggCA  agtatgtcgc  gcCAttgtgc
201 cacttcttcg  gcggacggTG  ctctgcgaT  gctgCATTCG  TACagcagga
251 aatcgagggt  ttcttcgatg  acggGgatgg  AttccgTTTG  GataAgCTgc
301 ttgagttcgt  tcatgactGt  TCgGATAcgg  aaatcgggaa  aatgccgtct
351 gAaagggtt  CAGACGGCat  tggATTATTT  GCTGTGCAGG  AAgcgcgttg
401 cctcttccca  tttgcCGGAA  AtgATGTCCg  gtacggcctg  cAGGGATttg
451 gCGACGGcat  cgtcgatttg  ccgGcggtgc  ttCcgcgctc  ggtttGTTca
501 agacgtagcc  gaCGACGagg  ttgcggtcGC  CGGGGtggcC  GATGCCGAGG
551 CGCAGGCGGt  aatagtctgC  CGTGCCGAGT  TTTGCctgAA  TGTCTTTCAA
601 GCCGTTGTGT  CgcCGttgc  cgcCGCCGAG  TTTGAATTTg  ATCCGTCCGC
651 AAGGGATGTC  GAGTTCGTGC  TGGACGACGA  GGATTTCTTC  GGGTTTGATT
701 TTGTAGAACT  GTGCAAGCGC  GGCAACCGCC  TGTCCGGAAC  GGTTCATGAA
751 CGTGGCCGGT  TTGAGCAGCC  AAACATCGCC  GTCGGGCAGG  GCGGCAGCGG
801 CAACTTCGCC  GAAGAATTTT  TTTTCTTCTT  TAAACGAAGC  CTTCCATTTC
851 CACGCCAGTT  CGTCGAGGAA  CAAAAGCCC  GCATTGTGGC  GGGTCTGTTC
901 GTATTCTTTG  CCCGGGTTGC  CCAAGCCGAC  AACCATTTTG  ATTGTGttcg
951 acatgataTT  TtccgtgTTT  CTgTCGaatg  cggTctgaAG  GCTTCAGacg
1001 gcatggTtaT  TCTTCTTgaT  TTtgaACgcg  tgtgcggCGC  GCTTCTTTGG
1051 GGTGCATCAA  CAGCGGGCGG  TACACTTCGA  TCGGGTCGCC  GTCGCGCAGC
1101 GGCGTGTCTG  CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1968; ORF 615.ng>:

```

g615.pep
1   MWKRRRRGVG  SFEEQRIDAA  GKPOCGKQAE  AVARQLHAAS  SSSHVWQILD
51  RRRNLPPRAA  SMSRHCATSS  ADGASSMLHS  YSRKSRVSSM  TGMDSVWISC
101 LSSFMTVRIR  KSGKCRKLGL  QTAIDYLLCR  KRVASSHLPE  MMSGTACRDL
151 ATASSICRRR  FRARFVQDVA  DDEVAVAGVA  DAEAQAVIVC  RAEFCLNVFQ
201 AVVSAAAAAE  FEFDPsARDV  EFVVDDEDFE  GFDFVELCKR  GNRLSGTVHE
251 RGRFEQPNIA  VGQGGAGNFA  EEEFFFFFKRS  LPFPRQFVEE  PKARIVAGLF
301 VFFARVAQAD  NHFDCVRHDI  FRVSVECLGK  ASDGMVILLD  FERVCGALLW
351 GRSTAGGTLR  CGRRRAAACR  L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1969>:

```

m615.seq  Length: 1116
1   ATGCGGAAAA  GGCGGTGGCG  CGGTTTCGGC  AGCTTTGAAA  AGCAGTGAGT
51  AAATGCTGCC  TGCAAACCAC  AATGCCGAGA  GCAGGATAAA  GCGGTTGCGT
101 GGCAGATTCA  TGCTTGTTCC  TCTTCAAGCC  ATGTCTGGCA  TAGTTTGGAT
151 AGGCGCAGGA  ATTTTCCGCC  GCGTGCGGCC  AGCATATCGC  GCCAAACGGC
201 AATTTCTTCG  GCGGAGGGGG  CATCGTCTAT  GCTGCATTTC  TAGAGCAGGA
251 AATCGAGGGT  TTCTTCGATG  ACGGGGATGG  ATTCGGTTTG  GATAAGCTGC
301 TTGAGTTCGG  TCATGACTGT  TCGGATATGG  AAATCGGGAA  CATGCCGTCT
351 GAAAGGGCTT  CAGACGGCAT  CGGGTCATTT  GCTGTGCAGG  AAGCGGGTTG
401 CTTCTTCCCA  TTTGCCGGCA  AGGATGTCGG  GTATGGCTTG  CAGGGATTTC
451 GCGACGGCAT  CGTCAATCTG  TCGGCGGTGT  .TCCGTACTG  GGTTTGTTCA
501 GGACATAGCC  GACGACGAGG  TTGCGGTCGC  CCGGGTGCC  GATGCCAGG
551 CGCAGGCGGT  AATAGTCTGC  CGTGCCGAGT  TTTGCCTGAA  TGTCTTTCAA
601 GCCGTTGTGT  CCGCCGTTGC  CGCCGCCGAG  TTTGAATTTG  ATCCGTCCGC
651 AGGGAATGTC  GAGTTCGTGC  TGGACGACGA  GGATTTCTTC  GGGTTTGATT
701 TTGTAGAACT  GTGCAAGCGC  GGCAACTGCC  TGTCCGGAAC  GGTTCATGAA
751 CGTGGCAGGT  TTGAGCAGCC  AAACGTCGCC  GTCGGGCAGG  GCGGCACGGG

```

986

```

801 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCCATTTT
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTT
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGTCTGAATG CTGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTGATCAA CAGCGGGCGG TACACTTCGA TGCGGTGCGC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1970; ORF 615>:

```

m615.pep Length: 372
1 MRKRRWRGFG SFEKQXVNAA CKPQCREQDK AVAWQIHACS SSSHVWHS LD
51 RRRNFP PRAA SISRQTAISS AEGASSMLHS XSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRC XRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSAVAAAE FEFDP SAGNV EFVVDDEDF FGFDFVELCKR GNCLSGTVHE
251 RGRFEQPNVA VGQGGTG DFA EEEEEFFKXS LPFPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCVX HDI FRVSVECC LK ASDGMVILL DFERVCGALLW
351 GRSTAGGTLR CGRRRAAACR L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m615/g615 86.8% identity in 371 aa overlap

```

m615.pep      10      20      30      40      50      60
MRKRRWRGFGSFEKQXVNAAACKPQCREQDKAVAWQIHACSSSSHVWHS LDRRNFP PRAA
| ||| || ||||:| ::|| |||| :| :||| |:| | |||||: ||||
g615          10      20      30      40      50      60
MWKRRRRRGVGSFEEQRIDAAGKPQCGKQAEAVARQLHAASSSSHVWQILD RRRNLPPRAA

m615.pep      70      80      90      100     110     120
SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL
|:| |:| |||: ||||| ||||| ||||| ||||| ||||| ||||| |||||
g615          70      80      90      100     110     120
SMSRHCATSSADGASSMLHSYSRKSRSVSSMTGMDSVWISCLSSFM TVRIRKSGKCR LKGL

m615.pep     130     140     150     160     170     180
QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRCXRTGFVQDIADDEVAVARVA
||| :||| ||||| ||||| ||||| ||||| ||| :|||: ||||| ||
g615          130     140     150     160     170     180
QTALDYLLCRKRVASSHLPEMMSGTACRDLATASSICRRCFRARFVQDVADDEVAVAGVA

m615.pep     190     200     210     220     230     240
DAEAQAVIVCRAEFCLNVFQAVVSAVAAAEFEFDP SAGNV EFVVDDEDF FGFDFVELCKR
||||| ||||| ||||| ||||| ||||| ||||| ||||| :||| ||||| |||||
g615          190     200     210     220     230     240
DAEAQAVIVCRAEFCLNVFQAVVSAVAAAEFEFDP SARDVEFVVDDEDF FGFDFVELCKR

m615.pep     250     260     270     280     290     300
GNCLSGTVHERGRFEQPNVAVGQGGTG DFA EEEEEFFKXS LPFPRQFVEE PKTRIVACLF
|| ||||| ||||| :||| :||| ||||| ||||| ||||| ||||| ||||| ||
g615          250     260     270     280     290     300
GNRLSGTVHERGRFEQPNIAVGQGGAGNFAEEEEFFKRS LPFPRQFVEE PKARIVAGLF

m615.pep     310     320     330     340     350     360
VFFARVAQADNHFDCVX HDI FRVSVECC LK ASDGMVILL DFERVCGALLWGRSTAGGTLR
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g615          310     320     330     340     350     360
VFFARVAQADNHFDCVR HDI FRVSVECC LK ASDGMVILL DFERVCGALLWGRSTAGGTLR

m615.pep      370
CGRRRAAACRLX
|||||
g615          370
CGRRRAAACRLX
370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1971>:

```
a615.seq
1   ATGCGGAAAC GGC GCGCGGCG CGGTGTCGGC AGCTTTGAAG AGCAGCGAAT
51  AGATGCCGCC GGCAAACAC AATGCGGAAA GCAGGCTGAA GCGGTTGCGC
101 GGCAGCTTCA TGCCGCCTCC TCGTCCAGCC ACGTTTGGCA GATTTTGGAC
151 AGGCGCAGGA ATTTGCCGCC GCGTGCAGCA AGTATGTCGC GCCATTGTGC
201 CACTTCTTCG GCGGATGGTG CGTCGTCGAT GCTGCATTGC TACAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTCGGTTTG GATAAGCTGC
301 TTGAGTTCGG TCATGACTGT TCGGATATGG AAATCGGGAA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CGGGTCATTT GCTGTGCAGG AAGCGGGTTG
401 CCTCTTCACA TTTGCCGGCA AGGATGTCGG GTATGGCTTG CAGGGATTG
451 GCGACGGCAT CGTCAATCTG TCGGCGGTG. TTCCGTACTG GGTTTGTTC
501 GGACATAGCC GACGACGAGG TTGCGGTCGC CCGGGTGGCC GATGCCGAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTTGCCTGAA TGTCTTTCAA
601 GCCGTTGTGT CCACCGTTGC CGCCGCCGAG TTTGAATTG ATCCGTCCGC
651 AGGGAATGTC GAGTTCGTCG TGGACGACGA GGATTTCTTC GGGTTTGATT
701 TTATAAACT GCGCAAGGGC GGCAACTGCC TGTCCGGAAC GGTTTCATGAA
751 CGTGGTTCGG TTGAGCAGCC AGACATCGCC GTCGGGCAGG GTAGCACGGG
801 GACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCCATTTC
851 CAGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGCCGAATG CCGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTGATCAA CAGCGGGCGG TACACTTCGA TGCGGTCGCC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1972; ORF 615.a>:

```
a615.pep
1   MRKRRRRGVG SFEEQRIDAA GKPQCGKQAE AVARQLHAAS SSSHVWQILD
51  RRRNLPPRAA SMSRHCAATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRX FRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSTVAAAE FEFDPAGNV EFVVDDEFF GFDFIKLRKG GNCLSGTVHE
251 RGRLEQPDIA VGQGSTGDEA EEEEEFFK*S LPFPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCV*HDI FRVSAECLRK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAAACR L*
```

m615/a615 90.3% identity in 371 aa overlap

	10	20	30	40	50	60
m615.pep	MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAWQIHACSSSSHVWHS�DRRRNFPPRAA					
				:		
a615	MRKRRRRGVGSFEEQRIDAAAGKPQCGKQAEAVARQLHAASSSSHVWQILDRRRNLPRAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m615.pep	SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
	: :					
a615	SMSRHCAATSSADGASSMLHSYSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m615.pep	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXRTGFVQDIADDEVAVARVA					
a615	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXFRTGFVQDIADDEVAVARVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m615.pep	DAEAQAVIVCRAEFCLNVFQAVVSAAAEFEFDPAGNVFVVDDEFFGFDFVELCKR					
a615	DAEAQAVIVCRAEFCLNVFQAVVSTVAAAEFEFDPAGNVFVVDDEFFGFDFIKLRKG					
	190	200	210	220	230	240
	250	260	270	280	290	300

988

```

m615.pep  GNCLSGTVHERGRFEQPNVAVGQGGTGDFAEFFFFFKXSLPFRQFVEEPKTRIVACLF
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a615       GNCLSGTVHERGRLEQPDIAVGQGSTGDFAEFFFFFKXSLPFRQFVEEPKTRIVACLF
           250      260      270      280      290      300

           310      320      330      340      350      360
m615.pep  VFFARVAQADNHFDVCVXHDFRVSVECCLKASDGMVILLDFERVCGALLWGRSTAGGTLR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a615       VFFARVAQADNHFDVCVXHDFRVSAECLRKASDGMVILLDFERVCGALLWGRSTAGGTLR
           310      320      330      340      350      360

           370
m615.pep  CGRRRAAACRLX
           |||||:|||||
a615       CGRRRAAACRLX
           370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1973>:

```

g616.seq
1  atgtcgaaCA CAATCAAAAT GGTGTGTCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACCCGCCACA ATGCGGGCTT TTGGTTCCTC GACGAACTGG
101 CGTGGAAATG GAAGGCTTCG TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTTGCCCGCG CGCCCTGCC CGACGGCGAT GTTTGGCTGC TCAAACCGGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGGT TGCCGCGCTT GCACAGTTCT
251 ACAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATC
301 CCTTGGCGAC GGATCAAATT CAAACTCGGC GcgggcaacG gcgGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGG CACGGcagac tattaCCGCC
401 TCGCCTCGG CATCGgcaC CCCGGCgacc gcaacctCGT CGtcggtac
451 gtcttgAAcA aaccgagcgc gGaagcaccg Ccgggcaatc gacgatgCCG
501 TCGccaaATC CCTGcaggcc gtaccCGACA TcaTTTCCGg caaatgggaa
551 gaggcaacgc gcTTCCTGCA CAGCAAATAA TccaatGCCG TCTGaagccc
601 ttTcagacgg cattttcccg atttccgTAT CcGAaCagtc atgaacgaac
651 tcaagcAGcT tatCCAAAcg gaaTccatcC ccgtcatcga agaaaccctc
701 gatttctcgc tGTACGAATG cagcAtcgac gaagCACCgt ccgccgaaga
751 agtggcacaa TGcgcgacac tactTGccgc acgcgGcgGC AAATtCtTgc
801 gcctgtccaa aatctgcCaa aCGTGGcTGG ACgAGGAGGC GGCatgAAgc
851 tGCCGcgcaA CGgcttcaGc ctgctTCCG CATTGTGGTT TGCCGGCGGc
901 atctAtTcGc tgctcttcaA AGCTGccgaC ACCGCGCCGC CGCCGTtTCC
951 ACATtTcgaC AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAaatCTTgt
1001 tTctGGCCAA AGCATTCAAA ACCGGAaAAC TTCCCATCCC CTACCGCAGC
1051 CTGATTGCGT TCGCCTTCTG TTTTGGCCGTC GGCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGCGAA CCGGCAGTTT GGGCGATGTC CTTGCCgACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTGCCG CGCGTTCTGC CTGCCGcccg
1201 gactaa

```

This corresponds to the amino acid sequence <SEQ ID 1974; ORF 616.ng>:

```

g616.pep
1  MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEKKKFFGE
51  VARAALPDGD VWLLKPATFM NRSGQVAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHNGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVGy
151 VLNKPSAEAP PANRRRRIQI PAGRTRHHFR QMGRGNALPA QQIIQCRLKP
201 FQTAFSRFPY PNSHRTQAA YPNGIHPRHR RNPRFPVRM QHRRSTVRRR
251 SGTMARHTCR TRRQIPAPVQ NLENVAGRGG GMKLPRNRFs LLSALWFAGG
301 IYSLLFKAAD TAPPPFPFHD KAAHLALFFA QILFLAKAFK TGKLPiPYRS
351 LIAFAFCFAV GSECAQWFT ATRTGS LGDV LADLTGAALA LFAARSACRP
401 D*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1975>:

```

m616.seq
1  ATGTCAAACA CAATCAAAAT GGTGTGTCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAACTGG
101 CGTGGAAATG GAAGGCTTCA TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTTGCCCGTG CGCCCTGCC CGACGGCGAC GTTTGGCTGC TCAAACCTGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGAGT TGCCGCGCTT GCACAGTTCT
251 ACAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCTTGGCGAC GGATCAAATT CAAACTCGGC GCGGCAACG GCGGACACAA
351 CGGCTTGAAA GACATTcAGG CAAACTCGG CACGGCAGAC TATTACGCC
401 TCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCTGAACA AACCCAGTAC GGAACA.CCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGGGAA

```

```

551 GAAGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCTC
701 GATTTCTCTG TCTACGAATG CAGCATAGAC GATGCCCCCT CCGCCGAAGA
751 AATTGCCGTT TGGCGCGATA TGCTGGCCGC ACGCGCGCGA AAATTCCTGC
801 GCCTATCCAA ACTATGCCAG ACATGGCTTG AAGAGGAACA AGCATGAATC
851 TGCCACGCAA CCGCTTTATC CTGCTCTCGG CATTGTGGTT TGCAGGCAGC
901 ATTTACTCAC TGCTTTTCAA AGCTGCCGAA ACCGCGCCAC CGCCTTTTCC
951 GCATTTTTCG AAAGTGGCGC ACCTCGCCCT GTTTTTCGCA CAAATCTGGC
1001 TTCTGACCAA AGCATTGAGA ACCGACAACC GCCCATCCC CTATCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTCCGCCCT TTCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTC CTTGCCGACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTACCG CGCGAGCTGC CTGCCGCCCG
1201 GACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1976; ORF 616>:

**m616.pep**

```

1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51 VARAALPDGD VWLLKPATFM NRSGQAVAAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGGHNLK DIQAKLGTD YRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTDXRRCRQI PASHTRHPCR QMGRSNPLPA QMTRCRLKP
201 FQTACSRFPY PSHDRTQAA YPNRIHPRHR RNPFPALRM QHRRCLRRR
251 NCRLARYAGR TRRKIPAPIQ TMPDMAXRGT SMNLPRNRFI LLSALWFAGS
301 IYSLLFKAAE TAPPPFPHFD KVAHLALFFA QIWLTKAFR TDNRPIPYRS
351 LMVFALCFAL FSECAQAWFT ATRTGS LGDV LADLTGAALA LFTARAACRP
401 D*

```

**m616/g616** 86.0% identity in 401 aa overlap

m616.pep	10	20	30	40	50	60
	MSNTIKMVVGLGNGPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
g616	MSNTIKMVVGLGNGPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
	10	20	30	40	50	60
m616.pep	70	80	90	100	110	120
	VWLLKPATFMNRSGQAVAAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGNGGGHNLK					
g616	VWLLKPATFMNRSGQAVAAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGNGGGHNLK					
	70	80	90	100	110	120
m616.pep	130	140	150	160	170	180
	DIQAKLGTDYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRQIPASHTRHPCR					
g616	DIQAKLGTDYYRLRLGIGHPGDRNLVVGYYLNKPSAEAPPANRRRCRQIPAGRTRHHFR					
	130	140	150	160	170	180
m616.pep	190	200	210	220	230	240
	QMGRSNPLPAQOMTRCRLKPFQTACSRFPYPNSHDRTQAAYPNRIHPRHRRNPRFPALRM					
g616	QMGRGNALPAQQTICRLKPFQTAFSRFPYNSHRTQAAYPNGIHRHRRNPRFPVVRM					
	190	200	210	220	230	240
m616.pep	250	260	270	280	290	300
	QHRRCLRRRNCRLARYAGTRRKIPAPIQTMPDMAXRGTSMNLPRNRFILLSALWFAGS					
g616	QHRRSTVRRSGTMAHTCRTRQIPAPVQNLPNVAGRGGMKLPNRNFSLLSALWFAGG					
	250	260	270	280	290	300
m616.pep	310	320	330	340	350	360
	IYSLLFKAAETAPPPFPHFDKVAHLALFFAQIWLTKAFRTDNRPIPYRSLMVFALCFAL					
g616	IYSLLFKAADTAPPPFPHFDKAAHLALFFAQILFLAKAFKTKGLPIPYRSLIAFAFCFAV					
	310	320	330	340	350	360
m616.pep	370	380	390	400		
	FSECAQAWFTATRTGSLGDVLADLTGAALALFTARAACRPDX					
g616	GSECAQAWFTATRTGSLGDVLADLTGAALALFAARSACRPDX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1977>:



990

```

a616.seq
  1 ATGTCAAACA CAATCAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
 51 ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAAC TGG
101 CGTGGAATG GAAGGCTTCA TTTAAGAAG AAAAAAATT CTTGCGCGAA
151 GTCGCCCGTG CTACCCGCGC CGACGCGGAT GTCTGGCTGC TCAAGCCGAC
201 CACGTTTCATG AACCGTTCCG GACAGGCACT TGCCGCCCTT GCGCAGTTTT
251 ATAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCTGCGGAC GGATCAAATT CAAACTCGGC GCGGCAACG GTGGACACAA
351 CGGCTTGAAA GACATTCAGG CAAACTCGG CACGGCAGAC TATTACCGCC
401 TCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCAGTAC GGAA CACCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCGACA TCCTTGCCGG CAAATGTGAA
551 GAGGCAACCC GCTTCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCTC
701 GATTTCTGTC TGTACGAATG CAGCATCGAC GACGCACCAT CCGCCGAAGA
751 AGTGCACAA TGGCGCGACA TACTTGCCGC ACGCGCGCGC AAATTCCTGC
801 GCCTGTCCAA AATCTGCCAA ACGTGGCTGG ACGAGGAGGC GGCATGAAGC
851 TGCGCGCAA CCGCTTCAGC CTGCTTCCG CATTGTGGT TGCCGGCGGC
901 ATCTATTGCG TGCTCTCAA AGCTGCCGAC ACCGCGCCGC CGCCGTTTCC
951 GCATTTGAC AAAGCAGCAC ACCTGCCCCT GTTTTTCGCA CAAATCTGGC
1001 TTTTGACAA AGCATTCAAA ACCGAAAAC TTCCCATCCC CTACCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGATTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTT CTTGCCGATA
1151 TGGCAGGTAC GGTCTCGCA CTCTTGCCG CCCGCGCCGC CGACCGCCGC
1201 GACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1978; ORF 616.a>:

```

a616.pep
  1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
 51 VARATLPDGD VWLLKPTTFM NRSGQAVAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHNGLK DIQAKLGTA YRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTD*RCRRQI PASHTRHPCR QM*RGNPLPA QMTRCRLKP
201 FQTACSRFFY PNSHRTQAA YPNRIHPRHR RNPRFPAVRM QHRRRTIRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRG GMKLPRNRF LLSALWFAGG
301 IYSLLFKAAD TAPPPFPFHD KAAHLALFFA QIWLTKAFK TGKLPIPYRS
351 LMVFALCFAL FSECAQA*FT ATRTGS LGDV LADMAGTVLA LFAARAADRP
401 D*

```

m616/a616 90.0% identity in 401 aa overlap

```

              10      20      30      40      50      60
m616.pep      MSNTIKMVVGLG NPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD
a616           MSNTIKMVVGLG NPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARATLPDGD
              10      20      30      40      50      60

              70      80      90      100     110     120
m616.pep      VWLLKPATFMNRSGQAVAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGNGGHNGLK
a616           VWLLKPTTFMNRSGQAVAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGNGGHNGLK
              70      80      90      100     110     120

              130     140     150     160     170     180
m616.pep      DIQAKLGTADYYRLRLGIGHPGDRNLVVG YVLNKPSTEXPPTDXRCRRQIPASHTRHPCR
a616           DIQAKLGTADYYRLRLGIGHPGDRNLVVG YVLNKPSTEXPPTDXRCRRQIPASHTRHPCR
              130     140     150     160     170     180

              190     200     210     220     230     240
m616.pep      QMGRSNPLPAQMQMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRNRNPRFPALRM
a616           QMXRGNPLPAQMQMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRNRNPRFPAVRM
              190     200     210     220     230     240

              250     260     270     280     290     300

```

991

```

m616.pep  QHRRCP LRRRNCRLARYAGRTRRKIPAPIQTMPDMAXRGTS MNLPNRNFILLSALWFAGS
a616       QHRRRTIRRRSGT MARHTCRTRRQIPAPVQNL PNVAGRGGGMKLPNRNFSLLSALWFAGG
           250      260      270      280      290      300

           310      320      330      340      350      360
m616.pep  IYSLLFKAETAPPPFP HFDKVAHLALFFAQI WLLTKAFRTDNRPI PYRSLMVFALCFAL
a616       IYSLLFKAADTAPPPFP HDKAAHLALFFAQI WLLTKAFKTGKLPI PYRSLMVFALCFAL
           310      320      330      340      350      360

           370      380      390      400
m616.pep  FSECAQAWFTATRTGSLG DVLADLTGAALALFTARAACRPDX
a616       FSECAQAXFTATRTGSLG DVLADMAGTVLALFAARAADRPDX
           370      380      390      400

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1979>:

```

g619.seq
1  ATGCCGTCTG AAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCCGTT
51  GCGGGTCGCC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
101 TCAACGTCAA AGGAGATTGG GACTTTGTCT TGCACCTGCG CCTGACCAAG
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACTCAACT
201 CTTCCAAACG CTGACCAACA ACCCGATTCT GACCCCTTCG ATTTTGGGTT
251 TCGATTGCGT GTATGTGTTT TTGCAGACCT TGCTGgtGTT TACGTtgcGC
301 GCGGTGGGCT ATAcatccct gccgttgacg gGCAAATTCG GCTTTGAACT
351 GGTTGTTATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCCGTC
401 AGGGCGGGCG CGATTTGCCG CACATGATT TAAATCGGCGT GATTTTCGGG
451 ATTTTGTTCG GCAGCCTTTC CTCGCTGCTT TCGCGCATGA TAGACCCCGA
501 AGAATTTACC GCCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
551 GCAGCGAGCT TTTAGGCATA GGCGCGCTGG TCCTGCTCGT CAGCGCGGCG
601 GTCGTTTGGC ACGAACGCTA CCGCTCGGAC GTACACCTTT TGGGGCGCGA
651 CCAAGCCGTC AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCCGT TGTCGGCCCCG
751 GTGAGCTTTT TCGGGCTTCT CGCCGCTCTG CTTGCCAACC ACTTTTCCcC
801 gtCCGTGCGC CATTCGCTCC GCCTGCcgat gacggtttGC gtcgGcgGCA
851 TCCTCTTGgt cggCggacaA ACCGTATTCG AACACTTCTT GGGCATGAag
901 gCggTATTAA GCGTGGTGGT cgAATTTGCG ggcggactcG TTTTCTCTA
951 TCTCGTTTAA AAACACAAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1980; ORF 619.a>:

```

g619.pep
1  MPSEKNIGFM AGSSRPLRVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
51  LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSL YVF LQTL LVFTFG
101 GVGYTSLPLT GKFGFELVVM MGSLLLFYT LIRQGGRLDLP HMLIGVIFG
151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVRSELLGI GALVLLVSAA
201 VVWHERYRSD VHLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG
251 VSFFGLLAAS LANHFSPSVR HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301 AVL SVVVEFA GGLVFLYLVL KHKK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1981>:

```

m619.seq
1  ATGCCGTCTG AAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGCCCCGTT
51  GTGGGTCGCC TTTGCGCTGT TGCTGGTTTC CTGCGTCCTG TTTATGACGC
101 TCAACGTCAA AGGCGATTGG GATTTTGTTC TGCAACTGCG GCTGACCAAA
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACGCAACT
201 CTTCCAAACG CTGACCAATA ATCCGATTCT GACCCCTTCA ATTTTGGGTT
251 TCGATTGCGT GTATGTGTTT TTGCAGACCT TGCTGGTGT TACGTTCGGC
301 GCGGTGGGCT ATGCTTCCCT GCCGTTGACG GGCAAATTCG GCTTTGAACT
351 GGTCGTCATG ATGGGCGGCT CGCTGCTGCT GTTCTACACG CTCATCAAAC
401 AGGGCGGACG CGATTGTGCG CGCATGATT TAAATCGGCGT GATTTTCGGG
451 ATTTTGTTCG GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGATCCCGA
501 AGAATTTACC GCCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
551 ACAGCGAGCT TTTGGGCATA GGCGCGCTGA TTCTGCTCGT CAGCGCGGCG
601 GTCGTTTGGC GCGAACGCTA CCGCTTGAC GTTTACCTTT TGGGGCGTGA
651 CCAAGCCGTC AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCCGT GGTCGGCCCC
751 GTAAAGCTTTT TCGGGCTTCT CGCCGCTCTG CTTGCCAACC ACTTTTCCcC
801 GTCGGTCAAA CATTCGCTCC GCCTGCCGAT GACGGTTTGT ATCGGCGGCA
851 TCCTCTTGgt CCGGCGACAG ACCGTGTTCT AACACCTGCT CGGTATGCAG

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901 GCAGTGTGA GCGTAGTAGT AGAATTGGCC GGCGGACTCG TTTTCCTCTA  
 951 TCTCGTTTAA AACACAAAA AATGA

This corresponds to the amino acid sequence <SEQ ID 1982; ORF 619>:

m619.pep  
 1 MPSEKNIGFM AGSSRPLWVA FALLLVSCVL FMTLNVKGDW DFVLQRLRLTK  
 51 LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLTVF LQTLLVFTFG  
 101 GVGYASLPLT GKFGFELVVM MGGSLLLFYT LIKQGGRDLS RMILIGVIFG  
 151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA  
 201 VVWRERYRLD VYLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG  
 251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC IGGILLVGGQ TVFEHLLGMO  
 301 AVLSVVVEFA GGLVFLYLVL KHKK\*

m619/g619 95.1% identity in 324 aa overlap

m619.pep	10	20	30	40	50	60
	MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQRLRLTKLAALLMVAYA					
g619	MPSEKNIGFMAGSSRPLRVAFALLLVSCILFMTLNVKGDWDFVLHLRLTKLAALLMVAYA					
	10	20	30	40	50	60
m619.pep	70	80	90	100	110	120
	VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLLVFTFGGVGYASLPLTGKFGFELVVM					
g619	VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLLVFTFGGVGYTSLPLTGKFGFELVVM					
	70	80	90	100	110	120
m619.pep	130	140	150	160	170	180
	MGGSLLLFYTLIKQGGRDLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
g619	MGGSLLLFYTLIRQGGRDLPMLILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
	130	140	150	160	170	180
m619.pep	190	200	210	220	230	240
	NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
g619	NTVRSELLGIGALVLLVSAAVVWHERYRSDVHLLGRDQAVNLGISYTRNTLWILLWIAAL					
	190	200	210	220	230	240
m619.pep	250	260	270	280	290	300
	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMO					
g619	VATATAVVGVPVSFFGLLAASLANHFSPSVRHSVRLPMTVCVGGILLVGGQTVFEHFLGMK					
	250	260	270	280	290	300
m619.pep	310	320				
	AVLSVVVEFAGGLVFLYLVLKHKKX					
g619	AVLSVVVEFAGGLVFLYLVLKHKKX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1983>:

a619.seq  
 1 ATGCCGCTCTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCCGTT  
 51 GTGGGTTGCC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC  
 101 TCAACGTCAA AGGCGATTGG GATTTTGTTT TGCACCTGCG CCTGACCAAG  
 151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGGTT CGACCCAGCT  
 201 TTTTCAAACG CTGACCAACA ATCCGATTCT GACCCCTTCG ATTTGGGTT  
 251 TCGATTTCGT GTATGTGTTT TTGCAGACCT TGCTGGTGTT TACGTTCCGC  
 301 GCGGTGGGCT ATGCTTCCCT GCCGTGACG GGCAAATTCG GCTTTGAACT  
 351 GGTCTGTTATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCAAAC  
 401 AGGGCGGGCG CGATTTCGCG CGTATGATTT TAATCGGCGT GATTTTCGGG  
 451 ATTTTGTTC GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGACCCCGA  
 501 AGAATTTACG GCGGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC  
 551 ACAGCGAGCT TTTAGGCATA GGCGCGCTGA TTCTGCTCGT CAGCGCGGCG  
 601 GTCGTTTGGC GCGAACGCTA CCGCTTGAC GTACACCTTT TGGGCGCGCA  
 651 CCAAGCCATA AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC  
 701 TGCTTTGGAT TGCCGCGCTG GTGGCGACGG CGACCGCCGT TGTCGGCCCC

993

```

751 GTAAGCTTTT TCGGGCTTCT CGCCGCCTCG CTTGCCAACC ACTTTTCCCC
801 GTCGGTCAAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT GTCGGCGGCA
851 TCCTCTTGGT CGGCGGACAG ACCGTATTCT AACACTTCTT GGGCATGAAG
901 GCGGTATTAA GCGTGGTGGT CGAATTGCG GCGGGA CTCT TTTCTCTA
951 TCTCGTTTTA AGACACAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1984; ORF 619.a>:

```

a619.pep
1  MPSEKNIGFM AGSSRPLWVA FALLLVSCIL FMTLNVKGDW DFLVHLRLTK
51  LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLTVF LQTLVFTFG
101 GVGYASLPLT GKFGFELVVM MGSLLLFYT LIKQGGRLDP RMILIGVIFG
151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
201 VVWRERYRLD VHLLGRDQAI NLGISYTRNT LWILLWIAAL VATATAVVG
251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301 AVLSVVVEFA GGLVFLYLVL RHKK*

m619/a619 97.2% identity in 324 aa overlap

m619.pep      10      20      30      40      50      60
MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQRLRLTKLAALLMVAYA
a619          10      20      30      40      50      60
MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLHRLRLTKLAALLMVAYA

m619.pep      70      80      90      100     110     120
VGVSTQLFQTLTNNPILTPSILGFDSLTVFLLQTLVFTFGGVGYASLPLTGKFGFELVVM
a619          70      80      90      100     110     120
VGVSTQLFQTLTNNPILTPSILGFDSLTVFLLQTLVFTFGGVGYASLPLTGKFGFELVVM

m619.pep     130     140     150     160     170     180
MGSLLLFYTLIKQGGRLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
a619         130     140     150     160     170     180
MGSLLLFYTLIKQGGRLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF

m619.pep     190     200     210     220     230     240
NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL
a619         190     200     210     220     230     240
NTVHSELLGIGALILLVSAAVVWRERYRLDVHLLGRDQAINLGISYTRNTLWILLWIAAL

m619.pep     250     260     270     280     290     300
VATATAVVGFPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ
a619         250     260     270     280     290     300
VATATAVVGFPVSFFGLLAASLANHFSPSVKHSVRLPMTVCVGGILLVGGQTVFEHFLGMK

m619.pep     310     320
AVLSVVVEFAGGLVFLYLVLKHKXX
a619         310     320
AVLSVVVEFAGGLVFLYLVLRHKKX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1985>:

```

g620.seq
1  ATGAAGAAAA CCCTGTTGGc AATTGTTGCC gtTTTCGCCT TAAGTGCCTG
51  CCGGCagcg gaAGaggcac cgccgCCTTT ACCCCGGCAG AtTAGCGacc
101 gttcggtcg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1986; ORF 620.ng>:

g620.pep

```

1  MKKTLAIVA VFALSACRQA EEAPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51 KAQIFLNGKP DQPWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGGAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1987>:

m620.seq

```

1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
51 CCGGCAGGCG GAAGAGGGAC CGCCGCCTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCGAGA TTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTTC GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTGTTCGGT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1988; ORF 620>:

m620.pep

```

1  MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51 KAQIFLNGKP DQPWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGGAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*

```

m620/g620 97.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g620	MKKTLAIVAVFALSACRQAEEAPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWMDAKKAFYVIDS					
g620	DQPWFSTVQMFGYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
g620	GFIGGGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1989>:

a620.seq

```

1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
51 CCGGCAGGCG GAAGAGGGAC CGCCGCCTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCGAGA TTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTTC GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTGTTCGGT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1990; ORF 620.a>:

a620.pep

```

1  MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51 KAQIFLNGKP DQPWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGGAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*

```

995

m620/a620 100.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLLAIVAVSALSACRQAE	EGPPPLPRQISDRSVGHYCS	MNLTEHNGPKAQIFLNGKP			
a620						
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMF	GYTKLPPEEPKGI	RVYVTDMG	NVTDW	TNP	NADTEWMDAKKAFYVIDS
a620						
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGMAEDALP	FGNKEQAEKFAK	DKGKGVVGFDD	MPD	TYIFKX	
a620						
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1991>:

g622.seq

```

1  ATGCAactta  ccgctgtcgg  ACTCAATCAT  CAAACCGCAC  CTTTAAGCAT
51  ACGGGAaaag  ctggCGTTTG  CCGCCGCCGC  CCTGCCAGAA  gccgTccgCA
101 ATCTTGCCCG  AAGCAATGCG  GCAACGGAGG  CGGTAATCCT  TTCTACCTGC
151 AACCGCACCG  AGCTTTACTG  CGTCGGCGAT  TCGGAAGaaa  TCATCCGATG
201 GCTTGCCGAT  TACCACAGTT  TGCCGATTGA  AGAAATCCGT  CCGTATCTGT
251 ACACGCTGGA  TATGCAGGAA  ACCGTGCGCC  ACGCCTTCCG  CGTGCCTGTC
301 GGCTTGGATT  CGATGGTTTT  GGGCGAGCCG  CAGATTTTGG  GGCAGATTAA
351 AGATGCGGTG  CGTGCGGCTC  AAGAACAGGA  AAGTATGGGG  GCAAAACTCA
401 ATGCCCTGTT  CCAAAAAACC  TTTTCCGTTG  CTAAAGAAGT  CCGTACCGAT
451 ACCGCTGTCT  GCGAAAATTC  GGTTCGATG  GCTTCCGCGT  CCGTCAAGTT
501 GCGGGAACAG  ATTTTCCCG  ACATCGGCGA  TTTGAACGTA  TTGTTTATCG
551 GCGCAGGCGA  AATGATTGAG  CTGGTTGCCA  CTTATTTTGC  CGCCAAAAAT
601 CCCCggctGA  TGACGGTTGC  CAACCGGAGC  CTGGCGCGTG  CACAGGAGTT
651 GTGCGACAAG  CTCGGTGTTA  ACGCCGAACC  GTGCCTGCTG  TCCGATCTGC
701 CTGCCATTCT  GCACGATTAC  GACGTGGTGG  TTTCTTCAAC  GGCAGGCCAG
751 CTTCCGATAG  TCGGCAAAGG  CATGGTCGAA  CGCGCATTGA  AACAGCGTCA
801 GAGTATGCCG  TTGTTTATGC  TTGACTTGGC  CGTGCCGCGC  GATATTGAAG
851 CGGAAGTCGG  CGATTTGAAC  GATGCGTATC  TTTATACGGT  GGACGATATG
901 GTCAACATCG  TCCAAAGCGg  caaggaggca  aggcagaaag  ccgccgcCgc
951 cgccgaaacg  ctggTGTCGG  AAAAGGTTGC  CGAATTTGTG  AGGCAGCAGC
1001 AGGCGAGGCA  GagggttcCG  CTGATTAAGG  CCTTGC GGGA  CGAGGGCGAG
1051 AAAGCGCGCA  AGCAGGTGTT  GGAATATGCG  ATGAAACAGC  TTGCCAAAGG
1101 CGcaacCGCG  AAGaggttt  TGgaacggct  gtccgtcCAA  CTGACCAACA
1151 AGCTGCTGCA  TTCGCCAACT  CAAACCTTGA  ATAAGGCGGG  GGAAGAAGAT
1201 AAAGatttGG  TTCATGCCgt  cGCGCAGATt  tatcatttGG  ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1992; ORF 622.ng>:

g622.pep

```

1  MQLTAVGLNH  QTAPLSIREK  LAFAAAAALPE  AVRNLARSNA  ATEAVILSTC
51  NRTELYCVGD  SEEIIRWLAD  YHSLPIEEIR  PYLYTLDMQE  TVRHAFRVAC
101 GLDSMVLGEP  QILGOIKDAV  RAAQEQUESM  AKLNALFQKT  FSVAKEVRTD
151 TAVGENSVSM  ASASVKLAEQ  IFPDIGDLNV  LFIGAGEMIE  LVATYFAAKN
201 PRLMTVANRT  LARAQELCDK  LGVNAEPCLL  SDLPAILHDY  DVVVSSTASQ
251 LPIVQGMVE  RALKQRQSMP  LFMLDLAVPR  DIEAEVGLDN  DAYLYTVDDM
301 VNIVQSGKEA  RQAAAAAET  LVSEKVAEFV  RQQGGRQSV  LIKALRDEGE
351 KARKQVLENA  MKQLAKGATA  EEVLERLSVQ  LTNKLLHSPT  QTLNKAGEED
401 KDLVHAVAQI  YHLDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1993>:

m622.seq

```

1  ATGCAACTTA  CCGCTGTCTGG  ACTCAATCAT  CAAACCGCAC  CTTTAAGCAT
51  ACGGGAaaaag  CTGGCGTTTG  CCGCCGCCGC  CCTGCCTAAA  GCCGTCCGCA
101 ATCTTGCCCG  AAGCAATGCG  GCAACGGAGG  CGGTAATCCT  TTCTACCTGC
151 AACCGCACCG  AGCTTTACTG  CGTCGGTGAT  TCGGAAGAAA  TCATCCGATG
201 GCTTGCCGAT  TACCACAGTT  TGCCGATTGA  AGAAATCCGT  CCGTATCTGT
251 ACGCGCTGGA  TATGCAGGAG  ACTGTGCGCC  ATGCTTTCCG  CGTGCCTGTC

```

```

301 GGGCTGGATT CGATGGTGT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCCGTT AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCCGTTG CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAAACTC GGTTTCCATG GCTTCCGCTT CCGTCAAATT
501 GGCGGAACAG ATTTTCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCC GGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTAGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTTG TCGGCAAAGG CATGGTGGAG CGTGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTCATGC TTGATTGGC AGTGGCCGCT GACATTGAAG
851 CGGAAGTCGG CGATTGAAT GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCCG AGAAAGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCCG TTGATTAAGG CGTTGCGGGA CGAGGCGCAG
1051 AAAGCGCGCA AACAGGTGTT GGAAAATGCC ATGAAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGGAACGGCT GTCCGTCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTTGG TTCATGCCGT CGCGCAGATT TATCATTTGG ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1994; ORF 622>:

**m622.pep**

```

1  MQLTAVGLNH QTAPLSIREK LAFAAAAALPK AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYALDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQUESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHDY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGDIN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVPL IKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*

```

**m622/g622** 98.8% identity in 415 aa overlap

	10	20	30	40	50	60
m622.pep	MQLTAVGLNHQTAPLSIREKLAFAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD					
g622	MQLTAVGLNHQTAPLSIREKLAFAAAALPEAVRNLARSNAATEAVILSTCNRTELYCVGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m622.pep	SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
g622	SEEIIRWLADYHSLPIEEIRPYLYTLDQMOTVRHAFRVACGLDSMVLGEPQILGQIKDAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m622.pep	RVAQEQUESMGKKLNALFQKTFSSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
g622	RAAQEQUESMGAKLNALFQKTFSSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
g622	LFIGAGEMIELVATYFAAKNPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPFLMLDLAVPRDIEAEVGDINDAYLYTVDDM					
g622	DVVVSSTASQLPIVGKGMVERALKQRQSMPFLMLDLAVPRDIEAEVGDINDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
g622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
g622	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					

370 380 390 400 410

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1995>:

```
a622.seq
1  ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAGAG CTGGCGTTTG CCGCGGCCTG CCTGCCCGAA GCCGTCCGCA
101 ATCTTGCCCC AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGTACCG AGCTTTACTG TGTAGGTGAT TCGGAAGAAA TCATCCGTTG
201 GCTCGCAGAC TATCACAGCC TTCCCATAGA AGAAATCAGC CCCTACCTTT
251 ATACTTTGGG GATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC
301 GGCTTGGAAT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCGGTC AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTCTGTTG CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACTC GGTTCCTATG GCTTCCGCTT CCGTCAAGTT
501 GGCAGAGCAG ATTTTCCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GTGCGGGTGA GATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCC GGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTTT GCATGAGTAC GACGTGGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTG TCGGCAAAGG TATGGTGGAG CGCGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGA GACATTGAGG
851 CGGAAGTCGG AGATTTGAAC GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCCG AGAAGGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCCG TTAATCAGGG CATTGAGGGA TGAGGGAGAG
1051 AAAGCGCGCA AACAGGTCTT GGAAAATGCG ATGAAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGGAAAGGCT GTCGATCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTTGG TTCACGCCGT CGCGCAGATT TATCATTTGG ACAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1996; ORF 622.a>:

```
a622.pep
1  MQLTAVGLNH QTAPLSIREK LAFAAACLPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIS PYLYTLGMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHEY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGD LN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVL LIRALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLRLRSIQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*
```

m622/a622 98.1% identity in 415 aa overlap

```

10      20      30      40      50      60
m622.pep  MQLTAVGLNHQTAPLSIREKLAFAAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD
          |||:|||||
a622      MQLTAVGLNHQTAPLSIREKLAFAAACLPEAVRNLARSNAATEAVILSTCNRTELYCVGD
          10      20      30      40      50      60

70      80      90      100     110     120
m622.pep  SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
          |||:|||||
a622      SEEIIRWLADYHSLPIEEISPYLYTLGMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
          70      80      90      100     110     120

130     140     150     160     170     180
m622.pep  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
          |||:|||||
a622      RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
          130     140     150     160     170     180
```



998

	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
a622	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHEY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDAYLYTVDDM					
a622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
a622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIRALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVOLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
a622	MKQLAKGATAEEVLERLSIQLTNKLHSPQTLNKAGEEDKDLVHAVAQIYHLDKX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1997>:

## g624.seq

```

1  ATGATCCGTT ATCTTTTAAT TGCCTGCGGC GGCATCTCCC TGCTGTTGGG
51  GATAATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTAC
101 TCTCCGCCGC CTGCTGGGCA AAGGCAtccc cgcgcTTTCa ccgCTGGCTG
151 CACcgGCacc gCTATTTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTCCCG CGCAAAGCCA AGATTTTCGC CATCAGCATG AtaaccgcAt
251 cctgcctcat gatctTTtgg CattTTCCCC aacnctggtg ggteGGGGCG
301 GTTTCATCGG TTTTTTGTTC CCTTGTcacc ATacggatgt gGcacAGacc
351 cgaatCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1998; ORF 624.ng>:

## g624.pep

```

1  MIRYLLIACG GISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM ITASCLMIFW HFPQXWWVGA
101 VSSVFCSLVT IRMWHRPES*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1999>:

## m624.seq

```

1  ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCC TACTGTTGGG
51  TATCATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTGC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTTA CCGCTGGCTG
151 CACCGGCACC GCTATTTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTCCCG CGCAAAGCCA AAATATTTCGC CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTGTG CAGTTTCCCC AACGCTGGTG GGTGGGGCGG
301 GTTTCATCGG TTTTTTGTTC CCTTGTGCGC ATATGGATGT GGCGCAGGCC
351 CGAATCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2000; ORF 624>:

## m624.pep

```

1  MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFYRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRRPES*

```

m624/g624 91.6% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACGCISLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV					
g624	MIRYLLIACGGISLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFHRWLHRHRYFGPMV					
	10	20	30	40	50	60

999

	70	80	90	100	110	120
m624.pep	HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX					
	:     :     :     :     :     :					
g624	HNWEQNGAVPRKAKIFAISMITASCLMIFWHFPQXWWVGAVSSVFCSLVTIRMWHRPESX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2001>:

```
a624.seq
1  ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCT TGCTGTTGGG
51  TATCATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTGC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTCA CCGCTGGCTG
151 CACCGGCACC GCTATTTTCG TCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTTCG CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTTGG CAGTTTCCCC AACGCTGGTG GGTGCGGGCG
301 GTTTCATCGG TTTTTTGTTC CCTGTGCGCC ATATGGATGT GCGCAGGCC
351 CGAATCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2002; ORF 624.a>:

```
a624.pep
1  MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRRPES*
```

m624/a624 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACGCISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV					
	:     :     :     :     :     :					
a624	MIRYLLIACGCISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFHRWLHRHRYFGPMV					
	10	20	30	40	50	60

	70	80	90	100	110	120
m624.pep	HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX					
	:     :     :     :     :     :					
a624	HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2003>:

```
a625.seq
1  ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAAACC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2004>:

```
g625.seq
1  atGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGtcTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC AttgCCGCGC
101 CGGtcgttCc CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATATATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAAACC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TGATTTTGcc
351 gTAA
```

This corresponds to the amino acid sequence <SEQ ID 2005; ORF 625.ng>:

```
g625.pep
1  MFATRKMKKM TMCTRRVRSW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA
```

1000

51 VLSLGVPFKS PQTkmppEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT  
101 KLNGMRKSNV QKAVILP\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2006>:

m625.seq  
1 ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT  
51 ACGGTTTGG TTGGCTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC  
101 CGGTCGTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG  
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC  
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT  
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC  
301 AAACGAAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC  
351 GTAA

This corresponds to the amino acid sequence <SEQ ID 2007; ORF 625>:

m625.pep  
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPmie ASAVPTASRA  
51 VLSLGVPFKS PQTkmppEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT  
101 KLNGMRKSNV QKAVILP\*

m625/g625 98.3% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
g625	MFATRKMKKMTMCTRRVRSWLAFFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTkmppEMVYRASSSRMKG IYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
g625	PQTkmppEMVYRASSSRMKG IYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

This corresponds to the amino acid sequence <SEQ ID 2008; ORF 625.a>:

a625.pep  
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPmie ASAVPTASRA  
51 VLSLGVPFKS PQTkmppEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT  
101 KLNGMRKSNV QKAVILP\*

m625/a625 100.0% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
a625	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTkmppEMVYRASSSRMKG IYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
a625	PQTkmppEMVYRASSSRMKG IYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2009>:

g627.seq  
1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTGAAA TCCTCGGCAG  
51 CCGTTACGCC CTGCAAAACC TTGTCCGCGA TGTATCCTG ATTACATTGA  
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA  
151 TTCAACTTTG AACCCTATCGC CGAAGTGGGC AAATCTTCC TCGGCATCTT  
201 CATCACCATC TTCCCCGTCC TGAGCATCTT GAAAGCAGGC GAGGCAGGCG  
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT  
301 AATACGATGT ATTTCTGGAT GAGCGGCATA TTGTCTGGCAT TCTTGGATAA  
351 CGCGCCCACT TATCTCGTGT TTTTCAATAT GGCGGGCGGC GATGCCCAAG  
401 CCTTAATGAC GGGTCCCTGT TTTTATTcgc TGCTGGCGGT TTCTAtgggT  
451 tCGGTATTCA TGGGCGCACT GaccTACATc gGCAAcgcac cgaactTCAT

1001

```

501 GGTcaaggcc aTTGCCGaaC agcgcgGCgt accgaTGCcg actTTCTTcc
551 ggtaTAtgat gtggtcggtc gcCTTCCTGa caCCCGTCTT CatcgTACAT
601 ACCTCgtCT TTTTCgTttt cAAACTACTg taa

```

This corresponds to the amino acid sequence <SEQ ID 2010; ORF 627.ng>:

```

g627.pep
  1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL ITLTAVSMAI TPKQVRAGNE
 51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
101 NTMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGPL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFRYMMWSV AFLTPVFIVH
201 TLVFFVFKLL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2011>:

```

m627.seq
  1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
 51 CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCACATCGC CGAAGTGGGC AAACCTCTCC TCGGCATCTT
201 CATCACCATC TTTCCCGTCC TGAGCATCTT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTGATGAC GGGTACCCTG TTTTCATTCG TGCTGGCGGT TTCTATGGGT
451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501 GGTC AAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTTCTTCG
551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
601 ACCCTTATCT TTTTCGTTTT CAAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2012; ORF 627>:

```

m627.pep
  1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
 51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGTL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
201 TLIFFVFKLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m627/g627 97.6% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVIL	IALTAVSMAITPKQVRAGNEFNFEPIAEVG				
g627	MSGLWKPEHPGFEILGSRYALQNLVRDVIL	ITLTAVSMAITPKQVRAGNEFNFEPIAEVG				
	10	20	30	40	50	60

1002

	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
g627	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINTMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVPMP					
g627	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVPMP					
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					
g627	TFFRYMMWSVAFLTPVFIVHTLVFFVFKLLX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2013>:

```

a627.seq
1  ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
51  CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
101 CCGCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCACATCG CGAAGTGGGC AAACCTCTCC TCGGCATCTT
201 CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTCGGCAT TCTTGATAA
351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GCGGGGCGGC GATGCCCAAG
401 CCTTGATGAC GGGTTCCTTG TTTTCATTCG TGCTGGCGGT TTCTATGGGT
451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501 GGTCAGGCC ATTGCCGAAC AGCGCGCGCT ACCGATGCCG ACTTTCTTCG
551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
601 ACCCTTATCT TTTTCGTTT CAAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2014; ORF 627.a>:

```

a627.pep
1  MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
51  FNFEPIAEVG KLFLGIFITI FVLVSILKAG EAGALGGVVS LVHDTAGHP
101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGSL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
201 TLIFFVFKLL *

```

m627/a627 99.5% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
a627	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
a627	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVPMP					
a627	YLVFFNMAGGDAQALMTGSLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVPMP					
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					

1003

a627                    TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX  
                          190                    200                    210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2015>:

g628.seq  
 1    ATGTGCGTGC   CACTCAAGCC   GGCAGGATGC   GGGCCGCCAA   ATTCATGTGT  
 51   TTCGATATTG   GCAGCATTTT   CAGACGGCAC   GTCTGCGCCT   GCTGCTTTAC  
 101   ACACATGGAT   TTTACGTTTCG   GTCAGGCGGC   TCAATACCAA   CAGGCCGCGT  
 151   TTGAAGTCTT   CGGCGGCTTC   TTTGATGATG   ACCGTAGGGT   CGGCAGCCAG  
 201   CGGATTGGTG   TCCATCGCAT   TGACGAAGAT   GGCGAACGGC   TCGGCATCTA  
 251   CGGCAGGGAT   TTTGCTGAAC   GGACGGGTGC   GAAGCGCAGT   CCATAAGCCT  
 301   GATTGAATCA   GGTGCGGCG   CACTTTTTCG   CTGCTCAATT   TTGCCAGCGC  
 351   TTCAGGTacg   TAG

This corresponds to the amino acid sequence <SEQ ID 2016; ORF 628.ng>:

g628.pep  
 1    MCVPLKPAGC   GPPNSCVSIL   AAFSDGTSAP   AALHTWILRS   VRRLLNTNRPR  
 51   LKSSAASLMM   TVGSAASGLV   SIALTKMANG   SASTAGILLN   GRVRSVAVHKP  
 101   D\*IRLRRTFS   LLNFASASGT   \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2017>:

m628.seq  
 1    ATGTGCGTGC   CACTCAAACC   GGCAGGATGC   GGGCCGCCGA   ATTCATGTGT  
 51   TTCGATGTTG   GCAGCATTTT   CAGACGGCAC   GTCTGCGCCA   GCTGCCTTAC  
 101   AACATGGAT   TTTGCGTTTCG   GTCAAACGGC   TCAATACCAA   CAGGCCGCGT  
 151   TTGAAATCCT   CGGCGGCTTC   TTTGATAATG   ACCGTAGGGT   CGGCAGCCAG  
 201   CGGATTGGTG   TCCATCGCAT   TGACGAAGAT   GGCGAACGGC   TCGGCATCGA  
 251   CGGCAGGAAT   TTTGCTGAAC   GGACGGGTGC   GCAGCGCAGT   CCACAAACCG  
 301   GATTGGATCA   GGTGCGGCG   CACTTCTTCG   CCGCTTAAGT   TTGCCAGCGC  
 351   TTCAGGTGCG   TAG

This corresponds to the amino acid sequence <SEQ ID 2018; ORF 628>:

m628.pep  
 1    MCVPLKPAGC   GPPNSCVSML   AAFSDGTSAP   AALQTWILRS   VKRLNTNRPR  
 51   LKSSAASLIM   TVGSAASGLV   SIALTKMANG   SASTAGILLN   GRVRSVAVHKP  
 101   DWIRLRRTSS   PLKFASASGA   \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

**m628/g628** 93.3% identity in 119 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAAALQ	TWILRSVKRLNTNRPR	LKSSAASLIM		
g628	MCVPLKPAGCGPPNSCVSILA	AFSDGTSAPAAALHTWILRSV	RRLNTNRPR	LKSSAASLMM		
	10	20	30	40	50	60
	70	80	90	100	110	120
m628.pep	TVGSAASGLVSIALTKMANGS	ASTAGILLN	GRVRSVAVHKPDWIRLRRTSS	PLKFASASGA		
g628	TVGSAASGLVSIALTKMANGS	ASTAGILLN	GRVRSVAVHKPD	XIRLRRTFS	LLNFASASGT	
	70	80	90	100	110	120
m628.pep	X					
g628	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2019>:

```
a628.seq
1  ATGTGCGTGC  CACTCAAACC  GGCCGGATGC  GGGCCGCCGA  ATTCATGTGT
51  TTCGATGTTG  GCAGCATTTT  CAGACGGCAC  GTCCTGCGCA  GCTGCCTTAC
101 ACACATGGAT  TTTACGCTCG  GTCAAACGGC  TCAATACCAG  CAAACCTCGT
151 CTGAAATCCT  CGGCGGCTTC  TTTGATCACA  ACCACAGGGT  CTGCCGCCAG
201 CGGATTGGTG  TCCATCGCAT  TGACGAAGAT  GGCGAACGGC  TCGGCATCGA
251 CGGCAGGGAT  TTTGCTGAAC  GGACGGGTAC  GCAGCGCAGT  CCACAAACCG
301 GATTGGATCA  GATTGGGCG  CACTTCTTCG  CCGCTTAAGT  TTGCCAACGC
351 TTCGGGCGCG  TAG
```

a628.pep

1	MCVPLKPAGC	GPPNSCVSML	AAFSDGTSAP	AALHTWILRS	VKRLNTSKPR
51	LKSSAASLIT	TTGSAASGLV	SIATKMGANG	SASTAGILLN	GRVRSVHHP
101	DWIRLRRTSS	PLKFANASGA	*		

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFSDGTSAPAAALQTWILRSVKRLNTNRPRLKSSAASLIM					
a628	MCVPLKPAGCGPPNSCVSMLAAFSDGTSAPAAALHTWILRSVKRLNTSKPRLKSSAASLIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m628.pep	TVGSAASGLVSIALTKMANGSASTAGILLNGRVRSVAVHKPDWIRLRTSSPLKFASASGA					
	:					
a628	TTGSAASGLVSIALTKMANGSASTAGILLNGRVRSVAVHKPDWIRLRTSSPLKFANASGA					
	70	80	90	100	110	120

g629.seq

1	ATGACTGCca	aacCTTTTTTC	CCTCAACCTG	GCcaaCCTCC	TGCTGCCggc
51	ggtatTGTTT	GCCGTCAGcc	tGtcggTCGG	cattgcogaT	TTCCGCTGGT
101	CGGATGTGTT	TTCGCTGTCC	GACAGCCAGC	AAGTGAATGT	CATCAGCCGC
151	CTGCCGCGCA	CTCTTGcgaT	TGTGTTGACG	GGCgcgtcga	tacgcGtggc
201	gGGGAtgatt	atgcagATTC	TGATGCGCAA	CcgtTTTGTC	GAGCCTtcta
251	tggcgGGTGC	GGGCCAAAGt	gcgGCTTTGG	GTttgcttct	gAtgtccctg
301	ctgctgcctg	CcgcGccgct	gccggtcaAA	ATGTCGGtag	Ccgccgttgc
351	CGCGCTGATC	GGGATGTTGG	tctTtatgct	gtaataccgC	Cgctggccac
401	cgacggcgca	gctgatGTgT	ccgCTGGTGG	Gg.ttATTTT	CGCGCGCGTG
451	GttgaGGCGG	TGGCGACGTT	TGTCGCGTAT	GAGTTTGAGA	TGCTGCAAAT
501	GTTGGGCGTG	TGGCAGCAGG	GCGACTTTTC	AAGCGTGCTG	CTGGGGCGGT
551	ACGAGCTGCT	TTGGATTACG	GGCGGTTTGG	CGGTGTTTGC	CTACCTGATT
601	GCCGACCCGG	TGACGATTTT	GGGGCTGGGC	GAGACGGTGA	CGCTGAATTT
651	GGGTTTGAAC	CGACGCGCGG	TGTTGTGGTC	GGGTTTGATT	GTTGTGGCAC
701	TGATTACATC	GCTGGTCATT	GTAACGGTCG	GCAATATTCC	GTTTATCGGG
751	CTGGTCGTGC	CGAATATCGT	CAGCCGCCCTG	ATGGGCGACA	GGCTGCGCCA
801	AAGCCTGCCT	GCGGTCGCCC	TCTTGGGCGC	GTCTTTGGTT	TTATTGTGCG
851	ACATTATCGG	ACGCTATGAT	GTGTTTCCGT	TTGAAATTCC	GGTCTCCACG
901	GTTTTTGGTG	TGTTGGGTAC	GGCTTTGTTT	TTGTGGCTTT	TGTTGAGGAA
951	ACCCGCCTAT	GCCGTCTGA			

g629.pep'

1	MTAKPFSLNL	ANLLLPVLF	AVSLSVGIAD	FRWSDVFSLS	DSQQVMFISR
51	LPRTFAIVLT	GASIAVAGMI	MQILMRNRFV	EPSMAGAGQS	AALGLLLMSL
101	LLPAAPLPVK	MSVAAVAALI	GMLVFMLLR	RLPPTAQLMV	PLVGXIFGGV

1005

151 VEAVATFVAY EFEMLQMLGV WQQGDFSSVL LGRYELLWIT GGLAVFAYLI  
 201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG  
 251 LVVPNIIVSRL MGDRLRQSLP AVALLGASLV LLCDIIGRMI VFPFEIPVST  
 301 VFGVLGTALF LWLLLRKPAY AV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2023>:

m629.seq  
 1 ATGACTGCCA AACCTTTTTC CCTCAACCTG ACCAACCTGC TGCTGCTGGC  
 51 GGTGTTGTTT GCCGTGAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT  
 101 CTGATGTGTT TTTACTGTCC GACAGCCAGC AGGTCATGTT CATCAGCCGC  
 151 CTGCCGCGCA CGTTTGCATG TGTGCTGACG GCGCGCTCGA TGGCGGTGGC  
 201 CGGCATGATT ATGCAGATTG TGATGCGCAA CCGTTTGTG GAACCGTCGA  
 251 TGGTGGGCGC AAGCCAAAGC GCGGCTTTAG GTTTGCTGCT GATGACCCTG  
 301 CTGCTGCCCG CCGCGCCGCT GCCGGCGAAA ATGTCGGTTG CCGCCGTTGC  
 351 CGCGCTGATC GGGATGTTGG TCTTTATGCT GCTGATCCGC CGCCTGCCGC  
 401 CGACCGCGCA ACTGATGGTG CTTTGGTTCG GGATTATTTT CGGCGGTGTG  
 451 ATTGAGGCGG TAGCCACCTT TATCGCGTAT GAAAACGAAA TGCTGCAAAT  
 501 GCTCGGCGTG TGGCAGCAGG GCGATTTTTC GAGCGTGCTG CTGGGCGGGT  
 551 ACGAGCTGCT TTGGATTACG GCGGTTTGG CCGTGTGTTG CTATCTGATT  
 601 GCCGACCGGC TGACGATTTT GGGGCTGGGC GAAACGGTAA GCGTGAATTT  
 651 GGGTTTGAAC CGGACGCGCG GTTGTGTTG GGGTTTGATT ATTGTGGCTT  
 701 TGATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG  
 751 CTGGTCGTGC CGAACATCAT CAGCCGCTG ATGGGCGACA GGTTGCGCCA  
 801 AAGCCTGCCT GCGGTGGCCT TGCTGGGCGC ATCTTTGGTG TTGCTGTGCG  
 851 ACATTATCGG ACGCGTGATT GTGTTTCCGT TTGAAATTCC GGTCTCTACG  
 901 GTTTTGGTG TATTGGGTAC GGCTTTGTTT TTGTGGCTTT TGTTGAGGAA  
 951 ACCCGCTAT GCCGTCTGA

This corresponds to the amino acid sequence <SEQ ID 2024; ORF 629>:

m629.pep  
 1 MTAKPFSNLN LNLLLAFLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR  
 51 LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMVGASQS AALGLLMTL  
 101 LLPAAPLPAK MSVAAVAALI GMLVFMLLIR RLPPTAQLMV PLVGIIFGGV  
 151 IEAVATFIAY ENEMLQMLGV WQQGDFSSVL LGRYELLWIT GGLAVFAYLI  
 201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG  
 251 LVVPNIIVSRL MGDRLRQSLP AVALLGASLV LLCDIIGRVI VFPFEIPVST  
 301 VFGVLGTALF LWLLLRKPAY AV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m629/g629 95.7% identity in 322 aa overlap

	10	20	30	40	50	60
m629.pep	MTAKPFSNLNLTNLLLAFLFAVSLSVGVADFRWSDVFSLSDSQQVMFISR					
	:     :     :     :     :     :					
g629	MTAKPFSNLNLANLLPAVLFAVSLSVGIADFRWSDVFSLSDSQQVMFISR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m629.pep	GASMAVAGMIMQILMRNRFVEPSMVGASQSAAALGLLMTLLLPAAPLPAKMSVAAVAALI					
	:     :     :     :     :     :					
g629	GASIAVAGMIMQILMRNRFVEPSMAGQSAAALGLLMSLLLPAAPLPVKMSVAAVAALI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m629.pep	GMLVFMLLIRRLPPTAQLMVPLVGIIIFGGVIEAVATFIAYENEMLQMLGVWQQGDFSSVL					
	:     :     :     :     :     :					
g629	GMLVFMLLIRRLPPTAQLMVPLVGXIFGGVVEAVATFVAYEFEMLQMLGVWQQGDFSSVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m629.pep	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					
	:     :     :     :     :     :					



1006

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g629      LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           190      200      210      220      230      240
           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRMIVFPFEIPVST
           250      260      270      280      290      300
           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VFGVLGTALFLWLLLRKPAYAVX
           310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2025>:

```

a629.seq
1  ATGACTGCCA AACCTTTTTC CCTCAACCTG ACTAACCTCC TGCTGCTGGC
51  GGTGTTGTTT GCCGTCAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT
101 CGGATGTGTT TTCGCTGTCG GACAGCCAGC AGGTTATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGCATG TGTGTTGACG GCGCGCTCGA TGGCGGTGGC
201 GGGGATGATT ATGCAGATTC TGATGCGTAA CCGTTTTGTC GAGCCTTCTA
251 TGGCGGGCGC GGGTCAGAGT GCGGCTTTGG GTTGCTTCTG GATGTCCCTG
301 CTGCTGCCTG CCGCGCCGCT GCCGGTCAAA ATGTCGGTTG CCGCCGTTGC
351 CGCGTTAATC GGGATGTTGG TGTATTATGAT GCTTATCCGC CGCCTGCCGC
401 CGACGGCGCA ACTGATGGTG CCTTTGGTCG GGATTATTTT CGGCGGCGTG
451 GTTGAGGCGG TGGCCACCTT TATTGCGTAT GAAAACGAAA TGCTGCAAAT
501 GCTGGGCGTG TGGCAACAGG GCGATTTTTC CGGCGTGTTG CTCGGACGGT
551 ATGAACTGTT GTGGGCAACG GGGATTTTGG CTTTGTTTGC CTATTTGATT
601 GCCGACCAGC TGACGATTTT GGGTTTGGGC GAAACGGTAA GCGTGAACCT
651 GGGGCTGAAC CCGACGGCGA TTCTGTGGTC GGGGCTGATT ATTGTGGCTT
701 TGATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCG GTTTATCGGG
751 CTGGTCGTGC CGAACATCAT CAGCCGCGCTG ATAGCGGACA GGCTGCGCCA
801 AAGCCTGCCT GCGGTGGCTT TGCTGGGTGC GTCTTTGGTT TTATTGTGCG
851 ACATTATCGG ACGAGTGATT GTGTTTCCGT TTGAAATTCC GGTATCGACC
901 GTCTTCGGCG TATTGGGTAC GGCCTTGTTT TTATGGCTTT TGTTAAGGAA
951 ACCTGCTCAT GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2026; ORF 629.a>:

```

a629.pep
1  MTAKPFSLNL TNLLLLAVLF AVSLSVGVD FRWSDVFSLS DSQQVMFISR
51  LPRTFAIVLT GASMAGMI MQILMRNFV EPSMAGAGQS AALGLLMSL
101 LLPAAPLPVK MSVAAVAALI GMLVFMLLR RLPPTAQLMV PLVGIIFGGV
151 VEAVATFIAY ENEMQLMGV WQQGDFSGVL LGRYELLWAT GILALFAYLI
201 ADQLTILGLG ETVSVNLGLN RTAILWSGLI IVALITSLVI VTVGNIPFIG
251 LVVFNIIISRL IGDRLRQSLP AVALLGASLV LLCIDIIGRVI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAH AV*

m629/a629  95.7% identity in 322 aa overlap

           10      20      30      40      50      60
m629.pep  MTAKPFSLNLTNLLLLAVLFAVSLSVGVD FRWSDVFSLS DSQQVMFISR LPRTFAIVLT
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      MTAKPFSLNLTNLLLLAVLFAVSLSVGVD FRWSDVFSLS DSQQVMFISR LPRTFAIVLT
           10      20      30      40      50      60
           70      80      90      100     110     120
m629.pep  GASMAGMIMQILMRNFVEPSMVGASQSAALGLLMTLLLPAAPLPKMSVAAVAALI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      GASMAGMIMQILMRNFVEPSMAGAGQSAALGLLMSLLLPAAPLPVKMSVAAVAALI
           70      80      90      100     110     120
           130     140     150     160     170     180
m629.pep  GMLVFMLLRRLPPTAQLMVPLVGIIFGGVIEAVATFIAYENEMQLMGVWQQGDFSSVL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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1007

```

a629      GMLVFMMLIRRLPPTAQLMVPLVGIIFGGVVEAVATFIAYENEMLQMLGVWQQGDFSGVL
           130      140      150      160      170      180

           190      200      210      220      230      240
m629.pep  LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           ||||| || ||:|||||:|||||:|||||:|||||:|||||
a629      LGRYELLWATGILALFAYLIADQLTILGLGETVSVNLGLNRTAILWSGLIIVALITSLVI
           190      200      210      220      230      240

           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           |||||:|||||:|||||:|||||:|||||:|||||
a629      VTVGNIPFIGLVVPNIISRLIGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           250      260      270      280      290      300

           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||
a629      VFGVLGTALFLWLLLRKPAHAVX
           310      320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2027>:

```

g630.seq (partial)
1  aTgatGATT  TGGTGTGGCT  ggctttgttt  ccccccattgt  tttacggcat
51  gtacaacgtc  GGCGCACAGG  CATTCGGTGC  CTTAACGCCC  GAtttgctgc
101 aacaaagcat  cgcccacgac  ggcaattacg  ccctcgccaa  cgctttgggc
151 atcaatatgt  cccccgaaGc  ggcggtgtTg  ggcaaaatgc  tgctcgGCGC
201 GATttacttc  ctgccgattt  acgcgaccgt  aTTTATTGTG  GGcggtctct
251 ggGaagtCTT  GTTCGCATCc  gtACGCAAAC  ACGAAATCAA  CGAAGGTTTC
301 TTCGTTACTT  CGATTCTGTT  TGCTTAATC  GTCCGCCCA  CGCTGCCGCT
351 GTGGCAGGCG  GCTTTGGGTA  TTTCTTTCGG  CGTTGTGGTT  GCGAAAGAAG
401 TATTCGGCGG  TACAGGTAAA  AACTTCATGA  ACCCTGCGCT  GGCAGGCCGC
451 GCCTTCCTGT  TCTTCGCCTA  CCCCGCCAAC  TTGAGCGGCG  ATGCGGTTTG
501 GACGGCGGTT  GACGGCTATT  CCGGCGCAAC  CGCGCTGGCG  CAATGGGCGG
551 CACACGGTGC  AGACGGCCTG  AAAAACGCCG  TAACCGGTCA  AACCATCACT
601 TGGATGGACG  CGTTTATCGG  CAAACTGCCC  GGCTCCATCG  GCGAAGTCTC
651 CACTTTGGCA  CTCTTAATCG  GCGGCGCGTT  TATCGTGTTC  GCCCGCATCG
701 CTtcttgGCG  CATTATTGCC  ggCGTGATGA  TCGGTatGat  tGcgatgTCT
751 tCgctgatta  agttcatCGg  ttctgacacc  aaagctatgt  ttgctatgca
801 cttggtacat  ggcacttggT  GGAaagatGa  ttAtcactca  ctgtacatta
851 aa.....

```

This corresponds to the amino acid sequence <SEQ ID 2028; ORF 630.ng>:

```

g630.pep
1  MMILVWLALF  PPMFYGMYNV  GAQAFGALTP  DLLQOSIAHD  GNYALANALG
51  INMSPEAGVL  GKMLFGAIYF  LPIYATVFIV  GGFWEVLFA  VRKHEINEGF
101 FVTSILFALI  VPPTLPLWQA  ALGISFGVVV  AKEVFGGTGK  NFMNPALAGR
151 AFLFFAYPAN  LSGDAVWTAV  DGYSGATALA  QWAAHGADGL  KNAVTGQTIT
201 WMDAFIGKLP  GSIGEVSTLA  LLIGGAFIVF  ARIASWRIIA  GVMIGMIAMS
251 SLINFIGSDT  KAMFAMHLVH  GTWWKDDYHS  LYIK....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2029>:

```

m630.seq
1  ATGATGATTT  TGGTGTGGCT  GGCTTTGTTC  CCTGCCATGT  TCTACGGTAT
51  GTACAACGTC  GGCGCGCAGG  CATTCGGTGC  GTTAACGCC  GATTGTGCTGC
101 AACAAAACAT  CGCCAACGAC  TGGCATTACG  CCTTGCCAA  CGCTTTGGGC
151 ATCAATATGT  CGTCTGAAGC  GGGCGTGTCT  GACAAAATG  TGTTTGGCGC
201 GATTTACTTC  CTGCCGATTT  ACGCGACTGT  ATTTGTTGT  GGCGGTTTCT
251 GGGAAAGTTT  GTTCGCCACC  GTGCGCAAAC  ACGAAATCAA  CGAAGGTTTC
301 TTCGTTACTT  CGATTCTGTT  TGCTTAATC  GTCCGCCCA  CGCTGCCGCT
351 GTGGCAGGCG  GCTTTGGGTA  TTTCTTTCGG  CGTTGTGGTT  GCGAAAGAAG
401 TATTCGGCGG  TACAGGTAAA  AACTTCATGA  ACCCTGCGCT  GGCAGGCCGT
451 GCTTTCCTGT  TCTTCGCCTA  CCTGCCAAC  TTGAGCGGCG  ATGCGGTTTG
501 GACGGCGGTT  GACGGCTATT  CCGGCGCAAC  CGCACTGGCG  CAATGGGCGG
551 CACACGGTGC  AGACGGCCTG  AAAAACGCCG  TAACCGGTCA  AACCATCACT
601 TGGATGGACG  CGTTTATCGG  CAAACTGCCC  GGCTCCATTG  GCGAAGTCTC
651 CACTTTGGCA  CTCTTAATCG  GCGGCGCGTT  TATCGTGTTC  GCCCGCATCG
701 CTCTTTGGCG  CATTATTGCC  GCGGTGATGA  TCGGTATGAT  TGCGATGTCT
751 TCGCTGTTC  ACTTCATCGG  TTCGGACACC  AACGCTATGT  TTGCTATGCC

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1008

801 TTGGTACTGG CACTTGGTGG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA  
 851 TGGCGACCGA CCCTGTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG  
 901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC  
 951 GGCTTACCCC GAAGGCATGA TGTGCGCAT TCTGTTTGCC AACCTGTTTG  
 1001 CCCCATTTC GACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG  
 1051 GCGCGCAGCA ATGGCTAA

This corresponds to the amino acid sequence <SEQ ID 2030; ORF 630>:

m630.pep  
 1 MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQONIAND WHYAFANALG  
 51 INMSSEAGVS DKMLFGAIYF LPIYATVFVV GGFWEVLFAT VRKHEINEGF  
 101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR  
 151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVGTQTIT  
 201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS  
 251 SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW  
 301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIFDYF VAQANIKRRK  
 351 ARSNG\*

m630/g630 93.5% identity in 275 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALF	PAMFYGMYNV	GAQAFGALTP	DLLQONIAND	WHYAFANALG	INMSSEAGVS
g630	MMILVWLALF	PPMFYGMYNV	GAQAFGALTP	DLLQSI	AHDGNYALANALG	INMSPEAGVL
	10	20	30	40	50	60
	70	80	90	100	110	120
m630.pep	DKMLFGAIYF	LPIYATVFVV	GGFWEVLFAT	VRKHEINEGF	FVTSILFALI	VPPTLPLWQA
g630	GKMLFGAIYF	LPIYATVFIV	GGFWEVLFAS	VRKHEINEGF	FVTSILFALI	VPPTLPLWQA
	70	80	90	100	110	120
	130	140	150	160	170	180
m630.pep	ALGISFGVVV	AKEVFGGTGK	NFMNPALAGR	AFLLFFAYPAN	LSGDAVWTAV	DGYSGATALA
g630	ALGISFGVVV	AKEVFGGTGK	NFMNPALAGR	AFLLFFAYPAN	LSGDAVWTAV	DGYSGATALA
	130	140	150	160	170	180
	190	200	210	220	230	240
m630.pep	QWAAHGADGL	KNAVGTQTIT	WMDAFIGKLP	GSIGEVSTLA	LLIGGAFIVF	ARIASWRIIA
g630	QWAAHGADGL	KNAVGTQTIT	WMDAFIGKLP	GSIGEVSTLA	LLIGGAFIVF	ARIASWRIIA
	190	200	210	220	230	240
	250	260	270	280	290	300
m630.pep	GVMIGMIAMSS	LFNFIGSDTN	NAMFAMPWYW	HLVVGGFAIG	MLFMATDPVS	SASFTNVGKWW
g630	GVMIGMIAMSS	LINFIGSDTK	AMFAM---	HLVHG	TWKKDDYHSLYIK.	
	250	260	270	280		
	310	320	330	340	350	
m630.pep	YGALIGVMCV	LIRVVNPAYP	EGMMLAILFAN	NLFAPIFDYF	VQAQANIKRRK	ARSNGX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2031>:

a630.seq  
 1 ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT  
 51 GTACAACGTC GGCGCACAGG CATTTCGGTG GTTAACGCCC GATTTGCTGC  
 101 AACAAAGCAT CGCCAACGAC TGGCATTACG CCCTTGCCAA CGCTTTGGGC  
 151 ATCAATATGT CGTCTGAAGC GGGCGTGTG GGCAAAATGC TGTTCCGCGC  
 201 GATTTACTTC CTGCCGATTT ACGCGACCGT ATTTATTGTC GGCGGTTTCT  
 251 GGAAGTTTT GTTCGCCACC GTGCGCAAAC ATGAAATCAA CGAAGGTTTC  
 301 TTTGTTACCT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT  
 351 GTGGCAGGCA GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG  
 401 TATTCGGCGG TACAGGTAAA AACTTCATGA ACCCTGCGCT GGCAGGCCGT  
 451 GCCTTCCTGT TCTTCGCCTA CCCTGCCAAC TTGAGCGGCG ATGCGGTTTG  
 501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCGCTGGCG CAATGGGCGG  
 551 CACACGGTGC AGACGGCTG AAAAACGCCA TAACCGGTCA AACCATCACT  
 601 TGATGGATG CGTTTATCGG CAAACTGCCC GGCTCCATCG GCGAAGTCTC  
 651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG

1009

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701 CTTCTTGCGC CATTATTGCC GCGGTGATGA TCGGTATGAT TGCCATGTCT
751 TCGCTGTTCA ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC
801 TTGGTACTGG CATTTGGTCG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCCGTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGCGCAT TCTGTTTGCC AACCTGTTTG
1001 CCCCATTTCG GACTATTTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2032; ORF 630.a>:

```

a630.pep
1  MMILVWLALF PAMFYGMYNV GAQAFGALT PDLLQQSIAND WHYALANALG
51  INMSSEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAITGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLFNFIGSDT NAMFAMPWYW HLTVGGFAIG MLFMDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIDYF VAQANIKRRK
351 ARSNG*

```

m630/a630 98.3% identity in 355 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALFPAMFYGMYNVGAQAFGALT	PDLLQQNIANDWHYAFANALGINMSSEAGVS				
a630	MMILVWLALFPAMFYGMYNVGAQAFGALT	PDLLQQSIANDWHYALANALGINMSSEAGVL				
	10	20	30	40	50	60
m630.pep	DKMLFGAIYFLPIYATVFVVG	GFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA				
a630	GKMLFGAIYFLPIYATVFIVG	GFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA				
	70	80	90	100	110	120
m630.pep	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTA	VDGYSGATALA				
a630	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTA	VDGYSGATALA				
	130	140	150	160	170	180
m630.pep	QWAAHGADGLKNAVTGQTITWMDAFIGKLP	GSIGEVSTLALLIGGAFIVFARIASWRIIA				
a630	QWAAHGADGLKNAITGQTITWMDAFIGKLP	GSIGEVSTLALLIGGAFIVFARIASWRIIA				
	190	200	210	220	230	240
m630.pep	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLFMDPVS	ASFTNVGKWW				
a630	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLFMDPVS	ASFTNVGKWW				
	250	260	270	280	290	300
m630.pep	YGALIGVMCVLIRVVNPAYPEGMMLAILFANL	FAPIDYFVAQANIKRRKARSNGX				
a630	YGALIGVMCVLIRVVNPAYPEGMMLAILFANL	FAPIDYFVAQANIKRRKARSNGX				
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2033>:

g635.seq

```

1  ATGACCCGGC GACGGGTCGG CAAGCAAAAC CGTATTGCCA TCCACTCCGC
51  GCAATACCGA AAAATGGTCG TCTTTGCGGT ATTCAGATA CACGATGACG
101 GGGATTTTCA ACTGCGCGAG CTGTTGCGAA GACAGGGCAT AGCCTTTCGC
151 CTCAAAACCC AAATCGGGCA TAATGCGCCG CATATCCTCA AACGACGCGC
201 GCATCTGTTT CTTACCCAGT TTTTCCAACA CTTCTTCTTC CGTCAGCTTT
251 TGCCCGTAAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGAGGA

```

q635.ppt

1 MTRRRVGKQN RIAIHSAYR KMVVFVAFQI HDDGDFQLRE LFERQGIAPR  
51 LKTQIGHNAP HILKRRAHLF LTQFFQHFFF RQLLPVKIVQ KRRHRSRPAG  
101 KIQILLYNIE IPPREPTLOF DESVNNRIIV KHRCSIOTIR QGSVPD\*

m635.seq

1	ATGACCCAGC	GACGGGTCTGG	CAAGCAAAAC	CGTATTGCCG	TCTATACCGC
51	GCAATACCGA	GAAATGATCA	TCCTTGGCGT	ATTTCAGGTA	CACGATGACG
101	GGGATTTCGA	ACTGTGCAAG	CTCGTCGAAA	ACCCAGGCAT	AGCCTTTCGC
151	TTCAAAACCC	AAATCAGGCA	TAATGCGCCG	CATATCCCTA	AACGACGCGG
201	GCATCTGCTC	CTTATCCAGT	TTTTTTAACA	CGTCTCTTTC	CGTCAGCTTG
251	TGCGCGTAAA	AATTGTTCAA	AAAGGTCACC	ACCGAAGCCG	CGCCGCAGGA
301	AAAAATCCAA	TCCTGCTTTA	CAATATTGAA	ATCGCGCCTT	TCTTTCCAAC
351	TCTGCAGCTT	GATTTTTCCT	TAAGCAACAG	GATTATATGT	GATTAA

m635 . pep

```

1  MTQRRVGKQN RIAVYTAQYR EMIILAVFQI HDDGDLQLCK LLERQGIAGR
51  FKTQIRHNAP HILKRRGHLL LIQFF*HVLF RQLLPVKIVQ KRHHRSRPAG
101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D*

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	10	20	30	40	50	60
m635.pep	MTQRRVGKQNRIAYVTAQYREMIILAVFQIHDDGDLQLCKLLERQGIAFREKTQIRHNAP   ::            :        : ::             :   :             :					
g635	MTRRRVGKQNRIAHSAQYRKMVVFAVFQIHDDGDFQLRELFERQGIARLKTQIGHNAP  					
	10	20	30	40	50	60
	70	80	90	100	110	120
m635.pep	HILKRGRGHLLLIQFFXHVLFRLLPVKIVQKRHRHSRPAGKIQILLYNIEIAPFFPTLHF         :     :       :					
g635	HILKRRAHLFLTQFFQHFFFRQLLPVKIVQKRHRHSRPAGKIQILLYNIEIPPRFTLQF  					
	70	80	90	100	110	120
	130					
m635.pep	DFSISNRRIVDX       :					
g635	DFSNNRRIIVKHRCISIQTIRQGSVPDX  					
	130	140				

a635.seq

1	ATGACCCAGC	GACGGGTCGG	CAAGCAAAAC	CGTATTGCCG	TCTATACCGC
51	GCAATACCGA	GAAATGATCA	TCCTTGCGGT	ATTTTCAGAT	CACGATGACG
101	GGGATTTCGA	ACTGTGCAAG	CTGCTCGAAA	GACAGGGCAT	AGCCTTTTCG
151	CTCAAAACCC	AAATCAGGCA	TGATGCGCCG	CATATCTCTA	AACGACGCGC
201	GCATCTGCTC	CTTATCCAGC	TTTTTCAACA	CGTCCTCTTC	CGTCAGCTTT
251	TGCCCGTGAA	AATTGTTCAA	AAGCGTCGCC	ACCGAAGCCG	CCCCCGCAGGA
301	AAAAATCCAAA	TCCTGCTTTA	CAATATTGAA	ATCGCGCCTT	TCTTTCCAAC
351	TCTGCACATT	GATTTTTCCA	TAAGCAACAG	GATTATAGTG	GATTAA

a635.pep

```

1  MTQRRVGKQN  RIAVYTAQYR  EMIILAVFQI  HDDGDLQLCK  LLERQGIAFR
51  LKTQIRHDAP  HILKRRALL  LIQLFQHVLF  RQLLPVKIVQ  KRRHRSRPAG
101 KIOILLYNIE  IAPFEPTLHE  DFSISNRIIV  D*

```

10                      20                      30                      40                      50                      60

1011

```

m635.pep    MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGI AFRFKTQIRHNAP
a635        MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGI AFRFKTQIRHDAP
              10      20      30      40      50      60

              70      80      90      100     110     120
m635.pep    HILKRRGHLLLIQFFXHVLFRLQLPVKIVQKRHRHRSRPAGKIQILLYNIEIAPFFPTLHF
a635        HILKRRRAHLLLIQLFQHVLFRLQLPVKIVQKRHRHRSRPAGKIQILLYNIEIAPFFPTLHF
              70      80      90      100     110     120

              130
m635.pep    DFSISNRIIVDX
a635        DFSISNRIIVDX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2039>:

```

g638.seq
1  ATGATTGGCG GACAGTTTAT CGTAGttgGc atTGTAGGCA AAAACGCACT
51  TGCCCGCTTT GTTGATAATA ttgtcGTGAA TAtcGGAATA GTTGACATAG
101 TTAGAGCATGA TGCCCTAATC GCGGCTGCCG ACGGCGATAT TGTCGAACAC
151 TTTGAGCCGT TCGGAAAACA TCAGCACATA GCCCATATTG TtgcCCACGG
201 AAATATTGCC GCTGacttcg ctgtcgTTGG TGTACATATA GTGGACGGCG
251 AAACGCAGGT CGCTGAAGCG GTTGTTTTGA TAGGTGTTGT GCGTGCTGGT
301 ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG ccgACGACCT
351 GCGCgcccgg CgcgtTCCAA ACGGTAACGC CATTGCCGCG CTCATTACAG
401 CGCAAGGTcg catcgCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGA AGGTATACGC CGAACGAATT ATCAAAAATA TTGTGTGTGT
501 CAACCAGGGC GCGCGGGGCG GCTTTTTCGA GATAAATACC GGCATCCATT
551 GCTGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCTTGTCG CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTCAATCG TAATCGGTTT GTCGATATAA
701 AGTTTGGTTT GATATAcGCC GGAAGCCAGT TTGATCGTAT CGCCCGCCCG
751 GCGCGCGGCA AAAATTTTCG CAAGGTTGTC TTGCGGGGAA ACGTGGACGA
801 CCGCTGCCGA TGCCGTCTGA AAAATGCTGC CGGCGGCAAG TATCAGCAG
851 GCCTTCAGCC ATATACGGAG CCGGATGTG TGCATAGTGT CCCTCTGTTT
901 CGTTCGGTAT GGCGGAACAA AATAAGCAT CATTCAAATG TGCCTGTTTT
951 TATAGCGAAA CCGCCTGAAA CCGTACGGCA AGCGGTTTGG CTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2040; ORF 638.ng>:

```

g638.pep
1  MIGGQFIVVG IVGKNALARF VDNIVVNIGI VDIVEHDALI AAADGDIVEH
51  FEPFGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQVAEA VVFIGVVRAG
101 IGNAVPPFG NVVADDLRAG RVPNGNAIAA LIHAQGRIAD DFILAHHRIG
151 TRMKVYAERI IKNIVVFNQG ARGGFFEINT GIHCWQAHG TGNGQVAERY
201 VRRVYGYGTP ALVPFDGCGT VGRPFNRNRF VDIKFGLIYA GSQFDRIARP
251 GAGKNFGKV VLRGNVDDGCR CRLKNAAGGK YQHGLQPYTE RGCVHSVPLF
301 RSVWPNKIKH HSNVPVFIK PPETVRQAVW L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2041>:

```

m638.seq
1  ATGATTGGCG AAAAGTTTAT CGTAGTTGGC ATTATAGGCA AATACGCACT
51  TGCTGCTTGT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTAGACATAA TGCCCTGATC GCGGCTGCCG ACGGCGATAT TGTCGAATAC
151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACCGG
201 AAATATTGCC GCTGATTTTC CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGCAAAAT CGCTGAAGCG GTTGTTTTGA TAGGTGTTGT GCGTGCTGGT
301 ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG CCGACGACCT
351 GCGCACCAGG TGCGTTCCAA ACGGTAACGC CGTTGCCGCG CTCGTTACAG
401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGC AGATATACGC CGACCGAATT ATCAAAAATA TTGTGTGTGT
501 CAATCAGGGC GCGCGGGGCA GTTCTTTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCTGTGCG CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTCAATCG TAATCGGTTT GTCAATGTGA
701 AGTTTGGTTT TATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 GGCGCGGGCA AATGCGGGAT ACCGATCAGC ATAATCGGTT CGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2042; ORF 638>:

m638.pep

```

1  MIGEKFIVVG IIGKYALACL VDNVVVNIGI VDIVEHNALI AAADGDIVEY
51  FEPLGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFGVVRAG
101 IGKNAVPPFG NVVADDLRTG CVPNGNAVAA LVHAQSRVAD DFILAHHRIG
151 RTMQIYADRI IQNIVVFNOG ARGSF FEINT GIHCGQAHTG TGNGQVAERY
201 VRRVYGYGTP APVAFDGGCT VGRPFNRNRF VNVKFGFIYA GSQFERIARP
251 GAGKCGIPIS IIGS*

```

m638/g638 88.2% identity in 254 aa overlap

m638.pep	10	20	30	40	50	60
	MIGEKFIVVG IIGKYALACL VDNVVVNIGI VDIVEHNALI AAADGDIVEY FEPLGKHQHI					
g638	MIGGQFIVVG IIVGKNALARF VDNIVVNIGI VDIVEHDALI AAADGDIVEH FEPFGKHQHI					
m638.pep	70	80	90	100	110	120
	AHIVAHGNIAADFAVVG VHI VDGETQIAEA VVFGVVRAG IGKNAVPPFG NVVADDLRTG					
g638	AHIVAHGNIAADFAVVG VHI VDGETQVAEAVVFIGVVRAG IGKNAVPPFG NVVADDLRTG					
m638.pep	130	140	150	160	170	180
	CVPNGNAVAA LVHAQSRVAD DFILAHHRIG RTMQIYADRI IQNIVVFNOG ARGSF FEINT					
g638	RVPNGNAIAALIHAQGR IADDFILAHHRIG RTMKVYAERI IKNIVVFNOG ARGSGF FEINT					
m638.pep	190	200	210	220	230	240
	GIHCGQAHTG TGNGQVAERY VRRVYGYGTP APVAFDGGCT VGRPFNRNRF VNVKFGFIYA					
g638	GIHCWQAHTG TGNGQVAERY VRRVYGYGTP ALVPFDGGCT VGRPFNRNRF VDIKFGLIYA					
m638.pep	250	260				
	GSQFERIARPGAGKCGIPISIIGSX					
g638	GSQFDRIARPGAGKNFGKVVL RGNVDDGCRCLKNAAGGKYQHGLQPYTERGCVHSVPLF					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2043>:

a638.seq

```

1  ATGATTGGCG GACAGTTTAT CGTAGTTGGC ATTGTAGGCA AAAACGCACT
51  TGCCCGCTTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTGAGCATGA TGCCTTGCTC GCGGCTGCCG ACGGCGATAT TGTCAAACAC
151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACCGG
201 AAATATTGCC GCTGATTTTC CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGCAAAT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGCTGGT
301 ATTGGA AAAA ATGCCGTCCC GCCCTTTGGA AATATCGTTG CCGACGACCT
351 GCGCGCCGGG CGCGTTCCAA ACGGTAACGC CATTGCCGCG CTCGTTACG
401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCCCGCACCA TCGCATCGGC
451 AGAACCATGC AGATAGACGC CGACCGAATT ATCCAAAATA TTATTGTGTT
501 CAATCAGGGC GCGCGGGGCA GTTTCCTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 TTCGGCGCGG TGTACGGCTA TGGTACGCCG GCTCCTGTCT CCTTCGATGG
651 TTGCAGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATGTGA
701 AGTTTGTTT GATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 GGCGCGGGCA AATGCGGGAT ACCGATCAGC ATAATCGACT CATGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2044; ORF 638.a>:

a638.pep

```

1  MIGGQFIVVG IIVGKNALARF VDNVVVNIGI VDIVEHDALV AAADGDIVKH
51  FEPLGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFIGVVRAG
101 IGKNAVPPFG NIVADDLRTG RVPNGNAIAA LVHAQSRVAD DFILPHHRIG
151 RTMQIDADRI IQNIIIVFNQ ARGSF FEINT GIHCGQAHTG TGNGQVAERY
201 VRRVYGYGTP APVSFDGCRT VGRPFNRNRF VDVKFGLIYA GSQFERIARP

```

1013

251 GAGKCGIPIS IIDSW\*

m638/a638 91.3% identity in 264 aa overlap

	10	20	30	40	50	60
m638.pep	MIGEKFIVVGIIGKYALACLV	DNVNVNIGIVDIVEH	NALIAAADGDIVEY	FEPLGKHQHI		
a638	MIGGQFIVVGIVGKNALARF	VDNVVNIGIVDIVEH	DALVAAADGDIVKH	FEPLGKHQHI		

	70	80	90	100	110	120
m638.pep	AHIVAHGNIAADFAVVG	VHIVDGETQIAEAVV	FVGVVRAGIGKNA	VPPFGNVVADDL	RTG	
a638	AHIVAHGNIAADFAVVG	VHIVDGETQIAEAVV	FIGVVRAGIGKNA	VPPFGNIVADDL	RRAG	

	130	140	150	160	170	180
m638.pep	CVPNGNAVAALVHAQSR	VADDFILAHHRIGR	TMQIYADRIIQNI	VFNQGARGSF	FEINT	
a638	RVPNGNAIAALVHAQSR	VADDFILPHHRIGR	TMQIDADRIIQNI	IVFNQGARGSF	FEINT	

	190	200	210	220	230	240
m638.pep	GIHCGQAHTGTGNGQVA	ERYVRRVYGYGTPAP	VAFDGCGTVGRPF	NRNRFVNVKFG	FIYA	
a638	GIHCGQAHTGTGNGQVA	ERYVRRVYGYGTPAP	VSFDGCRTVGRPF	NRNRFVDVVKF	GLIYA	

	250	260
m638.pep	GSQFERIARPGAGKCGIP	ISIIGSX
a638	GSQFERIARPGAGKCGIP	ISIIDSX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2045>:

## g639-1.seq

```

1  ATGAGCCTGC CAGCAATGGA TGCCGGTATT TATCTCGAAA AAGCCGCCCC
51  GCGCGCCCTG GTTGAACACA ACAATATTTT TGATAATTCG TTCGGCGTAT
101 ACCTTCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GATGCGACCT TGCGCGTGAA TGAGCGCGGC AATGGCGTTA CCGTTTGGA
201 CGCGCCCGGC GCGCAGGTCG TCGGCAACGA CATTCCAAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACACA CCTATAAAA CAACCGCTTC
301 AGCGACCTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAGT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTT
401 CCGAACGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGATTAG
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTACAG ACAATATTAT
501 CAACAAAGCG GGCAAGTGCG TTTTGCCTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATGCA CTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGGAAG
651 CCAGGTCAAA TATGTCAGTA CGCGCTTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA CTGGAGCGAC AACAGCCCGT TCGATTTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCGACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAATGGGC GCAGGCGCAG TTTCCCGCCG TTCTGCCCGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCAAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGT TGCTCAAAGA AGCCGAAACG CGGCAGTCGG
1001 AACGGGCGAG GCGGAAAAC GGTCTTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2046; ORF 639-1.ng>:

## g639-1.pep

```

1  MSLPAMDAGI YLEKAAPRAL VEHNIFDNS FGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101  SDLRFVHYM YTNDSEVSGN ISVGNMGGYV LMFSERLKVF DNIAVGSRD*
151  GIMLNIVNYS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGMHFTA
201  AIEGTSLHDN SFINNGSQVK YVSTRELDWS EGGHGNYSWD NSPFDLNGDG
251  FGDSAYRPDG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAF FPAVLPGGVV
301  DSKPLMKPYA PKIQTRYQAM KDELLEAET RQSERGRAEN GSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2047>:



1014

## m639-1.seq

```

1  ATGAGCTGTC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAAGTGGCCC
51  GCGCGCCCTG ATTGAACACA ACAATATTTT GGATAATTCG GTCGGCGTAT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AACGGCGTTA CCGTTTGGAA
201 CGCACCCTGG GCGCAGGTCG TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACACA CCTACAAAA CAACCGCTTC
301 AGCGATTTCG GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTATTC GACAATATCG CCGTCGGCAG CCGCGATCAG
451 GGCATTATGC TCAACTATGT CAACTATTCG GATATTCACG ACAACATTAT
501 CAACAAGGCA GGCAAGTGCG TATTTCCTTA TAATGCCAAC TACGATAAAC
551 TTTTCGCCAA TCATTTTGAA AACTGTCAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCTT GCATGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGGTCAA TACGTCAGCA CGCGCTTCT CGATTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG CCGCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TTTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAATGGGC GCAGGCGCAG TTCCCGCGCG TTCTGCCTGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCGCAAAATC AAACCGGTTA
951 TCAGGCGATG AAGGACGAGC TACTCAAAGA AGTCGAAACG CGGCAGTCGG
1001 AATGGGCGAG GCGGAAAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2048; ORF 639-1>:

## m639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFNTS THNTYKNNRF
101 SDLRFVHYM YTNDSISGN ISVGNMGYV LMFSERLKVF DNIAGVSRDQ
151 GIMLNYYNYS DIHDNIINKA GKCVFAYNAN YDKLFANHFE NCQIGIHFTA
201 AIEGTSLHDN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRENG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAF FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLKEVET RQSEWGRAEN GSLN*

```

g639-1/m639-1 95.9% identity in 344 aa overlap

	10	20	30	40	50	60
g639-1.pep	MSLPAMDAGIYLEKAAPRALVEHNNIFDNSFGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
g639-1.pep	NGVTVWNAPGAQVVGNDISKGRDGIFNTSTHNTYKNNRFSDLRFVHYMYTNDSEVSGN					
m639-1	NGVTVWNAPGAQVVGNDISKGRDGIFNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
	70	80	90	100	110	120
g639-1.pep	ISVGNMGYVLMFSERLKVFNDIAGVSRDXGIMLNYYNYSIDIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMGYVLMFSERLKVFNDIAGVSRDQGIMLNYYNYSIDIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
g639-1.pep	YDKLSANHFENCQIGMHFTAIEGTSLHDNSFINNGSQVKYVSTRFLDWSEGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTAIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
	190	200	210	220	230	240
g639-1.pep	NSPFDLNGDGFSDSAYRPGDIIDQIIWRAPVSRLLMNSPAISIVKWAQAFPAVLPGGVV					
m639-1	NSAFDLNGDGFSDSAYRPNGIIDQIIWRAPVSRLLMNSPAISIVKWAQAFPAVLPGGVV					
	250	260	270	280	290	300
g639-1.pep	DSKPLMKPYAPKIQTRYQAMKDELLKEAETRQSERGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLNX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2049>:

## a639-1.seq

```

1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAACTGCCCC
51  GCGCGCCCTG ATTGAACACA ATAATATTTT GGATAATTCG GTCGGCGTCT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GGGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AATGGCGTTA CCGTTTGAA
201 CGCGCCCGGC GCGCAGGTCT TCGGCAACGA TATTCCAAA GGGCGGGACG
251 GCATTTTTTC CAATACCAGC ACGCACAACA CCTATAAAAA CAACCGCTTC
301 AGCGATTTCG GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTT
401 CCGAGCGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGACCAA
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTACAG ACAACATTAT
501 CAACAAAGCG GCGAAGTGGC TTTTGCCTA CAATGCCAAC TACGATAAAC
551 TGTCGGCCAA TCATTTTGAA AACTGCCAAA TCGGCATACA CTTACCGCC
601 GGCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGGTCAA TACGTCAGCA CGCGCTTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCACCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAATGGGC CAGGCGCAA TTTCCCGCCG TTTGCCTGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGGGC TGCTCAAAAA AGTCGAAACG CGGCAGTTGG
1001 AATGGGGCAG GCGGGAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2050; ORF 639-1.a>:

**a639-1.pep**

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWVAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSEISGN ISVGNMGMV LMFSERLKVF DNIAGVSRDQ
151 GIMLNYYNYS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGIHFTA
201 AIEGTSLDN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRPNG IIDQIIWRAP VSRLLMNSPA ISIVKWAQQA FPAVLPGGVV
301 DSKPLMKPYA PKIOTRYQAM KDGLLKKVET RQLEWGRAEN GSLN*

```

**a639-1/m639-1** .98.8% identity in 344 aa overlap

a639-1.pep	10	20	30	40	50	60
	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
a639-1.pep	70	80	90	100	110	120
	NGVTVWVAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
m639-1	NGVTVWVAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
	70	80	90	100	110	120
a639-1.pep	130	140	150	160	170	180
	ISVGNMGMVLMFSERLKVF DNIAGVSRDQ GIMLNYYNYS DIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMGMVLMFSERLKVF DNIAGVSRDQ GIMLNYYNYS DIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
a639-1.pep	190	200	210	220	230	240
	YDKLSANHFENCQIGIHFTAAIEGTSLDNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTAAIEGTSLDNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
	190	200	210	220	230	240
a639-1.pep	250	260	270	280	290	300
	NSAFDLNGDGFSDSAYRPNGIIDQIIWRAPVSRLLMNSPAISIVKWAQQAQFPAVLPGGVV					
m639-1	NSAFDLNGDGFSDSAYRPNGIIDQIIWRAPVSRLLMNSPAISIVKWAQQAQFPAVLPGGVV					
	250	260	270	280	290	300
a639-1.pep	310	320	330	340		
	DSKPLMKPYAPKIQTRYQAMKDGLLKKVETRQLEWGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLNX					
	310	320	330	340		

1016

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2051>:

```

g640.seq
  1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGC
 51  TATGTCCTGT TTTTCAATCC GGCGTATGTC TCGGTTTCGG GCGCGGATAA
101  CGGCGTTTTT TACCGCCTTT GTCTTTTGA CGGcggcACT GCCCGCTTAT
151  GcggAgcgTc tgcctGATTT TCTGgcgAAA ATacAgcctT CGGAAATTTT
201  TCCGGGTGCG GATCGTTACG GCAAGCCGGA aggcAAGCCT AtggtTGCCC
251  GCgtttACAA AGgcgATGAG CAGCTCGGTT TGGTTTATAT CACGACCGAT
301  GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATCGATA CGCTGATGGC
351  TTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GATCATCACG
401  AACCGATTAT GCTGATCGGT ATCCCGCAAT CGCGTGTCGA TAAGTTCATC
451  GACAAATATA TCGGTCTGAA TTTTATTAAA AATCCGCCGA CCCCGAGCGT
501  GCGCGCGGGC GACATCATCA GcggTGCGAC TgttaCACTG ATGGTGGTTA
551  ACGACAGCAT CCAGCGTTCG TACAAGGTCA TTGCCAACCA ATACCGTCTG
601  GGTTCCGACA AGGCCCTTCA GACGGCATCC GCTTCCGATG TTCGGGAAGC
651  CGCGCCTGCG TCAGAAACCC GTCCGCGCCG TATGGCAAAT CCCGACAAGC
701  AGGATATTTT GTCTTGGGAC GAACTTTTGA AACAAAAGGC CGTCGGCCAT
751  CTGCATATCA CGCTCGATCA AATCAACAAA CTGTTTGAGA AAGGCGGCAA
801  GGCCGGCGTG GCCGATCACG CCGAACAGGG CGATCCTGAC GATACCTTTA
851  TTGATTTGTA TGTTCCTTG GTCAGCCAGC CTTCCATCGG TAAAAGCCTG
901  CTGGGTGAGG ACGGCTGGGC GCATCTGCAA AAACGGCTGA AACCCTGGCA
951  GCAGGCGGTT TTGGTTGCCG GAGAGGGCCG TTATTCTTGG AAAGGTTCCG
1001 GCTATGTGCG CGGCGGTATT TTCGACCGTA TCGAGATGAT TCAGGGGGAG
1051 AACAGCTTCC GTTTTACCGA TGCCCAACAC GAACGCGTCG TCGAGCTGTC
1101 TGCCGCCGAT GCGCCGCGTT TTAAAGAAGT TTCTTGTTT ACCATCCCTG
1151 AAGGCGTAGC GTTTGACGGT GCGGAGCCGT GGCGGCTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2052; ORF 640.ng>:

```

g640.pep
  1  MIHIISILKS IGISGIAMSC FSIRMSAFR ARITAFFTAF VFLTAALPAY
 51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101  AVNTRGYSSK PIDTLMALAN DGTIAGAKLV DHHEPIMLIG IPQSRVDKFI
151  DKYIGLNFIF NPPTPSVAPG DIISGATVTL MVVNDSIQRS YKVIANQYRL
201  GSDKALQTAS ASDVREAAPA SETRPRRMAN PDKQDILSWD ELLKQKAVGH
251  LHITLDQINK LFEKGGKAGV ADHAEQGDPD DTFIDLYVAL VSQPSIGKSL
301  LGEDGWAHLQ KRLKPGQAV LVAGEGRYSW KSGYVVRGGI FDRIEMIQGE
351  NSFRFTDAQH ERVELSAAD APRFKEVSF TIPEGVAFDG AEPWRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2053>:

```

m640.seq (partial)
  1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
 51  CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101  CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151  GCGGAGCGTC TGCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTTT
201  TCCGGGTGCG GACCGTTACG GCAAGCCGGA AGGTAAGCCT ATGGTTGCCC
251  GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301  GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGT
351  GTTGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GACCATCACG
401  AACCATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2054; ORF 640>:

```

m640.pep (partial)
  1  MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
 51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101  AVNTRGYSSK PIDTLMVLAN DGTIAGAKLV DHHEPIMLIG IPH...

```

m640/g640 96.5% identity in 143 aa overlap

	10	20	30	40	50	60
m640.pep	MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAAFVFLTAALPAYAERLPDFLAK					
g640	MIHIISILKSIGISGIAMSCFSIRMSAFRARITAFFTAFVFLTAALPAYAERLPDFLAK					
	10	20	30	40	50	60
	70	80	90	100	110	120

1017

```

m640.pep    IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMVLAN
g640        IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMALAN
              70      80      90      100     110     120

              130     140
m640.pep    DGTIAGAKLVDHHEPIMLIGIPH
g640        DGTIAGAKLVDHHEPIMLIGIPQSRVDKFIDKYIGLNFINKPPTPSVAPGDIISGATVTL
              130     140     150     160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2055>:

```

a640.seq (partial)
  1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
 51  CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101  CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151  GCGGAGCGTC TGCCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTGT
201  TCCGGGTGCG GACCGTTACA GCAAGCCGGA AGGTAAGCCT ATGGTTGCCC
251  GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301  GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGC
351  GTTGGCTAAA GACGGTACGA TAGCCGGAGC GAAATTGGTT GATCACCATG
401  AGTCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2056; ORF 640.a>:

```

a640.pep (partial) Length: 143
  1  MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
 51  AERLPDFLAK IQPSEIVPGA DRYSKPEGK PMVARVYKGE QLGLVYITTD
101  AVNTRGYSSK PIDTLMALAK DGTIAGAKLV DHESIMLIG IPH...

```

m640/a640 96.5% identity in 143 aa overlap

```

              10      20      30      40      50      60
m640.pep    MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAFVFLTAALPAYAERLPDFLAK
g640        MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAFVFLTAALPAYAERLPDFLAK
              10      20      30      40      50      60

              70      80      90      100     110     120
m640.pep    IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMVLAN
g640        IQPSEIVPGADRYSKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMALAK
              70      80      90      100     110     120

              130     140
m640.pep    DGTIAGAKLVDHHEPIMLIGIPH
g640        DGTIAGAKLVDHHEPIMLIGIPH
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2057>:

```

g642.seq
  1  ATGCGGTATC CGCCGCAATC GGCGGTTTTG CAGAATGCCG CGCGTTGCCT
 51  TTTGCGCCGC CCGAAATCTG CCTGCCGCCG TATTTGCCCG CTATCCGCAA
101  TATCGCAGT CCAATATATC TTTGCGGATG TCGTTCAGCA GGAAGGCTGT
151  GGTGCTTCG TGTTCTCCTT GTACGAAGAC AAAAAGTCGG GCGATGATTT
201  TGCCGATGAA GACTTTTTGC AGGGCGCAGG CGTCGGTCAG GGTGTGTTCC
251  TGCAGGAAGC TGCGGATGTC TTCGGGCAAA GCGTAgtCgc gGGCAACGGC
301  GGcaaagcgG ACatcggtTT Gcacggcgtc gagCAGGGtt tggTTTTTGT
351  CCAACTTAAT GCCTGCTTCT TTTTCTTCGG CGGTGGCGCG GACGAACCTG
401  TCGTAAATTT CGGCATAAAG CATATCGTTC GGCCTTCAA AAATCGTGAA
451  GGGGCGGATA TCGATGGCGA TATTGCCGGC TGGGTGTCCG CGTTCAAAAC
501  CCTTCGCGCC CAAGAGTTT TGCAACATTT GCGCGGCGGc gTAAGTGTAT
551  TCCGTGGCGa ggGTTTTGAc gatgTTCGCC TCCATCAATT GATGGGCGAc
601  ggGCGcgacg ggCGAAACGG AATGGCAGAC GTAGCGGTAA AGGATTTCCG
651  AAACCTGATG GCGGCGTTGG ATTTCCGGCG GTTCGTAATC GACGAATCTG

```

1018

```

701 ATATCGTTGC GGACATATCG GTTCAGGTTG TCAAGGATGT ATTCCATAAT
751 GCCGTGCGTC ATGCCGATCA GTTGCAAGCG GCTGCGGATA AAGATGTTTT
801 GGAACGCGCG CAAACCGGCA GCGTCGCCCC GGGAGAGTTT CATCACGGCG
851 GTTGCAAGCA TTTCGGCATC GATGCGGTTG ACGGCGTAAC GGACGGCGCG
901 CAGGCCTTCG GATGCGAGGG TTTTCGAGCG GATGTATGTT TTGGGGACGA
951 GCAGCAGGTC GATGactttg gcgagtttgC CgtttttgCG ctcctttgCG
1001 gcaacgaggA GGAAGTCGCT TTGCGAATG CCCTGCCAGT ATTTTCGCGC
1051 GttgACGTAA ATGGTTgtt cgtcggtata ttcgtagcag gactgcaTTT
1101 CGCGTGCAAt cgCcgcgccg gaggtTtcgg gttcggtaAc gcccaaacgg
1151 cggctttcgC ctTTGAAAAT CATGTCCAAA CCTTGTGCGA CTTGCgcttc
1201 gccgccgaac tCTTGCAAG GCTGCAACAC CAGCGCGCCT TCGATGCCGG
1251 TACGCAGCGT AACGGGCACG CCGTAATGCC CCGCAATCCT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2058; ORF 642.ng>:

```

g642.pep
  1 MRYPPQSAVL QNAARCLLR PKSACRRICP LSAISAVQYI FADVVOQEGC
 51 GVVFLLYED KKSDDFADE DFLQAGVGQ GVFLQEAADV FGQSVVAGNG
101 GKADIGLHGV EQGLVFEVLN ACFFFFGGGA DELVVNFGIK HIVRAFKNRE
151 GADIDGDIAG WVSFAKTLRA QEFLQHLRGG VSVFRGEGFD DVRLHQLMGD
201 GRDGRNGMAD VAVKDFGNLM AALDFAAFVI DESDIVADIS VQVVKDVFNH
251 AVRHADQLQA AADKDVLEA QTGSVAPGEF HHGGCRHFGI DAVDGVTDGA
301 QAFGCEGFAA DVCFGDEQV DDFGEFAVFA LFGGNEEEVA LRIALPVFRG
351 VDVNGLEFVGI FVAGLHFACN RRAGGFGFNG AQTAFAFEN HVQTLCDLRF
401 AAELLQLQLQH QRAFDAGTQR NGHVMRPNP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2059>:

```

m642.seq (partial)
  1 GCCTGCCGCC GTATTTGCCC GCTACCCGCA ATATCGGCAG TCCAATATAT
 51 CTTTGCGGAT GTCGTTGAGC AGGAAGGCTG CCGTGTCTTC GTGTTTCGCC
101 TGTACGAAGA CAAAGAGTCG GGCGATGATT TTGCCGATAA AGACTTTTTG
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTC CTGCAGGAAG CTGCGGATGT
201 CTTCAGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAATTCA TGCCTGCTTC
301 TTTTCTCTCG GCGGTGGCGC GGACAACTG GTCGTAAAT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATACCG
401 ATATTGCCGG CCGTGTGTCC GCGTTCAAAA CCCTTCGCAC CCAAGAGTTT
451 TTGCAACATT TGCGCGGCGG CGTAAGTGTA TTCCGTGGCG AGGGTTTTGA
501 CGATGTTGCG CTCCATCAGC TGATGGGCGA CGGGGGCAAC AGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GCGCGCGCCG
601 GATTTGCGCG CGTTCGTAAT CGACGAATTT GATGTCGTTG CGGACGTATC
651 GTTCCAGATT TTCAAGGATG TATTCCATAA TGCCGTGCGT CATGCCGATC
701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATACGGC GGTGTCAGGC ATTTCCGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTGCGCG CGTTGACGTA AATGGTTTGT
1001 CCGTCGATAT ATTCGTAGTA GGACTGCATT TCGCGTGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CACCCAAACC GCCGCCCTCG CCTTTGAAAA
1101 TCATCTCCAA ACCTTGCGCG ACTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2060; ORF 642>:

```

m642.pep (partial)
  1 ACRRICPLPA ISAVQYIFAD VVQQEGCGVF VFRLYEDKES GDDFADKDFL
 51 QGAGIGQGVF LQEAADVFRQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VDSDIAGGVS AFKTLRTQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGGN RRNGMADVAV KNLGNLMAAP
201 DFAAFVIDEF DVVADVFSQI FKDVFNHNAV HADQLQAAAD KDVLEAQTG
251 SVALGEFHG GCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFAVFALFG GNEEEVALRV ALPVFRGVDV NGLSVDIFVV GLHFACNRR
351 GGFGFGNTQT AALAFENHLQ TLRDLRFIAE LLQWLQHORA FDAGTQRNGH
401 AVMPRNP

```

1019

m642/g642 90.4% identity in 407 aa overlap

m642.pep				10	20	30	
				ACRRICPLPAISAVQYIFADV	VVQEGCGVFVRLYED		
g642	MRYPPQSAVLQNAARCLLRPKSACRRICPLSAISAVQYIFADV	VVQEGCGVFVLLYED		10	20	30	40
				40	50	60	70
m642.pep	KESGDDFADKDFLQAGIGQGVFLQEAADVFRQSVVAGDGGKAGIGLQAVEQGLV	FVQLH		70	80	90	
g642	KKSGDDFADEDFLQAGVGGQGVFLQEAADVFGQSVVAGNGGKADIGLHGVEQGLV	FVQLN		70	80	90	100
				100	110	120	
m642.pep	ACFFFFGGGADKLNVNFGIKHIVRAFKNREGADVDS	DIAGGVSAFKTLRTQEF	LOHLRGG				
g642	ACFFFFGGGADELNVNFGIKHIVRAFKNREGADIDG	DIAGVWSAFKTLRAQEF	LOHLRGG				
				130	140	150	160
m642.pep	VSVFRGEGFDDVRLHQLMGDGGNRRNGMADVAVK	NLGNLMAAPDFAAFVIDE	FVADV				
g642	VSVFRGEGFDDVRLHQLMGDGRDGRNGMADVAVK	DFGNLMAALDFAAFVIDE	SIVADIS				
				160	170	180	190
m642.pep	FQIFKDVFNHNAVRHADQLQAAADKDVLER	AQTGSVALGEFHHGGCRHFGID	AVDGVTDGA				
g642	VQVVKDVFNHNAVRHADQLQAAADKDVLER	AQTGSVAPGEFHHGGCRHFGID	AVDGVTDGA				
				220	230	240	250
m642.pep	QAFGCEGF	AADVCFGDEQQVDDFGEFAVF	FALFGGNEEEVALRVALPVFRGVDV	NGLSVDI			
g642	QAFGCEGF	AADVCFGDEQQVDDFGEFAVF	FALFGGNEEEVALRIALPVFRGVDV	NGLFVGI			
				280	290	300	310
m642.pep	FVVGLHFACNRRAGGF	GFNGTQTAAALAFENHLQTLRDLRFIAELLQWLQHQRAFD	AGTQR				
g642	FVAGLHFACNRRAGGF	GFNGAQTAAAFENHVQTLCDLRFIAELLQRLQHQRAFD	AGTQR				
				340	350	360	370
m642.pep	NGHAVMPRNP						
g642	NGHAVMPRNPX						
				400	410	420	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2061>:

a642.seq (partial)

```

1  GCCTGCCGCC GTATTTGCCG GCTATCCGCA ATATCGGCAG TCCAATATGT
51  CTTTGC GGAT GTCGTT CAGC AGGAAGGCTG CGGTGTCTTC GTGTTCCGCG
101 TGTACGAAGA CAAAGAGTCG GCGGATGATT TTGCCGATAA AGACTTTTGT
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTC CTGCAGGAAG CTGCGGATGT
201 CTTCCGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAACTTCA TGCCTGCTTC
301 TTTTCTTCG GCGGTGGCGC GGACAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTTCAAAA CCCTTCGCGC CCAAGAGTTT
451 TTGCAACATT TGCGCGGCGG CGTAAGTGTA TTCCGTGGCG AGGGTTTTGA
501 CGATGTTCCG CTCCATCAGT TGATGGGCGA CGGGTGCAAC GGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GGCGGCGCGG
601 GATTTCCGCG CGTTCGTAAT CGACGAATCT GATGTCGTTG CGGACGTATC
651 GTTCCAGGTT TTCAAGGGTG TATTCCATAA TGCCGTGCGT CATGCCGATC

```

1020

```

701 AGTTGCGAGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCGAGC ATTTCCGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTGCGCG CGTTGACGTA AATGGTTTGT
1001 CCGTCGGTAT ATTCGTAGTA AGACTGCATT TCTCGGGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CGCCTAAACC GCCGCCCTCG CCTTTGAAAA
1101 CCATGTCCAA ACCCTGTGCG ATTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2062; ORF 642.a>:

```

a642.pep Length: 407
1 ACRRICPLSA ISAVQYVFAD VVQQEGCGVF VFRLYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFGQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VDSDIAGGVS AFKTLRAQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGCN GRNGMADVAV KNLGNLMAAP
201 DFAAFVIDES DVVADVVSFQV FKGVFHNAVR HADQLQAAAD KDVLERAQTG
251 SVALGEFHHG GCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEQQVDDF
301 GFAVFALFG GNEEEVALRV ALPVFRGVDV NGLSVGIFV RLHFSGNRRA
351 GGFGFGNA*T AALAFENHVQ TLCDLRFIAE LLQWLQHORA FDAGTQRNGH
401 AVMPRNP

```

m642/a642 95.8% identity in 407 aa overlap

```

              10      20      30      40      50      60
m642.pep    ACRRICPLSAISAVQYIFADV VVQQEGCGVFVFRLYEDKESGDDFADKDFLQAGIGQGVF
              |||||  |||||:|||||
a642        ACRRICPLSAISAVQYVFADV VVQQEGCGVFVFRLYEDKESGDDFADKDFLQAGIGQGVF
              10      20      30      40      50      60

              70      80      90      100     110     120
m642.pep    LQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFFGGGADKL VVNFGIKHIV
              |||||  |||||:|||||
a642        LQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFFGGGADKL VVNFGIKHIV
              70      80      90      100     110     120

              130     140     150     160     170     180
m642.pep    RAFKNREGADVDSDIAGGVSAFKTLRTQEF LQHLRGGVSVFRGEGFDDVRLHQLMGDGCN
              |||||  |||||:|||||
a642        RAFKNREGADVDSDIAGGVSAFKTLRAQEF LQHLRGGVSVFRGEGFDDVRLHQLMGDGCN
              130     140     150     160     170     180

              190     200     210     220     230     240
m642.pep    RRNGMADVAVKNLGNLMAAPDFAAFVIDEFDVVADV SFQIFKDV FHNVRHADQLQAAAD
              |||||  |||||:||
a642        GRNGMADVAVKNLGNLMAAPDFAAFVIDESDVVADV SFQVFKGV FHNVRHADQLQAAAD
              190     200     210     220     230     240

              250     260     270     280     290     300
m642.pep    KDVLERAQTG SVALGEFHHGGCRHFGIDAVDGVTDGAQAF GCEGFAADVC FGDEQQVDDF
              |||||  |||||:|||||
a642        KDVLERAQTG SVALGEFHHGGCRHFGIDAVDGVTDGAQAF GCEGFAADVC FGDEQQVDDF
              250     260     270     280     290     300

              310     320     330     340     350     360
m642.pep    GFAVFALFGGNEEEVALRV ALPVFRGVDV NGLSVGIFV VRLHFSGNRRAGGFGFGNTQT
              |||||  |||||:|||||
a642        GFAVFALFGGNEEEVALRV ALPVFRGVDV NGLSVGIFV VRLHFSGNRRAGGFGFGNAXT
              310     320     330     340     350     360

              370     380     390     400
m642.pep    AALAFENHLQTLRDLRFIAELLQWLQHORA FDAGTQRNGHAVMPRNP
              |||||  |||||:|||||
a642        AALAFENHVQTLCDLRFIAELLQWLQHORA FDAGTQRNGHAVMPRNP

```

1021

370 380 390 400

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2063>:

**g643.seq**

```

1   ATGGTGTTCG CTTTGATGTT GTTGGCGACA ATCAGgTcgg CTACGCTGAc
51  gttgtancGt TTGGcaATGt tGaaCAgggt gtcgccTTCT ACAACGCGGT
101 GGATGCTGGC ATGGagcGGG GAGGTTTCGG CTTCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TGCCCGGCGT TtgCCGTCGG CGGCAACGGT
201 ATGTTGCGGA GATGAGGAAA TGTTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGagatGGTT TCTTCAGCCT GCCGGCGCag gTTGTTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTGGGGGGAt
351 GACCTGCGCg aGTGtTGCGG TTTGGGTTTC agacgGCATG GCAGTCTGTT
401 TTTcggTTTG a

```

This corresponds to the amino acid sequence <SEQ ID 2064; ORF 643>:

**g643.pep**

```

1   MVLPLMLLAT IRSATLTLXR LAMLNRVSPS TTRWMLAWSG EVSASPSAAL
51  ATRVSKRARR LPSAATVCCG DEEMLCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFGGMTCA SVAVWVSDGM AVCFSV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2065>:

**m643.seq**

```

1   ATGGTGTTCG CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
51  GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
101 GGATGCTGGC ATGGAGCGGG GAGATTTTCGG CTTCCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAGCGGT
201 ATGTTGCGGA GATGCGGAAA TTTTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAT
351 GATCTGCGCG AGTGTGCGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
401 TTTCGGTTTG A

```

This corresponds to the amino acid sequence <SEQ ID 2066; ORF 643>:

**m643.pep**

```

1   MVLPLMLLAT IRSATLTL*R LAMLNRVSPS TTRWMLAWSG EISASPSAAL
51  ATRVSKRTRR LPSAAVCCG DAEILCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFWGMICA SVAVWVSDGM AVCFSV*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 643 shows 94.9% identity over a 136 aa overlap with a predicted ORF (ORF643.a) from *N. gonorrhoeae*:

**m643/g643**

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
g643	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEVSASPSAALATRVSKRARR					
	10	20	30	40	50	60
m643.pep	70	80	90	100	110	120
	LPSAAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAAACMSFWGMICA					
g643	LPSAATVCCGDEEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAAACMSFGGMTCA					
	70	80	90	100	110	120
m643.pep	130					
	SVAVWVSDGMAVCFSVX					
g643	SVAVWVSDGMAVCFSVX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2067>:



1022

```

a643.seq
  1  ATGGTGTTC  CTTTGATGTT  GTTGGCGACA  ATCAGGTCGG  CTACACTGAC
 51  GTTGTAGCGT  TTGGCAATGT  TGAACAGGGT  GTCGCCTTCT  ACAACGCGGT
101  GGATGCTGGC  ATGGAGCGGG  GAGATTTCCG  CTTCCGCCGC  GGCAGCTTTG
151  GCTACGCGCG  TTTCCAAACG  TACCCGCGCT  TTGCCGTCGG  CGGCAACGGT
201  ATGTTGCGGA  GATGAGGAAA  TGTGTGTGTC  GGCAACTGTG  TCAGGCGTGC
251  CGATGACGGC  AGAGATGTTT  TCTTCAGCCT  GTCGGCGCAG  GTTGTTCGG
301  GCAACAAGCT  GCATGAGTTC  GTCTGCCGCC  TGCATGTCGT  TTTGGGGGAC
351  GATCTGCGCG  AGTGTGCGG  TTTGGGTTTC  AGACGGCATG  GCGGTCTGTT
401  TTTGCGTTTG  A

```

This corresponds to the amino acid sequence <SEQ ID 2068; ORF 643.a>:

```

a643.pep
  1  MVLPLMLLAT  IRSATLTL*R  LAMLNRVSPS  TTRWMLAWSG  EISASPSAAL
 51  ATRVSKRTRR  LPSAATVCCG  DEEMLCSATV  SGVPMTAEMV  SSACRRRLFR
101  ATSCMSSSAA  CMSFWGTICA  SVAVWVSDGM  AVCFSV*

```

m643/a643 97.1% identity in 136 aa overlap

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
a643	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m643.pep	LPSAAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAAACMSFWGMICA					
a643	LPSAATVCCGDEEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAAACMSFWGTICA					
	70	80	90	100	110	120
	130					
m643.pep	SVAVWVSDGMVAVCFVSX					
a643	SVAVWVSDGMVAVCFVSX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2069>:

```

g644.seq
  1  ATGCCGTCTG  AAAGGccgc  GGATTGTTC  CCGGTGCACT  TTGTGGTAAA
 51  GTTTAGAAAA  TTAACCTCTA  ACTGTGGCAG  GCGGTTTGAC  CGGCCGCCGA
101  TTAATGGGAA  CCGACAGAGG  AAGCCGATGA  TACACACCGA  ACCGAGCGCG
151  CAGCCGTCAA  CCATGGACAC  GGCTGCTTTT  TTAAagcaca  tcgaatCCGC
201  ATTcCCCCGC  ATTTTTTCAG  ACGGCATCGA  CCTGATGCGA  TACCTGCCCG
251  AAGACAAATG  GCTTGCCCTG  AAGCAGGCGG  GTTGTCTGTT  GCCCTTCCTC
301  GACAAAAAAC  ACGGCGGGCG  CAAGGGCAGT  CAGTTTGAAA  TCCAAGAAGT
351  CCTAAGGATT  GCGGGGCATT  ACGGCGTGCC  CGTTACGCTG  CGTACCGGCA
401  TCGAAGGCGC  GCTGGTGTG  CAGCCTCTGC  AAGagttcgg  cggcgaagcG
451  CAAGTCGCAC  AAGGTTTGGA  CATGATTTTC  AAagggcaaa  gccgcggttt
501  gggcgTtacc  gaaccgaAa  cctccggcgc  gGcgaTTGCA  CGCGAAAtgc
551  agtcctgcta  cgaatatacc  gacgaacaAA  CCATTTACGT  caaCGCCGCG
601  AAATACTGGC  AGGGCAATTC  GCAAAGCGAC  TTCTTcctcg  ttgccgccaa
651  agagcgcaaa  aacGGcaaac  tcgccaaagt  CATCGACCTG  CTGCTCGTCC
701  CCAAAACATA  CATCCGCTGC  GAAACCCCTG  CATCCGAAGG  CCTGCGCGCC
751  GTCCGTTACG  CCGTCAACCG  CATCGATGCC  GAAATGCGTG  CAACCGCCGT
801  GATGAAACTC  TCCCGGGGCG  ACGCTGCCGG  TTTGCGCGCG  TTCCAAAACA
851  TCTTTATCCG  CAGCCGCCTG  CAACTGATCG  GCATGACGCA  CGGCATTATG
901  GAATACATCC  TTGACAACCT  GAACCGATAT  GTCCGCAACG  ATATCAGATT
951  CGTGATTAC  GAACGCGCG  AAATCCAACG  CCGCCATCAG  GTTCCGAAA
1001  TCCTTTACCG  CTACGTCTGC  CATTCCGTTT  CGcccgtcgC  GCccgTCGCC
1051  CATCAATTGA  TGGAGGCGAA  catcgTCAAA  ACcctCGCCA  CGGAATACAC
1101  TTAcgcCGCC  GCGCAAAATG  TGCAAAAAC  CTGGGCGCG  AAGGGTTTG
1151  AACGCGGACA  CCCAGCCGGC  AATATCGCCA  TCGATATCCG  CCCCTTCACG
1201  ATTTTTGAG  GCCCGAACGA  TATGCTTTAT  GCCGAAATTT  ACGACCAGTT
1251  GTCCCGCGCC  ACCGCCAAG  AAAAGAAGC  AGGCATTAA  TTGGACAAAA
1301  accaaaCCCT  Gctcgacgcc  gtgCAAaccg  atGTCcgctt  tgCCGCGGTT
1351  GCCcgcGacT  ACGCTTTGCC  CGAAGACATC  CGCAGCTTCC  TGCAGGAACA
1401  CACCCTGACC  GACGCCTGCG  CCCTGCAAAA  AGTCTTCATC  GGCAAAATCA

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1023

1451 TCGCCCGACT TTTTGTCTTC GTACAGGAGG AACACGAAGA CACCACAGCC  
 1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG  
 1551 ATAG

This corresponds to the amino acid sequence <SEQ ID 2070; ORF 644.ng>:

g644.pep

1 MPSERPADCC PVHFVVKFRK LTLNCGRRFD RPPINGNRQR KPMIHTEPSA  
 51 QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL  
 101 DKKHGGRRKS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGEA  
 151 QVAQGDMIF KGESRRLGVT EPETSGAIA REMQSCYEY DEQTIYVNAA  
 201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA  
 251 VRYAVNRIDA EMPATAVMKL SRGDAAGLRA FQNIIFIRSRL QLIGMTHGIM  
 301 EYILDNLNRY VRNDIRFVDY ERREIQRHQ VSEILYRYVC HSVSPVAPVA  
 351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHPAG NIAIDIRPFT  
 401 IFEGPNDMLY AEIYDQFVRA TAEKEAGIK LDKNQTL LDA VQTDVRF AAV  
 451 ARDYALPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VQEEHEDTTA  
 501 FLLNDIRKDI LDCRYCG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2071>:

m644.seq

1 ATGCCGCTCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAA  
 51 GTTTAGAAAA TCAACTCTAA ACTGTGGCAG CGGGTTTGAC CGGCCGCCGA  
 101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG  
 151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TAAAGCACA TCGAATCCGC  
 201 ATTCCGCGCG ATTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCG  
 251 AAGACAAATG GCTTGCCCTG AAGCAGGCGG GTTGTCTGTT GCCCTTCCTC  
 301 GACAAAAAAT ACGGCGGGCG CAAGGGCAGC CAGTTTGAAA TCCAAGAAGT  
 351 CcTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA  
 401 TCGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG  
 451 CAAGTCGCGC AAGGTTTGGA GATGATTTTC AAAGGCGAGG GCGGCGGTTT  
 501 GGGTGTTACC GAACCCGAAA CCTCCGGCGC GGCGATTGCA CGCGAAATGC  
 551 AGTCCTACTA CGAATATATC GACGGACAAA CCATTTACGT CAACGCCGCG  
 601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA  
 651 AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC  
 701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CTGCGCGGCC  
 751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT  
 801 GATGAACTC TCCAGAGCG ACGCTGCCGG TTGCGCGCG TTCCAAACA  
 851 TCTTTATCCG CAGCCGCTG CAACTGATCG GCATGACGCA CGGCATTATG  
 901 GAATACATCC TTGAAATCT GGAACGATAC GTCCGCAACG ACATCAAATT  
 951 CGTCGATTAC GAACGCCGCG AAATCCGCGC CGCCATCAG GTTCCGAGA  
 1001 TTCTTTACCG CTACGCTGCG CATTCGCTT CGCCTGTGCG CCCCCTCGCC  
 1051 CATCAGCTGA TGGAGGCGAA CATCGTCAA ACCCTCGCCA CGGAATACAC  
 1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTTGGGTGCG AAGGGTTTTG  
 1151 AACCGCGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG  
 1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAGTT  
 1251 TGTCCGCGCC ACGCCGAAG AAAAAGAAG AGGCATGAAG TTGGACAAAA  
 1301 ACCAAACCCT GCTCGACCGC CTGCAAACCG ATGCCCGCTT TGCCGCCGTC  
 1351 GCCCGCGACT ACACCTTGCC TGAAGACATC CGCAGCTTCC TGCAGGAACA  
 1401 CACCTGACC GATGCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA  
 1451 TCGCCCGACT CTTGTCTTC GTACAGGCGA AACACGAAGA CACCGCAGCC  
 1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG  
 1551 GTAG

This corresponds to the amino acid sequence <SEQ ID 2072; ORF 644>:

m644.pep

1 MPSERSADCC PAHFVVKFRK STLNCGRRFD RPPINGNRQR KPMIHTEPSA  
 51 QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL  
 101 DKKYGGRRKS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGEA  
 151 QVAQGLEMIF KEGGGGLGVT EPETSGAIA REMQSYEYI DGQTIYVNAA  
 201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA  
 251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNIIFIRSRL QLIGMTHGIM  
 301 EYILENLERV VRNDIKFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA  
 351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT  
 401 IFEGPNDMLY AEIYDQFVRA TAEKEAGMK LDKNQTLDR LQTDARFAAV  
 451 ARDYTLPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VQAKHEDTAA  
 501 FLLNDIRKDI LDCRYCG\*

m644/g644 94.6% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pep	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
g644	MPSERPADCCPVHFVVKFRKLTNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					

1024

	10	20	30	40	50	60
m644.pep	70	80	90	100	110	120
g644	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI					
	70	80	90	100	110	120
m644.pep	130	140	150	160	170	180
g644	AGHYGVPVTLRTGIEGALVLQPLQEFGEAQAQGLEMIKKGEGGGLGVTEPETSAAIA					
	130	140	150	160	170	180
m644.pep	190	200	210	220	230	240
g644	REMQSYEYIDGQTIYVNAAKYWQGSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
	190	200	210	220	230	240
m644.pep	250	260	270	280	290	300
g644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNIIFIRSRLQLIGMTHGIM					
	250	260	270	280	290	300
m644.pep	310	320	330	340	350	360
g644	EYILENLERYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMANIVK					
	310	320	330	340	350	360
m644.pep	370	380	390	400	410	420
g644	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
m644.pep	430	440	450	460	470	480
g644	TAAEKEAGMKLDKNQTLDRQLTDARFAAVARDYTLPEDIRSFLQEHITLDACALQKVFI					
	430	440	450	460	470	480
m644.pep	490	500	510			
g644	GKIIARLFVQAKHEDTAAFLNDIRKDILDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2073>:

a644.seq

```

1  ATGCCGTCCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
51  GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
201 ATTCGCGCCG ATTTTTCGAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
251 AAGACAAATG GCTTGCCTTG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
301 GACAAAAAAT ACGGCGGGCG CAAGGGCAGC CAGTTTGAAA TTCAGGAAGT
351 CTTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTANNNNN NNNNNNNNNN
401 NNGAAGGCGC GCTGGTGTTC CAGCCACTGC AAGAGTTCGG CGATGAAGCG
451 CAAATCGCAC AGGGTTTGGG CATGGTTTTC AAAGGCGAGG GCGGCGGTTT
501 AGGCGTTACC GAACCCGAAA CCTCCGGCGC GCGGATTGCC CGAGAAATGC
551 AGTCTTACTA CGAATATACC GACGGACAAA CCATTTACGT CAACGCCGCG
601 AAATACTGGC AGGGCAATC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA
651 AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CTTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACGCCGCT
801 GATGAAATC TCCAGAGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA

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1025

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851 TCTTTATCCG CAGCCGCCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACACCC TTGAAAACCT GGAACGATAC GTCCGCAACG ACATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCGGCG CCGCCATCAG GTTTCCGAGA
1001 TTCTTTACCG CTACGTCTGC CATTCGGTTT CGCCCGTTGC ACCCGTCGCC
1051 CATCAACTGA TGGAGGCGAA CATCGTCAAA ACCCTCGCCA CGGAATACAC
1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTTGGGCGCG AAGGGTTTGT
1151 AACGCGGACA CACCGCCGGC AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTTGAAG GCGCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAGTT
1251 TGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
1301 ACCAAACCCCT GCTCGACCGC CTGCAAACCG ATGCCCGCTT TGCCGCCGTC
1351 GCCCGCGACT ACACTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCGTGACC GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCCGACT CTTTGTCTTC GTACAGGCGG AACACGAAGA CACCGCAGCC
1501 TTCTGTCTGA ACGACATCCG CAAAGACATA TTGGACTGCC GATATTGCGG
1551 ATAG

```

This corresponds to the amino acid sequence <SEQ ID 2074; ORF 644.a>:

```

a644.pep
1  MPERSADCC PAHFVVKFRK STLNCGRFRD RPPINGNRQR KPMIHTEPSA
51  QPSTMDTAAF LKHIESAFRR IFADGIDLMR YLPEDKWLAL KQAGLLLPFL
101 DKKYGGRKGS QFEIQEVLRI AGHYGVPVXX XXXXEGALVL QPLQEFGDEA
151 QIAQGLDMVF KEGGGGLGVT EPETSGAAIA REMQSYEYTDGQTIYVNA
201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNI FIRSRL QLIGMTHGIM
301 EYTLNLERI VRNDIRFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
351 HQLMLEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
401 IFEGPNDMLY AEIYDQFVRA TAEKEEAGMK LDKNQTLDR LQTDARFAAV
451 ARDYTLPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQAEHEDTAA
501 FLLNDIRKDI LDCRYCG*

m644/a644 97.3% identity in 517 aa overlap

10 20 30 40 50 60
m644.pep MPERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
|||||
a644 MPERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
10 20 30 40 50 60

70 80 90 100 110 120
m644.pep LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI
|||||
a644 LKHIESAFRRIFADGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI
70 80 90 100 110 120

130 140 150 160 170 180
m644.pep AGHYGVPVTLRTGIEGALVLQPLQEFGDEAQVAQGLEMI FKEGGGGLGVTEPETSGAAIA
|||||
a644 AGHYGVPVXXXXXXEGALVLQPLQEFGDEAQIAQGLDMVFKEGGGGLGVTEPETSGAAIA
130 140 150 160 170 180

190 200 210 220 230 240
m644.pep REMQSYEYIDGQTIYVNAAKYQWQNSQSD FLLVAAKERKNGKLAKVIDLLVPKTYIRC
|||||
a644 REMQSYEYTDGQTIYVNAAKYQWQNSQSD FLLVAAKERKNGKLAKVIDLLVPKTYIRC
190 200 210 220 230 240

250 260 270 280 290 300
m644.pep ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM
|||||
a644 ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM
250 260 270 280 290 300

310 320 330 340 350 360
m644.pep EYILENLERIYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMLEANIVK
||
a644 EYTLNLERIYVRNDIRFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMLEANIVK

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1026

	310	320	330	340	350	360
	370	380	390	400	410	420
m644 . pep	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
a 644	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m644 . pep	TAEKEAGMKLDKNQTLTDLRLQTDARFAAVARDYTLPEDIRSFLQEHTLTDACALQKVFI					
a 644	TAEKEAGMKLDKNQTLTDLRLQTDARFAAVARDYTLPEDIRSFLQEHTLTDACALQKVFI					
	430	440	450	460	470	480
	490	500	510			
m644 . pep	GKIIARLFVVFQAKHEDTAAFLNDIRKDILDCRYCGX					
a 644	GKIIARLFVVFQAEHEDTAAFLNDIRKDILDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2075>:

g645 . seq

```

1  ATGATGATGG TGTGGCGGTT GGGGATGTCG ATGCCGGTTT CGATGATGGT
51  GGAACAGAGC AACACATTGA ATCTTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCACGC AGTTGTCCGT GCGCCACGCC GATACGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTCTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAata cCTGTCTCC GCGTTTGAGT TCGCGCAACA
251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTGACAAA GGTTTTCACG
301 GCGAGGCGGC GGCTCGGTGC AGTGGTAATC AGCGAGAAGT CGCGCAGACC
351 TTCGAGCGCC ATGCTGAGGG TCGCGGAAT CGGCGTGGCG GTCATGGTTA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTT CTGTCCGACG
451 CCGAAGCGGT GTTCTTCATC GATAATCAAT AAACCTAAGT TTTGAATTT
501 TATGTCGTCC TGCACCAATT TGTGCGTACC GATAACGATA TCGACAGTAC
551 CGTCCGCCAT GCCTTCGAGC GTGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTGCGCGAA
651 GTTTTGCGCG TGCTGCTCGA CCAGAAGCGT GGTCGGGGCG AGTACGGCGA
701 CCTGTTTGCC GCCATCACC GCCACAAACG CGGCGCGAAG GCGGACTTCG
751 GTTTTGCCGA AACCGACATC GCCGCACACA AGTCGGTCCA TCGGCTTCGC
801 CTGCGTCAAA TCTTAAATCA CGGcggcgat ggcggcggc TGGTCTTCGG
851 TTCTCTCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 2076; ORF 645.ng>:

g645 . pep

```

1  MMMVLALGMS MPVSMMEQSS NTLNLCKKKS RMTCSSSRSR SCPCATPIRA
51  SGRVSSRSR IFSIVSTSLC RKNTCPPLRS SRNTASRTLP SLNGLTKVFT
101 ARRLGAVVI SEKSRRPSSA MLRVRGIGVA VMVRMSTLAR RRLSCSFCRT
151 PKRCSSTIN KPKFLNFMSS CTNLCVPITI STVPSAMPSS VALVALLLLK
201 RERLATFTGK SAKRSKFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT SRSIGFACVK SLITAAMAAA WSSVSS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2077>:

m645 . seq

```

1  ATGATGATGG TGTGGCGGTT GGGGATATCG ATACCGGTTT CGATGATGGT
51  GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTTTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAATA CCGTCTCTCC GCGTTTGAGT TCGCGCAACA
251 CGGCTTCGCG CACGCTGCCT TCGCTAAAGG GTTGACAAA GGTTTTGACG
301 GCGAGGCGGC GGCTGGGCGC GGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TTCCAACGCC ATACTTAAAG TACGCGGAAT CGGCGTGGCG GTCATGGTAA
401 GGATATCAAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTT CTGACGCACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTAAGT TTTGAATTT
501 GATGTCGTCC TGCACCAATT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCTGCCAT GCCTTCGAGC GCGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTGCGCGAA
651 GTTTTGCGCG TGCTGCTCGA CCAAAAGCGT GGTCGGAGCA AGTACGGCGA
701 CCTGTTTGCC GCCATCACC GCCACAAACG CGGCGCGCAG GCGGACTTCG
751 GTTTTGCCGA AGCCGACATC GCCGCACACA AGGCGATCCA TCGGCTTCGC
801 TTGCGTCAAA TCTTAAATCA CGGCGCGGAT GCGGCGGCC TGGTCTTCGG

```

1027

851 TTTCTTCGTA G

This corresponds to the amino acid sequence &lt;SEQ ID 2078; ORF 645&gt;:

m645.pep

```

1  MMMVLALGIS IPVSMMEQSN TLNRCCKKS RMTCSSSRSR SCPCATPMRA
51  SGRVSSRSR IFSIVSTSLC RKNTCPPLRS SRNTASRTL SLKGLTKVLT
101 ARRLGAVVI SEKSRSPSNA ILKVRGIGVA VMVRISTLAR RRLSCSF*RT
151 PKRCSSSIIT KPKFLNLMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
201 RERLATFTGK SAKRSAKFA CCSTKSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

```

m645/g645 93.7% identity in 286 aa overlap

	10	20	30	40	50	60
m645.pep	MMMVLALGISIPVSMMEQSN	TLNRCCKKS	RMTCSSSRSR	SCPCATPMRA	SGRVSSRSR	
g645	MMMVLALGMSMPVSMMEQSN	TLNRCCKKS	RMTCSSSRSR	SCPCATPIRA	SGRVSSRSR	
	10	20	30	40	50	60
	70	80	90	100	110	120
m645.pep	IFSIVSTSLCRKNTCPPL	SSRNTASRTL	PSLKGLTKVLT	ARRRLGAVVI	SEKSRSPSNA	
g645	IFSIVSTSLCRKNTCPPL	SSRNTASRTL	PSLNGLT	KVFTARRRLGAVVI	SEKSRSPSNA	
	70	80	90	100	110	120
	130	140	150	160	170	180
m645.pep	ILKVRGIGVAVMVRIST	LARRRLSCSF	FXRTPKRCSSSIIT	KPKFLNLMSS	CTSLCVPITI	
g645	MLRVRGIGVAVMVRIST	LARRRLSCSF	FCRTPKRCSSSIIN	KPKFLNLMSS	CTNLCVPITI	
	130	140	150	160	170	180
	190	200	210	220	230	240
m645.pep	STVPSAMPSSAALVALL	LLKRERLATFT	GSAKRSKFA	CCSTKSVVGA	STATCLPPIT	
g645	STVPSAMPSSVALVALL	LLKRERLATFT	GSAKRSKFA	CCSTRSVVGA	STATCLPPIT	
	190	200	210	220	230	240
	250	260	270	280		
m645.pep	ATNAARRATSVLPKPT	SPHTRRSIGFACVK	SLITAAMAAW	SSVSSX		
g645	ATNAARRATSVLPKPT	SPHTRSIGFACVK	SLITAAMAAW	SSVSSX		
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2079>:

a645.seq

```

1  ATGATGATGG TGTTGGCGTT GGAATGTCG ATACCGGTTT CGATGATGGT
51  GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCACGC ATGTTTTCGA TGGTATCCAC
201 TTCATTGTGC AGGAAAAATA CTTGCCCGCC GCGTTTGAGT TCGCGCAATA
251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTTGACAAA GGTTTTGACG
301 GCGAGGCGGC GGCTGGGCGC AGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TTCCAGCGCC ATACTTAAAG TACGCGGAAT CGGCGTAGCG GTCATGGTAA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTACGT TTTTGAATTT
501 TATGTCGTCC TGCACCAAGT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCCGCCAT GCCTTCCAGC GCGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAGC GGTGCGCAAA
651 ATTTTGCGCG TGCTGCTCGA CCAGAAGCGT GGTCGGTGCG AGTACGGCAA
701 CTTGTTTGCC ACCATTACC GCCACAACG CGGCGCGCAG GGCGACTTCG
751 GTTTTGCCGA AACCACATC GCCGCACACG AGGCGGTCCA TCGGCTTCGC
801 CTGCGTCAAA TCTTTAATCA CGGCGCGCAT GCGGCTGCG TGGTCTTCGG
851 TTTCTTCGTA G

```

This corresponds to the amino acid sequence &lt;SEQ ID 2080; ORF 645.a&gt;:

a645.pep

```

1  MMMVLALGMS IPVSMMEQSN TLNRCCKKS RMTCSSSRSR SCPCATPMRA

```

1028

```

51  SGSRVSSRSR MFSMVSTSLC RKNTCPPLRL SRNTASRTLPL SLNGLTKVLT
101 ARRLGAVVI SEKSRSPSSA ILKVRGIGVA VMVRMSTLAR RRLSCSF*RT
151 PKRCSSSIIT KPTFLNFMSS CTSCLVPITI STVPSAMPSS AALVALLLLK
201 RERLATFTGK SAKRSKFCA CCSTRSVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

m645/a645 96.9% identity in 286 aa overlap

      10      20      30      40      50      60
m645.pep  MMMVLALGISIPVSMVEQSNTLNRCCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645      MMMVLALGMSIPVSMVEQSNTLNRCCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
      10      20      30      40      50      60

      70      80      90     100     110     120
m645.pep  IFSIVSTSLCRKNTCPPLRLSSRNTASRTLPSLKGLTKVLTARRRLGAVVISEKSRSPSNA
      :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645      MFSMVSTSLCRKNTCPPLRLSSRNTASRTLPSLNGLTKVLTARRRLGAVVISEKSRSPSSA
      70      80      90     100     110     120

      130     140     150     160     170     180
m645.pep  ILKVRGIGVAVMVRISTLARRRLSCSFXRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645      ILKVRGIGVAVMVRMSTLARRRLSCSFXRTPKRCSSSIITKPTFLNFMSSCTSLCVPITI
      130     140     150     160     170     180

      190     200     210     220     230     240
m645.pep  STVPSAMPSSAALVALLLLKRELRATFTGKSAKRSKFCACCSTKSVVGASTATCLPPIT
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645      STVPSAMPSSAALVALLLLKRELRATFTGKSAKRSKFCACCSTRSVVGASTATCLPPIT
      190     200     210     220     230     240

      250     260     270     280
m645.pep  ATNAARRATSVLPKPTSPHTRRSIGFACVKS LITAAMAAWSSVSSX
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645      ATNAARRATSVLPKPTSPHTRRSIGFACVKS LITAAMAAWSSVSSX
      250     260     270     280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2081>:

```

g647.seq
1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAGGTGTCGA
51  TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCT
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTGCCGAGA TAGTAGGCGT AGTTGATGAC ACCGATGCCG
251 AGCGAACGGC GGTCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2082; ORF 647.ng>:

```

g647.pep
1  MQRLAADGIQ IFFVGVDGQF ALRINGLVKE RARSVFFGKV CRCFEQVILY
51  GFKGTVGQTE RGTVAVADTV FRQIVGVVDD TDAERTAVHS RGRGFYRIS
101 LII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2083>:

```

m647.seq
1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAAGTGTGCA
51  TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCA
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTGCCGAGA TAATAAGCAT AGTTAATCAC GCCGATGCCG
251 AGCGAACGGC GGCCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2084; ORF 647>:

```

m647.pep
1  MQRLAADGIQ IFFVSDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY

```

	10	20	30	40	50	60
m647 . pep	MQRLAADGIQIFFVSVDDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	:     :     :     :     :					
g647	MQRLAADGIQIFFVGVDDGQFALRINGLVKERARSVFFGKVCRCFEQVILYGFKGTVGQTE					
	10	20	30	40	50	60
	70	80	90	100		
m647 . pep	RGTVAVADTVFRQIISIVNHADAERTAASHSRGTRGFYRISLIIX					
	:     :     :     :					
g647	RGTVAVADTVFRQIVGVDDTDAERTAVHSRGTRGFYRISLIIX					
	70	80	90	100		

```
a647.seq
1 GTGCAAAGGC TCGTTACACA CAGCGTCCAA GTCTTTTTTG TAGGTGTCGA
51 TGGGCAGTTT GCCTTAGCGAA TAAACGGTTT GGTAAAGAG CAGTCACGCA
101 CCGTATTCCT TGGCAAGGTT TGCCGATGCT TTGACGAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAGCCG TCGTGTAGC
201 GGACACCGTT TTTCGCCAAA TAATACGCAT AGTTGATCAC GCCGATACCG
251 AGCGAACGGC GGCCCATAGT GGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA
```

```
a647.pap .
      1  VQRLVTHSVQ VFFVGVDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY
     51  GFKGTVGQTE RGAVAVADTV FRQIIRIVDH ADTERTAAHS GGTRGFYRIS
    101  LII*
```

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSV DQGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
a647	VQRLVTHSVQVFFVGVDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTVA VADTVFRQIIISIVNHADAERTA AHSRGTRGFYRISLIIX					
a647	RGAVAVADTVFRQIIRIVDHADTERTA AHSRGTRGFYRISLIIX					
	70	80	90	100		

```
g948.seq
1  ATGAACAGGC  GCAACGCGCG  GATCGAACGG  GCTGTGCGTA  TTGCAGTGTAT
51  CGACGTTTGT  AATGTAGATG  GCCCCGGTCC  CGGCACGCTC  TCGCATCAGC
101 TGGGAAAACA  GGTGCGCAGC  CGGAATGATA  CGCTTGCCTA  TGTTCGGGTC
151 TTGCTCGTAT  TTCGTATAGA  GCCGCTCAA  TTCGTCTTGG  TCGGCAAAAA
201 ACGCTTCGTA  CAACCCCGAA  ACCTCGTTGG  CGGAAAAACG  CGTAATGTTG
251 CGCCCTTAA  TACGGCGGGT  GTACAGCAG  CGGTTGATT  GCACGCATCA
301 ATCAAGCTGG  CGGATACGGT  TGTCTTCCAC  GCCCGGGTTG  TTTTTCAAAC
351 CCAGCAGGCT  TTCGGCTTCA  ATATGCCACA  AGGGGTAGAA  CAGGGTTGCC
401 GCGCGCGCG  GCACGCCATC  TTGCGAATC  GATTTGACCC  CGCCCTGAAA
451 CATCTTAAAG  AAGGGAATGC  AGCCGGATG  CCGGGCTTCA  CGCCCCCGGA
501 TTTCGCTGTC  CAGCCCGCGG  ATACGTCGG  CATGTATGCC  GATGCCCGGG
551 CGTTGGGAAA  CGTATTTCAC  AATCGCGCT  GTAGTGGCAT  TGATGGAATC
601 CAAACTATCG  TCGATTTCAA  TCAGCACACA  GCTTGA
```

g648.pgp



1030

```

1  MNRRNARIER AVRIAVIDVL NVDPAPGPTL LHQRGKQVGS RNDTLAYVRV
51  LLVFRIEPLK FVLVGKKRFV QPRNLVGRKQ RNVAAALNQAG VQQAVDLHAI
101 IKLADTVVFH APVVFQHQQA FGFNMPQGV E QGCRAAAHAT LRTFRDRRLK
151 HLKEGNAAGM PGFTAPDFAV QPADTSGIDA DARALGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2089>:

```

m648.seq
1  ATGAACAGGC GCGACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTTG AATGTAGATG CGCCCGGTTT CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCGGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTGATTT GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCCAC ACCCGGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCGCG GCACGCCGCC TTGCGAACAG GATTGACCG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGCGCTTCG CCGCCCGGA
501 TTTCGCTGTC CAAACCGCGG ATACGTCGGG CATGTATGCC GATGCCCGCA
551 CGCTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAAACTATCG TCGCATTCAA TCAGCACACA GCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2090; ORF 648>:

```

m648.pep
1  MNRRDARIER AVRIAVIDVL NVDPAPGPTL LHQRGKQVGS RNDALADIRV
51  LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAAALNQAG VQQAVDLHAV
101 IKLADTVVFH TAVVFQHQQA FGFDMPPQGV E QGCRAAAHAA LRTGFDRRLK
151 HFKEGNAAGM PRFAAPDFAV QTADTSGIDA DARTLGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

m648/g648 91.5% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDPAPGPTLLHQRGKQVGS	RNDALADIRVLLVFRIEPLK				
g648	MNRRNARIERAVRIAVIDVLNVDPAPGPTLLHQRGKQVGS	RNDTLAYVRVLLVFRIEPLK				
	10	20	30	40	50	60
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQ	RNVAAALNQAGVQQA	VDLHAVIKLTD	TVVFHTAVVFQHQQA		
g648	FVLVGKKRFVQPRNLVGRKQ	RNVAAALNQAGVQQA	VDLHAI	IKLADTVVFHAPVVFQHQQA		
	70	80	90	100	110	120
	130	140	150	160	170	180
m648.pep	FGFDMPPQGV	EQGCRAAAHAA	LRTGFDRRLKH	FKEGNAAGMPRFAAPDFAV	QTADTSGIDA	
g648	FGFNMPPQGV	EQGCRAAAHAT	LRTFRDRRLK	HLKEGNAAGMPGFTAPDFAV	QPADTSGIDA	
	130	140	150	160	170	180
	190	200	210			
m648.pep	DARTLGNVFHN	NRAGSGIDGI	QTIVAFNQHTAX			
g648	DARALGNVFHN	NRAGSGIDGI	QTIVAFNQHTAX			
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2091>:

```

a648.seq
1  ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTTG AATGTAGATG CGCCCGGTTT CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCGGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTGATTT GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCCAC GCCCGGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCGCG GCACGCCACC TTGCGAACAG GATTGACTG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGTGCTTCG CCGCCCGGA

```

1031

501 TTTTCGCTGTC CAGTCCGCGG ATACGTCCGG CATTGATGCC GATGCCCCGA  
 551 CGCTGGGAAA CGTATTTTAC AATCGCGCTG GTAGTGGCGT TGATGGAATC  
 601 CAGGCTGTCG TCGCATTCGA TCAATACGCA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2092; ORF 648.a>:

a648.pep  
 1 MNRRNARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV  
 51 LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVIDLHAV  
 101 IKLTDTVVFH APVVFQHQQA FGFDMPQGV E QGCRAAAHAT LRTGFDCRLK  
 151 HFKEGNAAGM PCFAAPDFAV QSADTSGIDA DARTLGNVFH NRAGSGVDGI  
 201 QAVVAFDQYA A\*

m648/a648 93.8% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGS	RNDALADIRVLLVFRIEPLK				
a648	:					
	10	20	30	40	50	60
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHTAVVFQHQQA					
a648						
	70	80	90	100	110	120
	130	140	150	160	170	180
m648.pep	FGFDMPQGV E QGCRAAAHAALRTGFDRRLKHFKEGNAAGMPRFAAPDFAVQTADTSGIDA					
a648						
	130	140	150	160	170	180
	190	200	210			
m648.pep	DARTLGNVFHN RAGSGIDGIQTI VAFNQHTAX					
a648	:    :    :    :					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2093>:

g649.seq  
 1 ATGCTTGCCA TACTGTTGTC TGCAATACTG GGA CTGGTAT CAACAACTGC  
 51 CGCTGCCGGT ACGTCAGAAC CCGCCACCG ACATACCAA CATATCAGCA  
 101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC  
 151 CGTGCCCGCT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC GCGAAAA  
 201 CAAAAAGGCG CGCAAAGCAT TCCGCACCCT GCCTTATGCG GAACAGAAAA  
 251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGG  
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2094; ORF 649.ng>:

g649.pep  
 1 MLAILLSAIL GLVSTTAAAG TSEPAHRHTK HISKANKQML HPECRKYLER  
 51 RAAWYRSQGN VQELRENNKA RKAFTLPYA EQKIQCAAAY EAFDDFDGGR  
 101 FRR\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2095>:

m649.seq  
 1 ATGCTTGCCA TACTGTTGTC TGCAATATTG GGA CTGGTAT CGACAACTGC  
 51 CGCTGCCGGT ACGTCAGAAC CCGCCACCG CGATACCAA CATATCCGCA  
 101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC  
 151 CGTGCCCGCT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC GCGAAAA  
 201 CAAAAAGGCG CGCAAAGCAT TCCGTCCCT GCCTTATGCG GAACAGAAAA  
 251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGT  
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2096; ORF 649>:

m649.pep

1032

```

1  MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51 RAAWYRSQGN VQELRENKKA RKAFRSLPYA EQKIQCRAAY EAFDDFDGGS
101 FRR*

```

m649/g649 96.1% identity in 103 aa overlap

```

              10      20      30      40      50      60
m649.pep      MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              |||||
g649          MLAILLSAILGLVSTTAAAGTSEPAHRHTKHIKANKQMLHPECRKYLERAAWYRSQGN
              10      20      30      40      50      60

              70      80      90      100
m649.pep      VQELRENKKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX
              |||||
g649          VQELRENKKARKAFRTLPHYAEQKIQCRAAYEAFDDFDGGRFRRX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2097>:

```

a649.seq
1  ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACCTGC
51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAAA CATATCCGCA
101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
201 CAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATAAG GAACAGAAAA
251 CCCAATGCCG GCGGCTTAT GAGGCTTCG ATGATTTCGA CGGCAGCAGG
301 TTCCGCCGTT AA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2098; ORF 649.a&gt;:

```

a649.pep
1  MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51 RAAWYRSQGN VQELRENKKA RKAFRSLPYK EQKTQCRAAY EAFDDFDGSR
101 FRR*

```

m649/a649 96.1% identity in 103 aa overlap

```

              10      20      30      40      50      60
m649.pep      MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              |||||
a649          MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              10      20      30      40      50      60

              70      80      90      100
m649.pep      VQELRENKKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX
              |||||
a649          VQELRENKKARKAFRSLPYKEQKTQCRAAYEAFDDFDGSRFRRX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2099>:

```

g650.seq
1  ATGTCCAAAC TCAAAACCAT CGCCCTGACC GCATCAGGTC TGTCCGTTTG
51 TCCGGGTTTC CTATATGCCC AAAACACCTC ATCACACCAA GTCCGTTTAG
101 CGATTATGCG GTTAAACTCT TCAATACTCG ACCTGCCACC GACAAAACAA
151 TATTTCGAAT CCGGCAGCCT GTGGGACGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCGCAG CTATTTCGAC AGGGTCGTCA ACCGGAGCCG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGCTACCGG CAGGCATTAC
451 GGCTTGAAAA AAACaccgGT TTACGacggc aggcacGacg TTtacgcaGc
501 taccgatgcc gcactCAACT AtctGcAATA TCTCTAtgga CTGTTCCGCG
551 ACTGGCCGCT CGCCTTTGCC GCCTACAACT GGGGTGAAGG CAACGTCGGA
601 CGCGCCGTCA ACCGCGCCCG CGACCAAGGG CTCGAACCGA CCTACGAAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCAAG CTGCTCGCCG
701 TCGCAACAT TATTGCCACC CCCCAATCTT TCGGCATGAA TATCAGCGAC

```

1033

```

751 ATAGACAACA AACCCCTATTT TCAGGCAGTC GAACCGGGGCC GTCCGCTCGA
801 caacGAagcC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTGAATCC TGCATTCAAC GTCCCCGCGt tcatCCCCAA AAaCaacgc
901 aaacTGCTGC TTCCTGTGCG GTCCGTCCAA ACCTTccaaa gcaACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTCa ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAGAC CCTTCATACG GCATCGGAat
1151 ccGTCGTTTC CATCGACATC GACAATACGC CcgacacCTa ccgttccaaT
1201 ATGCcggcag gcaCGGTGAA CGTCAGCATT gccCgaatcc aacCCgcccgc
1251 cgcaCAGACA gcggaacatta ccgtcgacc tttgcccga gaaaccgtcc
1301 gtacgggaac ccgatccct tgtccgcaTt accgaaccg ccctTGCAGC
1351 AGCCGCAGCG CaacctCAAA ccgAAAAACA GACTGCCATG CcgtctGA

```

This corresponds to the amino acid sequence <SEQ ID 2100; ORF 650.ng>:

```

g650.pep
1 MSKLTIALT ASGLSVC PGF LYAONTSSHQ VGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWDE LRQGRFMGEV NPFLVRRHES KFIASRSYFD RVVNRSRPYM
101 YHIANEVKKR NMPAEAAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWEGENVG
201 RAVNRARDQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYPQAV EPGRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKNKR
301 KLLLPAVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLHT ASESVVSIDI DNTPDITYRSN
401 MPAGTVNVSI ARIQPAQAQT ADITVAPLPQ ETVRTGTRSP CPHYRTRPCD
451 SRSATSNRKT DCHAV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2101>:

```

m650.seq
1 ATGTCCAAAC TCAAAACCAT CGCTCTGACC GCATCAGGTC TGTCGGTTTG
51 TCCGGGTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGGC CTTAAACTCT TCAATACTCG ACCTGCCCCC GACAAAACAA
151 TATTTCGAAT CCGGCAGCCT GTGGGGCGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC AGGATTATGG CAGTTTATGC CCGCTACCGG CAGGCATTAC
451 GGCCTGGAAA AAACACCGGT TTACGACGGC AGGCACGACG TTTACGCCCG
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGGG
551 ACTGGCCGCT TGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTGGAACCGA CCTACGAAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCAAG CTGCTCGCCG
701 TGCGCAACAT TATTGCCACT CCCCAATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCCCTATTT TCAGGCAGTC GAACCGGATC GTCCGCTCGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTAAACCC CGCATTCAAC GTCCCCGCGT TTATCCCCAA AAGCAAACGC
901 AAATGCTGCT TTCCTGTGCG GTCCGTACAA ACCTTCCAAA GCAACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTCa ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCGACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCGA AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCAGC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2102; ORF 650>:

```

m650.pep
1 MSKLTIALT ASGLSVC PGF LYAONTSSHQ IGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWGE LRQGRFMGEV NPFLVRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEAAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWEGENVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYPQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPAVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPDITYRSN
401 MPAGTVNVGI ARIRPAAQAQT ADITVAPLPQ KTVRTXTRSP CPYCRTPCPD
451 SRSATSNRKT DRHAV*

```

m650/g650 96.1% identity in 465 aa overlap

1034

	10	20	30	40	50	60
m650.pep	MSKLKTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
g650	MSKLKTIALTASGLSVCPGFLYAQNTSSHQVGLAIMRLNSSILDLPPTKQYFQSGSLWDE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m650.pep	LRQGFRMGVEVNPVLRHESKFIASHSYFNRVINRSRPYMYHIANEVKKRNMPAEAAALLP					
g650	LRQGFRMGVEVNPVLRHESKFIASRSYFDRVVNRSRPYMYHIANEVKKRNMPAEAAALLP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m650.pep	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
g650	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m650.pep	LFGDWPLAFAAYNWGEGNVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT					
g650	LFGDWPLAFAAYNWGEGNVGRAVNRARDQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m650.pep	PQSFGMNISDIDNKPYPQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKSKR					
g650	PQSFGMNISDIDNKPYPQAVEPGRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKNKR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m650.pep	KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
g650	KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m650.pep	NLVNAGRSILVAKNGKTLQTASESVSIDIIDNTPDTPYRSNMPAGTVNVGIARIQPAQAAT					
g650	NLVNAGRSILVAKNGKTLHTASESVSIDIIDNTPDTPYRSNMPAGTVNVSIARIQPAQAAT					
	370	380	390	400	410	420
	430	440	450	460		
m650.pep	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTDRAVX					
g650	ADITVAPLPQETVRTGTRSPCPHYRTRPCDSRSATSNRKTDCHAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2103>:

a650.seq

1	ATGTCCAAAC	TCAAAACCAT	CGCCCTGACC	GCGTCAGGTC	TGTCCGTTTG
51	TCCGGGTTTC	CTATACGCCC	AAAACACCTC	ATCACACCAA	ATCGGTTTGG
101	CGATTATGCG	CTTAAACTCT	TCAATACTCG	ACCTGCCACC	GACAAAACAA
151	TATTTCCAAT	CCGGCAGCCT	GTGGAGCGAG	CTGCGCCAAG	GCTTCCGGAT
201	GGGCGAAGTC	AATCCCGAAC	TGGTACGCCG	CCACGAAAGC	AAATTCATCG
251	CAAGCCACAG	CTATTTCAAC	AGGGTCATCA	ACCGGAGTAG	ACCCTATATG
301	TACCATATCG	CCAACGAAGT	CAAAAAACGC	AATATGCCCG	CCGAAGCCGC
351	CCTGCTTCCC	TTCATCGAAA	GCGCGTTCGT	CACCAAAGCC	AAATCACACG
401	TCGGCGCATC	GGCCTGTGG	CAGTTCATGC	CCGTACCGG	CAGGCATTAC
451	GGCCTGGAAC	AAACACCGGT	TTACGACGGC	AGGCACGACA	TTTACGCCGC
501	CACCGATGCC	GCACTCAACT	ATCTGCAATA	CCTCTATGGA	CTGTTCCGGC
551	ACTGGCCGCT	CGCCTTTGCC	GCCTACAAC	GGGGTGAAGG	CAACGTCGGA
601	CGCGCCATCA	ACCGCGCCCG	CGCCCAAGGG	CTCGAACC	CCTACGAAAA
651	CCTGCGTATG	CCCAACGAAA	CGCGCAACTA	TGTTCCCAAG	CTGCTCGCCG
701	TGCGCAACAT	CATTGCCGCC	CCCCAATCTT	TCGGCATGAA	TATCAGCGAC
751	ATAGACAACA	AACCGTATTT	TCAGGCAGTC	GAACCGGACC	GTCCGCTCGA
801	CAACGAAGCC	ATCGCCCGGC	TTGCCCGCAT	CACGCAAGC	GAGCTGCTCG
851	CCCTAAACCC	CGCATTCAAC	GTCCCCGCGT	TCATCCCCAA	AAGCAAACGC

```

901  AAACTGCTGC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951  CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CTTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCAACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCGGTATT GCCGAACCTG CCCTTGCAGC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2104; ORF 650.a>:

```

a650.pep
1   MSKLKTIALT ASGLSVCPGF LYAQTSSHQ IGLAIMRLNS SILDLPPTKQ
51  YFQSGSLWSE LRQGRMGEV NPVLRRHES KFIASHSYFN RVINRSRPFY
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDIAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAA PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPTNYSRN
401 MPAGTVNVGI ARIRPAAQQT ADITVAPLPQ KTVRTXTRSP CPYCRTCPCD
451 SRSATSNRKT DRHAV*

m650/a650 99.1% identity in 465 aa overlap

10      20      30      40      50      60
m650.pep MSKLKTIALTASGLSVCPGFLYAQTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE
|||||
a650     MSKLKTIALTASGLSVCPGFLYAQTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWSE
10      20      30      40      50      60

70      80      90      100     110     120
m650.pep LRQGRMGEVNPVLRRHESKFIASHSYFNRVINRSRPFYHIANEVKKRNMPAEAALLP
|||||
a650     LRQGRMGEVNPVLRRHESKFIASHSYFNRVINRSRPFYHIANEVKKRNMPAEAALLP
70      80      90      100     110     120

130     140     150     160     170     180
m650.pep FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG
|||||
a650     FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG
130     140     150     160     170     180

190     200     210     220     230     240
m650.pep LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT
|||||
a650     LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAA
190     200     210     220     230     240

250     260     270     280     290     300
m650.pep PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR
|||||
a650     PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR
250     260     270     280     290     300

310     320     330     340     350     360
m650.pep KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
|||||
a650     KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
310     320     330     340     350     360

370     380     390     400     410     420
m650.pep NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPDYRSNMPAGTVNVGIARIRPAAQQT
|||||
a650     NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPDYRSNMPAGTVNVGIARIRPAAQQT

```

	370	380	390	400	410	420
	430	440	450	460		
m650.pep	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTD	RAVX				
a650	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTD	RAVX				
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2105>:

g652.seq

```

1 ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGCG GTGCGAATGC
51 GACTTTGGCG GTCTCTATGG CCGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGTCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGTAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAAGCGGCCG
401 AAGCCGCGCG CTACAAGGCG GGCGAAGACG TATTATTCCG ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTTGCCGA ATACTTGGA GGCTTGTTA
551 ACGAATTCCC GATTATTTCC ATTGAAGACG GGATGGACGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAATTG GGCAAAAAAG TTCAATTGGT
651 CGGCGACGAC TTGTTCTGTA CCAATCCGAA AATCTTGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAAACGCA TTGCTGGTCA AAGTCAACCA AATCGGTACT
751 TTAAGCGAAA CCCTGAAAGc cgtcgatctg gCAAAATGCA accgctacGc
801 cagCGTGATG AGCCAccgct ccggCGAAAC CGAAGACAGT Accattgccc
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TTA AAAAccgG TTCTTTGAGC
901 cgtTCCGACC GCATGGCGAA ATACAACCAa ctGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCcgccctACT ACCCCGGCAA AGCCGCATTC TACCAACTGG
1001 GCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2106; ORF 652.ng>:

g652.pep

```

1 MIELDGTENK GN LGANATLA VSM AVARAAA EDSGLPLYRY LGGAGPMSLP
51 VPMNVINGG EHANN SLNIQ EFMIMPV GAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGFAPNLN SHKEALQLMV EAAEAAGYKA GEDVLFALDC
151 ASSEFYKD GK YHLEA EGRSY TNAEFAEYLE GLVNEFP IIS IEDGMDENDW
201 EGWKL LTEKL GKKVQLV GDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKA VDL AKCNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRM AKYNQ LLRIEEELAE AAYYPGKA AF YQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2107>:

m652.seq

```

1 ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGCG GTGCGAATGC
51 GACTTTGGCG GTTCTCTATGG CCGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGCCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCGCG CTACAAGGCG GGCGAAGACG TATTATTCCG ATTGGACTGC
451 GCCTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTTGCCGA ATATCTGGAA GGCTTGTTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GCATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAACTG GGCGGTAGAG TTCAATTGGT
651 TTGGCGACGAC TTGTTCTGTA CCAATCCAAA AATCTTGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAAACGCA TTGCTGGTCA AAGTCAATCA AATCGGTACT
751 TTGAGCGAGA CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
901 CGTTCCGACC GCATGGCGAA ATACAACCAA CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCGCGGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2108; ORF 652>:

m652.pep

```

1 MIELDGTENK GN LGANATLA VSM AVARAAA EDSGLPLYRY LGGAGPMSLP
51 VPMNVINGG EHANN SLNIQ EFMIMPV GAK SFREALRCGA EIFHALKKLC

```

1037

101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC  
 151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFFIIS IEDGMDENDW  
 201 EGWKKLLTEKL GGRVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT  
 251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS  
 301 RSDRMAKYNQ LLRIEEELAE AADYPSKAAF YQLGK\*

m652/g652 98.2% identity in 335 aa overlap

	10	20	30	40	50	60
m652.pep	MIELDGTENKGNLGNATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
g652	MIELDGTENKGNLGNATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m652.pep	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN					
g652	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m652.pep	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
g652	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m652.pep	GLVNEFFIISIEDGMDENDWEGWKKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA					
g652	GLVNEFFIISIEDGMDENDWEGWKKLLTEKLGKVKQLVGDDLFVTNPKILAEGIEKGVANA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652.pep	LLVKVNQIGTILSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS					
g652	LLVKVNQIGTILSETLKAVDLAKCNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS					
	250	260	270	280	290	300
	310	320	330			
m652.pep	RSDRMAKYNQLLRIEEELAEAADYPSKAAFYQLGKX					
g652	RSDRMAKYNQLLRIEEELAEAAAYPGKAAFYQLGKX					
	310	320	330			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2109>:

a652.seq

1	ATGATCGAAT	TGGACGGTAC	TGAAAACAAA	GGCAATTTGG	GTGCGAATGC
51	GACTTTGGCG	GTTTCTATGG	CGGTTGCACG	CGCCGCTGCC	GAAGACTCAG
101	GCCTGCCGCT	TTACCGCTAC	TTGGGCGGCG	CAGGCCCGAT	GTCCCTGCCC
151	GTACCGATGA	TGAACGTCAT	CAACGGCGGC	GAACACGCCA	ACAACAGCCT
201	GAACATCCAA	GAGTTTATGA	TTATGCCCGT	CGGCGCAAAA	TCCTTCCGCG
251	AAGCGTTGCG	CTGCGGTGCG	GAAATTTTCC	ACGCCTTGAA	AAACTGTGTC
301	GACAGCAAAG	GCTTCCCAC	CACAGTCGGC	GACGAAGGCG	GTTTCGCCCC
351	CAACCTGAAC	AGCCACAAA	AAGCCCTGCA	ACTGATGGTC	GAGGCGACCG
401	AAGCCGCCGG	CTACAAAGCG	GGCGAAGACG	TATTATTCGC	ATTGGACTGC
451	GCGTCCAGCG	AGTTCTACAA	AGACGGCAAA	TACCACTTGG	AAGCCGAAGG
501	CCGCTCCTAC	ACCAACGCGG	AATTGCGCGA	ATATCTGGAA	GGCCTGGTCA
551	ACGAGTTCCC	CATCATCTCC	ATCGAAGACG	GGATGGATGA	AAACGACTGG
601	GAAGGCTGGA	AACTGCTGAC	CGAAAACTG	GGCGGCAAA	TCCAACCTCGT
651	TGGCGACGAC	CTCTTCGTTA	CCAACCCGAA	AATCCTTGCC	GAAGGCATTG
701	AAAAAGGCGT	GGCAAACGCA	CTATTGGTCA	AAGTCAACCA	AATCGGTACT
751	TTGAGTGAAG	CCCTGAAAGC	CGTCGACTTA	GCCAAACGCA	ACCGCTACGC
801	CAGCGTAATG	AGCCACCGCT	CCGGCGAAAC	CGAAGACAGC	ACCATTGCCG
851	ACTTGGCAGT	CGCCACCAAC	TGTATGCAGA	TCAAAACCGG	TTCTTTGAGC
901	CGTTCGACC	GCATGGCGAA	ATACAACCAA	CTGCTGCGTA	TCGAGGAAGA
951	ATTGGCGGAA	GCCGCGGACT	ACCCAGCAA	AGCCGCATTC	TACCAACTGG
1001	GCAAATAA				

This corresponds to the amino acid sequence <SEQ ID 2110; ORF 652.a>:

a652.pep

1	MIELDGTENK	GNLGNATLA	VSMVARAAA	EDSGLPLYRY	LGGAGPMSLP
51	VPMNVINGG	EHANNSLNIQ	EFMIMPVGAK	SFREALRCGA	EIFHALKKLC
101	DSKGFPTTVG	DEGGFAPNLN	SHKEALQLMV	EATEAAGYKA	GEDVLFALDC



1038

151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPPIIS IEDGMDENDW  
 201 EGWKLLTEKL GGVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT  
 251 LSETLKAVDL AKRNRYSVM SHRSGETEDS TIADLAVATN CMQIKTGSLS  
 301 RSDRMAKYNQ LLRIEELAE AADYPSKAAF YQLGK\*

m652/a652 99.7% identity in 335 aa overlap

	10	20	30	40	50	60
m652.pep	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
a652	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m652.pep	EHANNSLNQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN					
a652	EHANNSLNQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m652.pep	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
a652	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m652.pep	GLVNEFPPIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA					
a652	GLVNEFPPIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652.pep	LLVKVNQIGTSLSETLKAVDLAKRNRYSVMSHRSGETEDSTIADLAVATNCMQIKTGSLS					
a652	LLVKVNQIGTSLSETLKAVDLAKRNRYSVMSHRSGETEDSTIADLAVATNCMQIKTGSLS					
	250	260	270	280	290	300
	310	320	330			
m652.pep	RSDRMAKYNQLLRIEEEELAEAADYPSKAAFYQLGKX					
a652	RSDRMAKYNQLLRIEEEELAEAADYPSKAAFYQLGKX					
	310	320	330			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2111>:

g652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GTGCGGCGCT ACCGAGCGGC GCATCCACCG GTCAGAAAGA AGCTTTGGAA
151 CTTCCGACAG GCGACAAATC CCGCTATTCC GGCAAAGCGC TATTGAAGGC
201 CGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATC GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAA GCAATTTGGG TCGAATGCG ACTTTGGCGG TCTCTATGGC
351 GGTTGCACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGGGGCGC AGGTCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCCGC GCGCAAAAT CTTTCGCGCA AGCGTTGCGC TCGGGTGGCG
551 AAATTTTCCA CGCCTTGAAA AAATGTGCG ACAGTAAAGG CTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTCGCCCGC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AAGCGGCCGA AGCCGCCGGC TACAAGGCGG
701 GCGAAGACGT ATTATTGCGA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAA ACCACTTGGG AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TACTTGGAAG GCTTGTTAA CGAATTCCCG ATTATTTCCA
851 TTGAAGACGG GATGGACGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAATTGG GCAAAAAAGT TCAATTGGTC GCGGACGACT TGTTCTGAAC
951 CAATCCGAAA ATTCTTGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAACCAA ATCGGTACTT TAAGCGAAAC CCTGAAAGCC
1051 TCGCATCTGG CAAAATGCAA CCGCTACGCC AGCGTGATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGTA CCATTGCCGA CTTGGCAGTG GCCACCAACT
1151 GTATGCAGAT TAAACCCGGT TCTTTAGGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCTACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2112; ORF 652-1.ng>:

1039

## g652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES G VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNLS NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEAAEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMD E NDWEGWKLLT
301 EKLGGKVQLV GDDLFTNPK ILAEGIEKGV ANALLVKVNQ IGTLSLTLKA
351 VDLAKCNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAAYPGK AAFYQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2113>:

## m652-1.seq

```

1  ATGAGCGCAA TCCTTGATAT TTTGCGCCGC GAAATTTTGG ACTCAGCGCG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTCGCGACG GCGACAAATC CCGTATTTCG GGCAAGGGCG TATTGAAGGC
201 GGTCGAACAC GTCACCAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TCGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTTCACGCG CCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGGCG AGGCCGATG TCCCTGCCG TACCGATGAT GAACGTCATC
451 AACGGCGGGC AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GGGCGAAAAT CTTCCGCGCA AGCGTTGCGC TCGGGTGGCG
551 AAATTTTCCA CGCCTTGAAA AACTGTGCG ACAGCAAAGG CTTCGGACC
601 ACAGTCGGCG ACGAAGGCGG TTTGCGCCCG AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCGGCG TACAAAGCGG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CCTCCAGCGA GTTCTACAAA
751 GACGGCAAAAT ACCATTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG CATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAAATGG GCGGTAGAGT TCAATTGGTT GCGGACGACT TGTTCGTAAC
951 CAATCCAAAA ATCTTGGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAATCAA ATCGGTACTT TGAGCGAGAC CCTGAAAGCC
1051 CTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 GCGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCGAGCAA GCCGATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2114; ORF 652-1>:

## m652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES G VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNLS NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMD E NDWEGWKLLT
301 EKLGGKVQLV GDDLFTNPK ILAEGIEKGV ANALLVKVNQ IGTLSLTLKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEADYPSK AAFYQLGK*

```

m652-1/g652-1 98.6% identity in 428 aa overlap

```

          10      20      30      40      50      60
m652-1  MSAIVDIFAREILDSRGNPTVECDVLLES GVMGRAAVPSGASTGQKEALELRDGDKSRY
g652-1  MSAIVDIFAREILDSRGNPTVECDVLLES GVMGRAAVPSGASTGQKEALELRDGDKSRY
          10      20      30      40      50      60

          70      80      90     100     110     120
m652-1  GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR
g652-1  GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR
          70      80      90     100     110     120

          130     140     150     160     170     180
m652-1  AAAEDSGLPLYRYLGGAGPMSLPVPMNVI NGGEHANNLSNIQEFMIMPVGAKSFREALR
g652-1  AAAEDSGLPLYRYLGGAGPMSLPVPMNVI NGGEHANNLSNIQEFMIMPVGAKSFREALR
          130     140     150     160     170     180

```

1040

	190	200	210	220	230	240
m652-1	CGAEIFHALKKL	CDSKGFPTTV	GDDEGGFAP	NLNSHKEAL	QLMVEATEA	AAGYKAGEDVLFA
g652-1	CGAEIFHALKKL	CDSKGFPTTV	GDDEGGFAP	NLNSHKEAL	QLMVEAAEA	AAGYKAGEDVLFA
	190	200	210	220	230	240
	250	260	270	280	290	300
m652-1	LDCASSEFYK	DGKYHLEA	EGRSYTNAE	FAEYLEGLV	NEFPIISIE	DGMDENDWEGWKLLT
g652-1	LDCASSEFYK	DGKYHLEA	EGRSYTNAE	FAEYLEGLV	NEFPIISIE	DGMDENDWEGWKLLT
	250	260	270	280	290	300
	310	320	330	340	350	360
m652-1	EKLGGVRVQ	LVGDDLFV	TNPKILAE	GIEKGVAN	ALLVKVNQ	IGTLSETLKA
g652-1	EKLGGVRVQ	LVGDDLFV	TNPKILAE	GIEKGVAN	ALLVKVNQ	IGTLSETLKA
	310	320	330	340	350	360
	370	380	390	400	410	420
m652-1	SVMSHRSGET	EDSTIADL	AVATNCMQ	IKTGSLSR	SDRMAKYN	QLLRIEEEEA
g652-1	SVMSHRSGET	EDSTIADL	AVATNCMQ	IKTGSLSR	SDRMAKYN	QLLRIEEEEA
	370	380	390	400	410	420
	429					
m652-1	AAFYQLGKX					
g652-1	AAFYQLGKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2115>:

a652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCCG GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTCGCGACG GCGACAAATC CCGTTATTCG GGCAAGGGCG TATTGAAGGC
201 GGTGCAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TGCGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTGTCACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGCGC AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCGAAAAT CTTTCGCCGA AGCGTTGCCG TGCGGTGCCG
551 AAATTTTCCA CGCCTTGAAA AACTGTGCG ACAGCAAAGG CTTCCCGACC
601 ACAGTCGCGC ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCGGCG TACAAAGCGG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG GATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAACTGG GCGGCAAAGT CCAACTCGTT GCGGACGACC TCTTCGTTAC
951 CAACCCGAAA ATCCTTGCCG AAGGCATTGA AAAAGGCGTG GCAAACGCAC
1001 TATTGGTCAA AGTCAACCAA ATCGGTACTT TGAGTGAAAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2116; ORF 652-1.a>:

a652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECVLLLES G VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRY S GKGVLKAVEH VNNQIAQAL I GIDANEQSYI DQIMIELDGT
101 ENKGNLGA N TLAVSMVAR AAAEDSGLPL YRYLGAGGPM SLPVPMNVI
151 NGGEHANN S L NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCD SKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAE G RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKVQL V GDDLFVTNPK ILAEGIEKGV ANALLVKVNQ IGTLSETLKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLSRSDRMAK
401 YNQLLRIEE E LAEADYPSK AAFYQLGK*

```

m652-1/a652-1 99.8% identity in 428 aa overlap

10 20 30 40 50 60

1041

```

m652-1      MSAIVDIFAREILDSRGNPTVECDVLLESGVMGRAAVPSGASTGQKEALELRDGDKSRY
a652-1      MSAIVDIFAREILDSRGNPTVECDVLLESGVMGRAAVPSGASTGQKEALELRDGDKSRY
              10      20      30      40      50      60

m652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
a652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
              70      80      90      100     110     120

m652-1      AAAEDSGPLPYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
a652-1      AAAEDSGPLPYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
              130     140     150     160     170     180

m652-1      CGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
a652-1      CGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
              190     200     210     220     230     240

m652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPIISIEDGMDENDWEGWKLLT
a652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPIISIEDGMDENDWEGWKLLT
              250     260     270     280     290     300

m652-1      EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
a652-1      EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
              310     320     330     340     350     360

m652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEELAEAAADYPSK
a652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEELAEAAADYPSK
              370     380     390     400     410     420

m652-1      AAFYQLGKX
a652-1      AAFYQLGKX
              429

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2117>:

```

g653.seq
1  ATGGCGGcgg aaccgatgcg gAtgccggag gtaAcgtaCG GTTTTCCGG
51 ATCGTTCGGG ATGGCGTTT TGTgacggT GATGTGCGCt ttgcccAAG
101 CGGCTtcggc ggtcttgcCg gtgaTTTCA TCGGTTGCAG GtcgacgaGG
151 AAaacgTGGC TTTCGGTGCG GCCGGAaAcg atgcgCaaac cgCGTttaac
201 caactcttcc gcCATGACGG CAGCATTGAT TTTCACTTGT FTTGCGTATT
251 GTTTGAactC GGGTTGcaac gcttctTTAA acgctACGGC TttgGCGGCG
301 ATAACGTgca tcaACGGAcc gCCTTGCAGG CTTGGGAAGA TGGAAGAGTT
351 CAGCGCTTTT TCGTGGGTAT TGTCACGGCA CAAAATCACA CCGCCGCGAG
401 GGCCGCGTAG GGTTTTGTGG GTGGTAGTgG ttACgaaGtc GCAGAtggc
451 ACGGGgttag gatattcgcc gccGGCAACC AgtccgGCAT Ag

```

This corresponds to the amino acid sequence <SEQ ID 2118; ORF 653.ng>:

```

g653.pep
1  MAAEPMRMPE VTYGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51 KTWLSVRPET MRKPRLTNSS AMTAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCINGPPCR LGKMEEFSAF SWVLSRHKIT PPRGPRRVLW VVVVTKSQNG
151 TGLGYSPPAT SPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2119>:

```

m653.seq
1  ATGGCAGCGG AGCCGATGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
51 ATCGTTCGGA ATGGCGTTT TGTGACGGT GATGTGCGCT TTGCCCAAAG
101 CGGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCAACGAGG

```

1042

```

151 AAAACGTGGC TTTCGGTGCG GCCGGAAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCATTGT TTTGCGTATT
251 GTTTGAACTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGACC GCCTTGCAAG CTTGGGAAGA TGGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTCGGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TCACGAAGTC GCAGAACGGC
451 ACCGGGTTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2120; ORF 653>:

m653.pep

```

1  MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRVLW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/g653 96.9% identity in 163 aa overlap

```

              10      20      30      40      50      60
m653.pep      MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
              |||||
g653           MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
              10      20      30      40      50      60

              70      80      90      100     110     120
m653.pep      MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
              |||||
g653           MRKPRLTNSSAMTAALIFTCFAYCLNSGCNASLNATALAAITCINGPPCRLGKMEEFSAF
              70      80      90      100     110     120

              130     140     150     160
m653.pep      SWVLSRHKITPPRGPRRVLWVVVTKSQNGTGLGYSPPATRPAX
              |||||
g653           SWVLSRHKITPPRGPRRVLWVVVTKSQNGTGLGYSPPATSPAX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2121>:

a653.seq

```

1  ATGGCGGCGG AACCGATGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
51  ATCATTCGGG ATGGCGTTTT TGTGACAGT GATGTGCGCT TTGCCAAAG
101 CAGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCAACGAGG
151 AAAACGTGGC TTTCGGTGCG GCCGGAAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCATTGT TTTGCGTATT
251 GTTTGAACTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGGCC ACCTTGCAAG CTTGGGAAGA TGGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTCGGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TAACGAAGTC GCAGAACGGC
451 ACGGGATTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2122; ORF 653.a>:

a653.pep

```

1  MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRVLW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/a653 100.0% identity in 163 aa overlap

```

              10      20      30      40      50      60
m653.pep      MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
              |||||
a653           MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
              10      20      30      40      50      60

              70      80      90      100     110     120
m653.pep      MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
              |||||
a653           MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
              70      80      90      100     110     120

              130     140     150     160
m653.pep      SWVLSRHKITPPRGPRRVLWVVVTKSQNGTGLGYSPPATRPAX
              |||||
a653           SWVLSRHKITPPRGPRRVLWVVVTKSQNGTGLGYSPPATRPAX

```

1043

130 140 150 160

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2123>:

```
g656.seq
1   ATGCCGCGTT TCTCCGGTTC GATTTCCTCG ATGATTTCCTCA TCGCGCGGAC
51  TTTtggcGCG CCGGAGAGTG TGCcggcagg gAAGGTGGCG GCGAGGATGT
101 CCATATTGGT AACGCCCTCT TTCAAACAGc ctTCGACGTT GGAAACGATG
151 TGCATCACAT GGGAGTATTT TTCAATCACC ATTTTGTCTCG TGACTTTGAC
201 TTCGCCTGTT TTGCTGATGC GTCCGACATC GTTGCGCCCC AAATCGATAA
251 GCATAACGTG TTCGGCgatt TCTTTGGCGT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGGT CTTCGGCGGG GGT'TTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATGACGTcat CGCGTTCGCG GCGGACGAGG ATTTCTGGGCG
401 AGGAACCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2124; ORF 656.ng>:

```
g656.pep
1   MPRFSGSISS MISIARTFGA PESVPAGKVA ARMSILVTPS FKQPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSIISITCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRRTR ISGEEPTMWK SPKS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2125>:

```
m656.seq
1   ATGCCGCGTT TGCTCGGTTC GACTTCTTCG ATGATTTCCTCA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTTCGACGTT GGAAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCTCG TAACTTTGAC
201 TTCGCCGTT TACTGATGC GGCCGACGTC GTTGCCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGGT CTTCGGCGGG GGT'TTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATAACGTCGT TCGGTCGCG TCGGACGAGG ATTTCTGGGCG
401 AGGAGCCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2126; ORF 656>:

```
m656.pep
1   MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPS FRRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT ITSLSRRRTR ISGEEPTMWK SPKS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m656/g656 91.0% identity in 144 aa overlap

```

              10      20      30      40      50      60
m656.pep      MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPSFRRPSTLETMCITWEYFSIT
g656           |||: || ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
              10      20      30      40      50      60

              70      80      90      100     110     120
m656.pep      ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT
g656           ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
              70      80      90      100     110     120

              130     140
m656.pep      ITSLSRRRTRISGEEPTMWKSPKSX
g656           :|| ||||:||||:||||:||||:||||
              130     140
m656.pep      MTSSRSRRTRISGEEPTMWKSPKSX
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2127>:

```
a656.seq
1  ATGCCGCGTT TGCTCGGTTC GACTTCTTCG ATGATTTCCTA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTGACGTT GGAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCTG TAACTTTGAC
201 TTCGCCCGTT TTACTGATGC GGCCGACGTC GTTGCCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTCG
301 TTGGCAAGGT CTTGGCGGG GGTTTTGGCG CGCAGGCGCG TGCCGGCGAT
351 GGGCGGACG ATGACATCGT CGCGTTCGCG GCGGACGAGG ATTCGGGCG
401 AGGAGCCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2128; ORF 656.a>:

```
a656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRTR ISGEEPTMWK SPKS*
```

m656/a656 98.6% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRPSTLETMCITWEYFSIT					
a656.	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRPSTLETMCITWEYFSIT					
	10	20	30	40	50	60
m656.pep	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP					
a656	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP					
	70	80	90	100	110	120
m656.pep	RRRVPAMGRT					
a656	RRRVPAMGRT					
	70	80	90	100	110	120
m656.pep	ITSLRSRTRISGEEPTMWKSPKSX					
a656	MTSSRSRTRISGEEPTMWKSPKSX					
	130	140				
m656.pep	ITSLRSRTRISGEEPTMWKSPKSX					
a656	MTSSRSRTRISGEEPTMWKSPKSX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2129>:

```
g657.seq
1  ATGAACACAC CCCCCATCCT TCCTCCCGCC ATGCTCGGCA TCCTCGGCGG
51  CGGACAATTa ggcagAATGT TTGCCGTTGC CGCTAAAACC ATGGGCTACA
101 AAGTAACCGT TCTCGATCCC GACCCGAATG CGCCGGCGGC GGAATTTGCC
151 GACCGCCATT TGTGCGCGCC GTTTGACGAC CGGGCCGCGT TGGACGAATT
201 GCGCAAAATGC GCGGCGGTTa cgACCGAATT TGAAaagtc aaTGCCGACG
251 CGATGCGCTC TCTGGCAAAG CATAACACG TTTCCCCCAG CGGCGACTGC
301 GTGTCCATTG CACAAAACCG CATTCAGGAA AAAGCGTGGA TACGCAAAGC
351 AGGCTTGCAA ACCGCGCCGT ATCAGGCGGT TTGCAAGGCC GAAGACATTA
401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
451 GGCTACGACG GCAAAGGTCA AATCCGCGTC AAAACGTTGG ACGAACTCAA
501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTTG GAAAAAATGG
551 TGGACTTGCG CGGCGAGATT TCCGTGATCG TATGCCGTCT GAACGATGAA
601 AACGTGCAAA CCTTCGACCC CGCCGAAAAC ATCCACGAAA ACGGCATCTT
651 GGCTTattc ATCGTCcccg CGCGGCTGAG TGCCGACGTG CAGCAACAGG
701 CGCGGCAGAC GCGGCAACgc tTGGCGGACG AATTGGATTA TGTCGGCgta
751 TTGGCGGTAG AAATGTTTGT TGTGCGCGAC ACACATGAAT TGCTCGTCAA
801 TGAAACCGCC CCGCGCACGC ACAATTCCGG CCACCATACG ATAGATGCCT
851 GCGCCGCAGA CCAGTTCCAA CAGCAGGTAC GCATTATGTG CAACctGCCG
901 cccGccgACA CCAAATTATT aTCCCcttgC TGTATGGCGA ATATTTGGGg
951 CGACGTTTGG CAGGAAGATG GCGGCGAACC GGATTGGCTG CCGTTGCAAA
1001 GCCGGCCGAA TGCACACCTG CACCTATACG GAAAAAAAAC CGCACAGAAA
1051 GGTGCGAAAA TGGGACACTT TaccgTTTTG ACCACCGATT CGGACaccgC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2130; ORF 657.ng>:

1045

g657.pep

1	MNTPPILPPA	MLGILGGGQL	GRMFAVAAKT	MGYKVTVLDP	DPNAPAAEFA
51	DRHLCAPFDD	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC
101	VSIAQNRIQE	KAWIRKAGLQ	TAPYQAVCKA	EDITEASAQF	LPGILKTATL
151	GYDGKGQIRV	CTLDELKAAF	AEHGGVDCVL	EKMVDLRGEI	SVIVCRLNDE
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQQARQTAQR	LADEL DYVGV



1046

251 LAVEMFVVG D THELLVNETA PRTHNSGHHT IDACAADQFQ QQVRIMCNLP  
 301 PADTKLLSPC CMANILGDVW QEDGGEPDWL PLQSRPNAHL HLYGKKTAQK  
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQSL\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2131>:

m657.seq  
 1 ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTTGGCA TCCTCGGCGG  
 51 CGGACAATTA GGCAGAATGT TTACCGTTGC CGCCAAAACC ATGGGCTACA  
 101 AAGTAACCGT TCTCGACCCC GATCCGGACG CGCCGGCAGC AGAATTTGCC  
 151 GACCGCCATT TGTGCGCGCC GTTTAACGAC CAAGCTGCTT TGGACGAATT  
 201 GGCAAAATGC GCGGCGGTGA CCACTGAATT TGAAAACGTC AATGCCGATG  
 251 CGATGCGCTT TTTGGCAAAA CATACCAATG TTTCCCTAG CGGCGATTGT  
 301 GTGGCGATTG CACAAAACCG CATTAGGAA AAGGCATGGA TACGCAAAGC  
 351 GGGATTGCAA ACCGCGCCGT ATCAAGTGGT TTGTAAGGCT GAAGACATCA  
 401 CTGAAGCAAG CGCGCAATTT TTGCCCAGCA TCCTGAAAAC GGCTACGTTG  
 451 GGCTACGACG GCAAAGGTCA AATCCGCGTA AAAACATTGG ATGAACTCAA  
 501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTTG GAAAAAATGG  
 551 TGGATTGCG CAGTGAAATT TCCGTAATCG TATGCCGTTT GAACAATGAC  
 601 AACGTGCAAA CTTTCGACCC TGCCGAAAAC ATCCACGAAA ACGGCATCTT  
 651 GGCTTATTCC ATCGTCCCG CGCGACTGAG TGCCGACGTG CAGCAACAGG  
 701 CGCGGCAGAT GGCGCAACGC TTGGCGGACG AATTGGATTA TGTCGGCGTA  
 751 TTGGCGGTAG AAATGTTTGT TGTCGGTGAC ACGCATGAAT TGGTCGTCAA  
 801 GCAAAATCGCC CCGCGCCCG ACAATTCCGG ACACCATACG ATAGATGCCT  
 851 GCGCAGCAGA CCAGTCCAG CAGCAGGTAC GCATTATGTG CAACCTGCCG  
 901 CCTGCCGATA CCAAATTACT GAGTTCTTGC TGTATGGCAA ATATTTTGGG  
 951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGCTG CCCTTGCAAA  
 1001 GCCATCCGAA TGCACACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA  
 1051 GGGCGGAAAA TGGGACACTT TACCGTTTTA ACCACCGATT CGGACACCGC  
 1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

This corresponds to the amino acid sequence <SEQ ID 2132; ORF 657>:

m657.pep  
 1 MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP DPDAPAAEFA  
 51 DRHLCAPFND QAALDELA KC AAVTTEFENV NADAMRFLAK HTNVSPSGDC  
 101 VAIAQNRIQE KAWIRKAGLQ TAPYQVCKA EDITEASAQF LPGILKTATL  
 151 GYDGKGQIRV KTLDELKAAF AEHGGVDCVL EKMVDLRSEI SVIVCRLNND  
 201 NVQTFDPAEN IHENGILAYS IVPARLSADV QQARQMAQR LADEL DYVGV  
 251 LAVEMFVVG D THELVVNEIA PRPHNSGHHT IDACAADQFQ QQVRIMCNLP  
 301 PADTKLLSSC CMANILGDVW QEDGGEPDWL PLQSHPNAL HLYGKKTAHK  
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQSL\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m657/g657 93.9% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPAM	LGILGGGQLGR	MFTVAAKTM	GYKVTVLDP	DPDAPAAEF	ADRHLCAPFND
g657	MNTPPILPPAM	LGILGGGQLGR	MFAVAAKTM	GYKVTVLDP	DPNAPAAEF	ADRHLCAPFDD
	10	20	30	40	50	60
	70	80	90	100	110	120
m657.pep	QAALDELA	KCAAVTTEF	ENVNADAM	RFLAKHTN	VSPSGDC	VAIAQNRIQE
g657	RAALDELA	KCAAVTTEF	ENVNADAM	RSKAKHTN	VSPSGDC	VSIAQNRIQE
	70	80	90	100	110	120
	130	140	150	160	170	180
m657.pep	TAPYQVCKA	EDITEASAQ	FLPGILKTAT	LGYDGKGQ	IRVKTLD	ELKAAFAEH
g657	TAPYQAVCKA	EDITEASAQ	FLPGILKTAT	LGYDGKGQ	IRVKTLD	ELKAAFAEH
	130	140	150	160	170	180

1047

	190	200	210	220	230	240
m657.pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQARQMAQR					
g657	EKMVDLRGEISVIVCRLNDENVQTFDPAENIHENGILAYSIVPARLSADVQQARQTAQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m657.pep	LADEL DYVGV LAVEMFVVGDTHELVVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP					
g657	LADEL DYVGV LAVEMFVVGDTHELLVNETAPRTHNSGHHTIDACAADQFQQQVRIMCNLP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m657.pep	PADTKLLSSCCMANILGDVWQEDGGE PDWLP LQSHPN AHLHL YGKKT AHKGRKM GHFTVL					
g657	PADTKLLSPCCMANILGDVWQEDGGE PDWLP LQSRPN AHLHL YGKKT AQKGRKM GHFTVL					
	310	320	330	340	350	360
	370	379				
m657.pep	TTDSDTAFQEAKKLHQSLX					
g657	TTDSDTAFQEAKKLHQSLX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2133>:

```

a657.seq
1  ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTCGGCA TTCTTGCGCG
51  CGGACAATTA GGCAGAAATG TTACTGTTGC TGCCAAAACC ATGGGCTACA
101 AAGTAACCGT ACTCGATCCC AACCCGAATG CGCCGGCAGC GGAATTTGCC
151 GACCGCCATT TGTGTGCGCC GTTTGACAAC CAAACCGCTT TGGAAGAATT
201 GGCAAAATGT GCGGCTGTTA CGACCGAGTT CGAAAACGTC AATGCCGATG
251 CGATGCGTTT TCTCGCCAAA CATACCAATG TTTCCCCCAG CGGCGACTGC
301 GTTGCCATCG CGCAAAACCG CATTCAAGAA AAGGCATGGA TACGCAAAGC
351 AGGCCTGCAA ACCGCGCCGT ATCAAGCAAT TTGCAAAGCC GAAGACATCA
401 CTGAAGAAAG CATACAATTT CTGCCCGGCA TCCTGAAAAC CGCTACATTG
451 GGCTATGACG GCAAAGGCCA AATCCGCGTC AAAACGGTGG ATGAACTCAA
501 AGCCGCGTTT GCCGAACACC GCGGCGTGGA TTGCGTTTTG GAAAAAATGG
551 TGGACTTGCG CGGCGAAATT TCCGTTATCG TATGCCGTCT GAACAATGAC
601 AACGTGCAAA CTTTCGATCC TGCCGAAAAC ATTCACGAAA ACGGTATCCT
651 CGCCTACTCC ATCGTCCCAG CCCGACTGAG TGCCGACATT CAGCAACAGG
701 CGCGACAAAT GGCGCAGCGT TTGGCCGATG AATTGAACTA CGTCGGCGTA
751 TTGGCGGTAG AAATGTTTGT TGTCGGCGAC ACGCATGAAT TGGTCGTCAA
801 CGAAATCGCG CCGCGTCCG ACATATCCGG CCACCATACC GTCGACGCCT
851 GCGCGGCAGA CCAATTCCAG CAACAGGTCC GCCTGATGTG CAACCTGCCA
901 CCTGTGACA CCAATTGCT GAGTTCTTGC TGTATGGCGA ATATTTTGGG
951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGTTT CCCCTGCAAA
1001 GCGGCGCGA CGCGCACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
1051 GGGCGGAAAA TGGGACACTT TACCATTTTA AGCACCGATT CGGACACCGC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2134; ORF 657.a>:

```

a657.pep
1  MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP NPNAPAAEFA
51  DRHLCAPFDN QTALEELAKC AAVTTEFENV NADAMRFLAK HTNVSPSGDC
101 VAIAQNRIQE KAWIRKAGLQ TAPYQAICKA EDITEESIQF LPGILKTATL
151 GYDGKGQIRV KTVDELKAAF AEHRGVDCVL EKMVDLRGEI SVIVCRLNND
201 NVQTFDPAEN IHENGILAYS IVPARLSADI QQARQMAQR LADELNYVGV
251 LAVEMFVVGDTHELVVNEIA PRPHNSGHHT VDACAADQFQ QQVRLMCNLP
301 PADTKLLSSC CMANILGDVW QEDGGE PDWF PLQSRPDAHL HLYGKKTAKH
351 GRKMGHFTIL STDSDTAFQE AKKLHQSL*

m657/a657 94.2% identity in 378 aa overlap

10 20 30 40 50 60
m657.pep MKNISLSPPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPDPDAPAAEFADRHLCAFPND

```

1048

```

|||||
a657      MKNISLSPPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPNPNAPAAEFADRHLCAFPDNDN
          10      20      30      40      50      60

          70      80      90      100     110     120
m657.pep  QAALDELAkCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ
          :|||:|||||
a657      QTALEELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ
          70      80      90      100     110     120

          130     140     150     160     170     180
m657.pep  TAPYQVVCKAEDITEASAQFLPGILKTATLGyDGKGQIRVKTLDelKAAFAEHGGVDCVL
          |||||:|||||
a657      TAPYQAICKAEDITEESIQLPGILKTATLGyDGKGQIRVKTVDelKAAFAEHRGVDCVL
          130     140     150     160     170     180

          190     200     210     220     230     240
m657.pep  EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQARQMAQR
          |||||:|||||
a657      EKMVDLRGEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADIQQARQMAQR
          190     200     210     220     230     240

          250     260     270     280     290     300
m657.pep  LADELdYVGVLAVEMFVVGDTHELVVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP
          |||||:|||||
a657      LADELNYVGVLAVEMFVVGDTHELVVNEIAPRPHNSGHHTVDACAADQFQQQVRLMCNLP
          250     260     270     280     290     300

          310     320     330     340     350     360
m657.pep  PADTKLLSSCCMANILGDVWQEDGGEFDWFLQSHPNahlhLYGKkTAHKGRKMghFTVL
          |||||:|||||
a657      PADTKLLSSCCMANILGDVWQEDGGEFDWFLQSRPDAHLHLyGKkTAHKGRKMghFTIL
          310     320     330     340     350     360

          370     379
m657.pep  TTDSDTAFQEAKKLHqSLX
          :|||||
a657      STDSDTAFQEAKKLHqSLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2135>:

```

g658.seq
1  ATGGTGGCCG GAATTGTGCG TGC GCGGGGC GGTTCATTG ACGAGCAATT
51 CATGTGTGTC GCCGACAACA AACATTCTA CCGCCAAtac GCCGACATAA
101 TCCAATTTCGT CCGCCAagcG TTGCGCCGTC TGCCGCGCCT GTTGCTGCAC
151 GTCGGCACTC AGCCGCGcgg gGACGATGga atAAGCCAAG ATGCCGTTTT
201 CGTGGATGTT TTCGGCGGGG TCGAAGGTTT GCACGTTTTC ATCGTTCAGA
251 CGGCATACGA TCACGGAAT CTCGCCGCGC AAGTCCACCA TTTTTCCTAA
301 AACGCAATCC ACGCCGCCGT GTTCGGCAAA CGCGGCTTTG AGTTCGTCCA
351 ACGTTTTGAC GCGGATTGTA CCTTTGCCGT CGTAGCCCAA CGTAGCCGTT
401 TTCAGGATGC CGGGCAAAAA TTGCGCGCTT GCTTCAGTAA TGTCTTCGGC
451 CTGCAAAACC GCCTGATACG GCGCGGTTTG CAAGCCTGCT TTGCGTATCC
501 ACGCTTTTTT CTGAATGCGG TTTTGTGCAA TGGACACGCA GTCGCCGCTG
551 GGGGAAACGT TGGTATGCTT TGCCAGAGAG CGCATCGCGT CGGCAttgac
601 gtTTTCAAAAT TCGGTcgtaA CCGCCGCGCA TTTTGCCAAT TCGTCCAACG
651 CGGCCCGGTC GTCAAACGGC GCGCACAAAT GGCGGTCGGC AAATTCGCCC
701 GCCGGCGCAT TCGGGTCGGG ATCGAGAACG GTTACTTTGT AGCCCATGGT
751 TTAGCGGCA ACGGCAACA TTctgcctAA

```

This corresponds to the amino acid sequence <SEQ ID 2136; ORF 658.ng>:

```

g658.pep
1  MVAGIVRARG GFIDEQFMCV ADNKHfYRQY ADIIQfVRQA LRRLPRLLLL
51 VGTQPRGDDG ISQDAVFVDV FGGVEGLHVF IVQTAYDHGN LAAQVHHFFQ

```

m658.seq

1	ATGGTGTCCG	GAATTGTGCG	GGCGCGGGGC	GATTTCGTTG	ACGACCAATT
51	CATCGGTGTC	ACCGCAACAA	AACATTTTCTA	CCGCCAATAC	GCGGACATAA
101	TCCAATTTCGT	CCGCCAAGCG	TTCGCGCCATC	TGCCCGCGCT	GTTCGTGCAC
151	GTCGCGACTC	AGTCGCGCGG	GGACGATGGA	ATAAGCCAAG	ATTGCGTTTT
201	CGTGGATGTT	TTCGCGAGGG	TCGAAAAGTTT	GCACGTTGTC	ATTGTTCAAA
251	CGGCAACATC	TTACGGAAAT	TTCACTGCGC	AAATCCACCA	TTTTTCCAA
301	AACGCAATCC	ACGCGCCCGT	GTTTCGGCAA	CGCGGCTTTG	AGTTATCCTT
351	ATGTTTTTAC	CGGGAATTGA	CCTTTGCCGT	CGTAGCCCAA	CGTAGCCGTT
401	TTCAGGATGC	CGGGCAAAAA	TTGCGCGCTT	GCTTCAGTGA	TGCTTTCAGC
451	CTTACAAAAC	ACTTGATACG	GCGCGGTTTG	CAATCCCGCT	TTGCGTATCC
501	ATGCCATTTTC	CTGAATTGCG	TTTTGTGCAA	TGCCACACA	ATCCCGCGTA
551	GGGCAAAACAT	TGGTATGTTT	TGCCAAAAAG	CGCATCGCAT	CGGCATTGAC
601	GTTTTCAAAT	TCAGTGGTCA	CCGCCGCGCA	TTTTGCCAAT	TCGTCCAAAG
651	CAGCTTTGGC	GTTAAACGCG	GCGCACAAA	GGCGGTCGGC	AAATTCTGCT
701	GCCGGCGCGT	CCGGATCCGG	GTCGAGAACG	GTTACTTTGT	AGCCCCATGGT
751	TTTGGCGGCA	ACGGTAAACA	TTCTGCCTAA		

m658.pep

1	MVSGIVRARG	DFVDDQFMRV	TDNKHFYRQY	ADIIQFVRQA	LRHLPRLLLH
51	VGTSQRGDDG	ISQDAVEFVDV	EGRVESLHVV	IVQTAYDYGK	FTAQIHFFFQ
101	NAIHAHAFDGK	RGDFEYTCFY	ADLTFVAVVQ	RSRFQDAGQN	LRACFSDFVS
151	LTNHLIRRG	QSRFAYPCLF	LNAVLCNRHT	IAARGNIGMF	CQKAHRIGID
201	VFKFSGHRR	FCQFVQSSLV	VKRRQAQMAVG	KFCCRRVRIG	VENGYFVAHG
251	FGGKGRKSA*				

Homology with a predicted ORF from *N. gonorrhoeae*

**m658/g658** 82.2% identity in 259 aa overlap

	10	20	30	40	50	60
m658.pep	MVSGIVRARGDFVDDQFM	RVTDNKHFYRQYADII	QFVRQALRHLPRLLL	HVGTSRGGDDG		
g658	:	:	:	:		
	10	20	30	40	50	60
m658.pep	ISQDAVFVDVFGRVESL	HVVIVQTAYDYGNF	TAQIHFFQNAIHA	AVFGKRGFEFI	QCFY	
g658		:		:  :		
	70	80	90	100	110	120
m658.pep	ISQDAVFVDVFGGV	EGLHVFIVQTAYD	HGNLAAQVHHFF	QNAIHA	AVFGKRGFEF	VQRFD
g658						
	70	80	90	100	110	120
m658.pep	ADLTFAVVAQRSRFQ	DAGQKLACFSDV	FSLTNHLIRRL	GLQSRFAYPCL	FLNAVLCNRHT	
g658				:  :		:
	130	140	150	160	170	180
m658.pep	ADLTFAVVAQRSRFQ	DAGQKLACFSNV	FGLANRLIRRL	GLQACFAYPR	FFLNAVLCNGHA	
g658						
	130	140	150	160	170	180
m658.pep	IAARGNIGMFCQKA	HRIGIDVFKFS	GHRRAFCQFV	QSSLVVKRRA	QMAVGKFC	CRRVRIG
g658	:	:	:  :	:  :	:  :	:  :
	190	200	210	220	230	240
m658.pep	IAARGNIGMFCQKA	HRIGIDVFKFS	GHRRAFCQFV	QSSLVVKRRA	QMAVGKFC	CRRVRIG
g658	:	:	:  :	:  :	:  :	:  :
	190	200	210	220	230	240
m658.pep	VENG	YFVAHGFGGNGK	SAX			
g658						
	250	260				

1:050

```

          :|||||:|||||
g658      IENGYFVAHGFSGNGKHSAX
          250      260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2139>:

```

a658.seq
1  ATGGTGGCCG GAATTGTGCG GACGCGGCGC GATTTCGTTG ACGACCAATT
51  CATGCGTGTC GCCGACAACA AACATTCTA CCGCCAATAC GCCGACGTAG
101 TTCAATTCAT CGGCCAAACG CTGCGCCATT TGTCGCGCCT GTTGCTGAAT
151 GTCGGCACTC AGTCGGGCTG GGACGATGGA GTAGGCGAGG ATACCGTTTT
201 CGTGAATGTT TTCGGCAGGA TCGAAAGTTT GCACGTGTC ATTGTTTCAGA
251 CGGCATACGA TAACGGAAAT TTCGCGCGCG AAGTCCACCA TTTTTTCCAA
301 AACGCAATCC ACGCCGCGGT GTTCGGCAAA CGCGGCTTTG AGTTCATCCA
351 CCGTTTTGAC GCGGATTTGG CCTTGGCCGT CATAGCCCAA TGTAGCGGTT
401 TTCAGGATGC CGGGCAGAAA TTGTATGCTT TCTTCAGTGA TGTCTTCGGC
451 TTTGCAAATT GCTTGATACG GCGCGGTTT CAGGCTGCTT TTGCGTATCC
501 ATGCCTTTTC CTGAATGCGG TTTTGCGCGA TGGCAACGCA GTCGCCGCTG
551 GGGGAAACAT TGGTATGTTT GGCGAGAAAA CGCATCGCAT CGGCATTGAC
601 GTTTTCGAAC TCGGTCGTAA CAGCCGCACA TTTTGCCAAT TCTTCAAAG
651 CGGTTTGGTT GTCAAACGGC GCACACAAAT GGCGGTCGGC AAATTCGGCT
701 GCCGGCGCAT TCGGTTGGG ATCGAGTACG GTTACTTTGT AGCCCATGGT
751 TTTGGCAGCA ACAGTAAACA TTCTGCCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2140; ORF 658.a>:

```

a658.pep
1  MVAGIVRTRR DFVDDQFMRV ADNKHFYRQY ADVVQFIGQT LRHLSRLLLN
51  VGTQSGWDDG VGEDTVFVNV FGRIESLHV IVQTAYDNGN FAAQVHHFFQ
101 NAIHAAVFGK RGFEEIHRFD ADLAFAVIAQ CSGFQDAGQK LYAFFSDVFG
151 FANCLIRRLG QACFAYPCLF LNAVLRDUNA VAAGGNIGMF GEKTHRIGID
201 VFELGRNSRT FCQFFQSGLV VKRRTQMAVG KFCRRRIRVG IEYGYFVAHG
251 FGSNSKHSAX*

```

m658/a658 75.3% identity in 259 aa overlap

	10	20	30	40	50	60
m658.pep	MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLLHVGTQSRGDDG					
a658	MVAGIVRTRRDFVDDQFMRVADNKHFYRQYADVQFIGQTLRHLSRLLLNVTQSGWDDG					
	10	20	30	40	50	60
m658.pep	ISQDAVFVDVFGRVESLHVIVIVQTAYDYGNTAQIHFFQNAIHAAVFGKRGFEFIQCFY					
a658	VGEDTVFVNVFGRIESLHVIVIVQTAYDNGNFAAQVHHFFQNAIHAAVFGKRGFEFIHRFD					
	70	80	90	100	110	120
m658.pep	ADLTFVAVQSRFQDAGQKLRACFSDVFSLTNHLIRRLGQSRFAYPCLFLNAVLCNRHT					
a658	ADLAFAVIAQCSGFQDAGQKLYAFFSDVFGFANCLIRRLGQACFAYPCLFLNAVLRDUNA					
	130	140	150	160	170	180
m658.pep	IAARGNIGMFCQKAHRIGIDVFKFSGHRRACQFVQSSLVVKRRRAQMAVGKFCRRVRIG					
a658	VAAGGNIGMFGKTHRIGIDVFELGRNSRTFCQFFQSGLVVKRRTQMAVGKFCRRRIRVG					
	190	200	210	220	230	240
m658.pep	VENGYFVAHGFSGNGKHSAX					
a658	IEYGYFVAHGFSGNSKHSAX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2141>:

1051

```

g661.seq
  1  ATGCACATCG GCGGTTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
 51  GGCGGGCATT GCGGACAAAC CCTTCCGCCG CCTCTGTCGG GCGTTTGGCG
101  CAGGTTGGGC GGTGTGCGAA ATGCTGGCCA GCGATCCGAC GCTCAGGAAT
151  ACCGGA AAAA CCctgcaccg cagtgaTTt gccgatgaag gCGGCATCGT
201  TGCCGTGCAG ATTGCCGGCA GCGACCcga acaGATGGCG Gatgcgggcg
251  gttacAACGT CGGACTCGGG GCGCAGGTCA TCGACATcaa TATGGGCTGC
301  cccgccaaga AAGTGTGCAA CGTCCAAGCC GGTAGCGCgc tGATGCAGGA
351  CGAGccgctg gttgcCgcca tTTtgaggc ggtggtcAAG GCGGCGGgcy
401  TACCCGTTAC cctCAAAACc cgtTtgggtt ggcacgacga cgatcaaaac
451  ctgcCcgccg tcgcaaaaat cgccgaagat tgcggcattg ccgccCttgc
501  cggtccacgg gcgCGCgcgC ACGCAAATGT ACAAAGGCGA GGCgcGTTAC
551  Gaactcatcg CCGAGACCAA AAGccgTCTG AACATCCCGG cctGggtCAA
601  CGGCGACATC actTCgccc AAAAAGCCGC CGccgTCCTC AAACAAACCG
651  CCGCCGACGG CATCATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTT
701  TTCCGCGATT TGAAGCATTA TGCCGAACAC GCGGTTTTAC CGCCTGCCTT
751  GAGTTTGGCA GAATGCAGAG CCGCCATTTT GAACCACATC CGCGCCATGC
801  ACGCGTTTTA TGGTGAGACC GTCGGTGTGC GCATCGCACG CAAACACATA
851  GGCTGGTACA TCGGCGAAAT GCCCGACGGC GAACAGGCGC GCGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2142; ORF 661.ng>:

```

g661.pep
  1  MHIGGYFIDN PIALAPMAGI ADKPFRRLCR AFGAGWAVCE MLASDPTLRN
 51  TGKTLHRSDf ADEGGIVAVQ IAGSDPEQMA DAARYNVGLG AQVIDINMGC
101  PAKKVCNVQA GSALMQDEPL VAAILEAVVK AAGVPVTLKT RLGWHDDQDN
151  LPAVAKIAED CGIAALAVPR ARAHANVQRR GALRTHRRDQ KPSEHPGLGQ
201  RRHHFAAKSR RRPQTNRRRR HHDRARRARQ AVVFPRFEAL CRTRRFTACL
251  EFGRMQSRHF EPHPRHARVL WXDRCARHRT QTHRLVHRRN ARRRTGAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2143>:

```

m661.seq
  1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
 51  GGCGGGCATT ACCGACAAAC CGTTCCGCCG ACTTTGCCGA GATTTTGGCG
101  CAGTTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151  ACTAGAAAAA CCTTGACCCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201  TGCCGTGCAG ATTGCCGGA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251  GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301  CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351  CGAGCCGCTG GTTGCCGCCA TTTTGGAAGC CGTCGTCCGT GCGGCAGGCG
401  TACCCGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
451  CTGCCCGTCA TCGCCAAAAT CGCCGAAGAT TCGGGCATCG CCGCCCTTGC
501  CGTCC.AC GG ACGCACGCGT ACGCAAATGT ACAAAGGCGA AGCGCGTTAC
551  GAACTCATCG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601  CGGCGACATT ACTTCGCGCG AAAAAGCCCA AGCCGTCTC AAACAAACCG
651  CCGCCGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTC
701  TTCCGCGATT TGAACATTA TGCCGAACAC GGTGTTTTGC CGCCTGCCTT
751  GAGTTTGGCA GAATGCGCCG CCGCTATTTT GAACCACATC CGCGCCATAC
801  ACGCGTTTTA CGGCGACACC GCCGGTGTGC GCATCGCACG CAAACACATA
851  GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2144; ORF 661>:

```

m661.pep
  1  MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
 51  TRKTLHRSDf ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
101  PAKKVCNVQA GSALMQNEPL VAAILEAVVR AAGVPVTLKT RLGWHDDHQN
151  LPVIAKIAED CGIAALAVXR THAYANVQRR SALRTHRRNQ MPSEHPGLGQ
201  RRHYFAAKSP SRPQTNRRRR HYDRARRARQ AVVLPRFETL CRTRCFACCL
251  EFGRMRRRYF EPHPRHTRVL RRHRCARHRT QTHRLVHRRN ARRRTDTS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m661/g661 88.5% identity in 295 aa overlap

1052

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNP	IAPMAGITDKP	FRRLCRDFGAG	WAVCEMLTSDPT	LRNTRKTLHRSDF	
g661	MHIGGYFIDNP	IAPMAGIADKP	FRRLCRAFGAG	WAVCEMLASDPT	LRNTGKTLHRSDF	
	10	20	30	40	50	60
	70	80	90	100	110	120
m661.pep	ADEGGIVAVQI	AGSDPQQMADA	ARYNVSLGAQL	IDINMGCPAKK	VKNVQAGSALM	QNEPL
g661	ADEGGIVAVQI	AGSDPEQMA	DAARYNVGLGA	QVIDINMGCP	AKKVCNVQAG	SALMQDEPL
	70	80	90	100	110	120
	130	140	150	160	170	180
m661.pep	VAAILEAVVRA	AGVPVTLKTRL	GWHDHQNLP	VIAKIAEDCG	IAALAVXRTH	AYANVQRR
g661	VAAILEAVVKA	AGVPVTLKTRL	GWHDHDDQN	LPVAKIAEDCG	IAALAVPRAR	AHANVQRR
	130	140	150	160	170	180
	190	200	210	220	230	240
m661.pep	SALRTHRRNQ	MPSEHPGLGQ	RRHYFAAKSP	SRPQTNR	RRRHDRARR	ARQAVVLP
g661	GALRTHRRDQ	KPSEHPGLGQ	RRHFAAKSRR	RPQTNRR	RRRHDRARR	ARQAVVFP
	190	200	210	220	230	240
	250	260	270	280	290	299
m661.pep	CRTRCFAAC	LEFGRMRRRY	FEPHPRHTR	VLRRHRC	CAHRTQTHRL	VHRRNARR
g661	CRTRRFTAC	LEFGRMQSR	HFEPHPRH	ARVLWXDR	CAHRTQTHRL	VHRRNARR
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2145>:

```

a661.seq
1   ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GGCGGGCATTT ACCGACAAAC CGTTCCGCCG ACTTTGCCGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTTGACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCCGCTG GTTGCCGCCA TTTTGGAGGC GGTGGTCAA GCGGCGGGCG
401 TACCCGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCGTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATTG CCGCCCTTGC
501 CG.TCCACGG ACGCACGCGC ACGCAAATGT ACAAAGGCGA AGCGGCTTAC
551 GACCTGATTG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601 CGGCGACATT ACCTCGCGC AAAAAGCCCA AGCCGTCTC AAACAAACCG
651 CCGCAGACGG CATTATGATA GGGCGCGCGC CGCAAGGCAG ACCGTGGTTC
701 TTCCGCGATT TGAAACATTA CGCCGAACAC GGTGTTTAC CGCCTGCCTT
751 GAGTTTGGCA GAATGTACCG CCACTATTTT GAACCACATC CGAGCCATGC
801 ACGCGTTTTA CGGCGACACC GCCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCGACGCG GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2146; ORF 661.a>:

```

a661.pep
1   MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQQMA DAARYNVSLG AQLIDINMG
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVK AAGVPVTLKT RLGWHDDHQN
151 LPVIAKIAED CGIAALAXPR THAHANVQRR SGLRPDCRNQ MPSEHPGLGQ
201 RRHYLAAKSP SRPQTNRRRR HYDRARRARQ TVVLPFRFETL RRTRCFTACL
251 EFGMRMYRHYF EPHPSHARVL RRHRRCAHRT QTHRLVHRRN ARRRTDTS*

```

m661/a661 94.6% identity in 298 aa overlap

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNP	IAPMAGITDKP	FRRLCRDFGAG	WAVCEMLTSDPT	LRNTRKTLHRSDF	

1053

```

a661      MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF
           10      20      30      40      50      60
           70      80      90      100     110     120
m661.pep  ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           |||||
a661      ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           70      80      90      100     110     120
           130     140     150     160     170     180
m661.pep  VAAILEAVVRAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR
           |||||
a661      VAAILEAVVKAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAXPRTHAHANVQRR
           130     140     150     160     170     180
           190     200     210     220     230     240
m661.pep  SALRTHRRNQMPSEHPGLQRRHYFAAKSPSRPQTNRRRRHYDRARRARQAVVLPFRFETL
           |::|
a661      SGLRPDCRNQMPSEHPGLQRRHYLAAKSPSRPQTNRRRRHYDRARRARQTVVLPFRFETL
           190     200     210     220     230     240
           250     260     270     280     290     299
m661.pep  CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRRHRRCAHRTQTHRLVHRRNARRRTDTSX
           |||||
a661      RRTRCFCTACLEFGRMYRHYFEPHPSHARVLRRHRRCAHRTQTHRLVHRRNARRRTDTSX
           250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2147>:

```

g663.seq
1  ATGTGTACCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCA GTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGGCCTGATC GGTTGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTGGCA
151 AAATGTTTTT CCGAATGGGA CGAAGAAAAG CGTAAAACCG TGTGAAACA
201 GCATTTCAAA CACATGGCAA AACTGATGCT CGAATACGGC TTATATTGGT
251 ACGCGtctGC CAAATGCCTG AAATCGCTGG TCGCTACCG CAATAAGCAT
301 TATTGGACG ACGCGCTGGC GGCGGGGAA AAAGTCATCA TCCTGTACCC
351 GCACTTTACC GCGTTTCGAGA TGCGGTGTA CGCGCTAAT CAGGATGCC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAg gccgcaACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAagggctg cgCGCCctcg TCAAACAGTT CCGCAAAAGC AGTGCGCCGT
551 TCCTGTATCT GCCCGATCAG GATTTCGGAC GCAACAATTC GGTTTTGTG
601 GATTTTTTCG GCATtcagaC GGCAACGATT ACCGGCTTGA GCCGATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCCGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAA TTCTATCCCG CTTGAAAATC CTTTCCGAGT
751 GAAGACGCGC AAGCCGACGC GCAACGTATG AACCGCTTTA TCGAAGAACG
801 CGTGCGCGAA CACCCGGAAC AATATTTCTG GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2148; ORF 663.ng>:

```

g663.pep
1  MCTEMKFIFF VLYVLQFLPF ALLHKIAGLI GSLAYLLVKP RRRIGEINLA
51  KCFPEWDEEK RKTVLKQHFH HMAKLMLEYG LYWYASAKCL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNNSVFEV
201 DFFGIQTATI TGLSRIAALA NAKVIPAIPIV READNTVTLO FYPAWKSFPF
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2149>:

```

m663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCA GTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGACCTGACG GGTTTGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTGGCA
151 AAATGTTTTT CCGAATGGAG TGAGGAAAAG CGTAAAACCG TGTGAAACA

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1054

```

201 GCATTTCAAA CACATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCTGC CGGACGTTTG AAATCGCTGG TGCGCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATATCC
401 CGCTGATCAG TATGTATTCC CATCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAG GCCGCAACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCGCGATCAG GATTTCGGAC GCAACGATTC GGTTTTGTG
601 GATTTTTTCG GTATTCAGAC GGCAACGATT ACCGGATTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCCGTC CGCGAGGCAG
701 ACAATACGGT TACATTGCAT TTCTACCCTG CTTGGAAATC CTTTCCGGGT
751 GAAGACGCGA AAGCCGACGC GCAGCGCATG AACCGTTTTA TCGAAGACAG
801 GGTGCGCGAA CATCCGGAAC AATATTTTTG GCTGCACAAG CGTTTTAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2150; ORF 663>:

```

m663.pep
  1 MCIEMKFIFF VLYVLQFLPF ALLHKIADLT GLLAYLLVKP RRRIGEINLA
 51 KCFSEWSEEEK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDIPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVVF
201 DFFGIQTATI TGLSRIAALA NAKVIPAI PV READNTVT LH FYPAWSFPG
251 EDAKADAQRM NRFIEDRVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

**m663/g663** 94.9% identity in 293 aa overlap

	10	20	30	40	50	60
m663.pep	MCIEMKFIFFVLYVLQFLPFALLHKIADLTGLLAYLLVKP	RRRIGEINLAKCFSEWSEEEK				
g663	MCTEMKFIFFVLYVLQFLPFALLHKIAGLIGSLAYLLVKP	RRRIGEINLAKCFPEWDEEK				
	10	20	30	40	50	60
m663.pep	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH	YLDDALAAGEKVIILYPHFT				
g663	RKTVLKQHFHMAKLMLEYGLYWYASAKCLKSLVRYRNKH	YLDDALAAGEKVIILYPHFT				
	70	80	90	100	110	120
m663.pep	AFEMAVYALNQDIPLISMYS HQKNKILDEQILKGRNRYHN	VFLIGRTEGLRALVKQFRKS				
g663	AFEMAVYALNQDVPLISMYS HQKNKILDEQILKGRNRYHN	VFLIGRTEGLRALVKQFRKS				
	130	140	150	160	170	180
m663.pep	SAPFLYLPDQDFGRNDSVVF	DFFGIQTATITGLSRIAALANAKVIPAI	PVREADNTVT	LH		
g663	SAPFLYLPDQDFGRNNSVVF	DFFGIQTATITGLSRIAALANAKVIPAI	PVREADNTVT	LQ		
	190	200	210	220	230	240
m663.pep	FYPAWSFPGEDAKADAQRMNRFIEDRVREH	HPEQYFWLHKR	FKTRPEGSP	DFYX		
g663	FYPAWSFPGEDAQADAQRMNRFIEERVREH	HPEQYFWLHKR	FKTRPEGSP	DFYX		
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2151>:

```

a663.seq
  1 ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
 51 TCTGCCGTTT GCGCTGCTGC ACAAACTTGC TGATCTGACA GGCTTGCTCG
101 CCTACCTTTT GGTCAAACCC CGCCGCCGTA TCGGCGAAAT CAATTTGGCA

```

1055

```

151 AAATGCTTTC CCGAGTGGGA CGGAAAAAAG CGTAAACCG TGTGAAACA
201 GCATTTCAAA CATATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCCGC CGGGCGTTTG AAATCACTGG TGCCTACCG CAACAAACAT
301 TATTTGGACG ACGCTCTGGC GGCAGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTCAAT CAGGATGTTC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAAC GTTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CCGCGCCTCG TCAAACAGTT CCGCAAAAGC AGCGGCGCGT
551 TTCTGTATCT GCCCGATCAG GATTTCGGAC GCAACGATTC GGTTTTGTG
601 GATTTCCTCG GTATTCCGAC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATCCCTGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAT TTCTACCCTG CTTGGGAATC CTTCCGAGT
751 GAAGATGCGC AGGCCGACGC GCAGCGCATG AACCGTTTGA TCGAGGAACG
801 CGTGC GCGAA CATCCCGAGC AGTATTTTGT GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2152; ORF 663.a>:

a663.pep

```

1 MCIEMKFIFF VLYVLQFLPF ALLHKLADLT GLLAYLLVKP RRRIGEINLA
51 KCFPEWDGKK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDVPLISMYH HQNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVFE
201 DFFGIRTATI TGLSRIAALA NAKVIPAIPIV READNTVTLH FYPAWESFSP
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

m663/a663 96.2% identity in 293 aa overlap

	10	20	30	40	50	60
m663.pep	MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKP	RRRIGEINLAKCFSEWSEEK				
a663	MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKP	RRRIGEINLAKCFPEWDGKK				
	10	20	30	40	50	60
	70	80	90	100	110	120
m663.pep	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH	YLDALAAGEKVIILYPHFT				
a663	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH	YLDALAAGEKVIILYPHFT				
	70	80	90	100	110	120
	130	140	150	160	170	180
m663.pep	AFEMAVYALNQDIPLISMYSHQNKILDEQILKGRNRYHN	VFLIGRTEGLRALVKQFRKS				
a663	AFEMAVYALNQDVPLISMYSHQNKILDEQILKGRNRYHN	VFLIGRTEGLRALVKQFRKS				
	130	140	150	160	170	180
	190	200	210	220	230	240
m663.pep	SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAALA	NAKVIPAIPVREADNTVTLH				
a663	SAPFLYLPDQDFGRNDSVFVDFFGIRTATITGLSRIAALA	NAKVIPAIPVREADNTVTLH				
	190	200	210	220	230	240
	250	260	270	280	290	
m663.pep	FYPAWKSPGEDAKADAQRMNRFIEDRVREHPEQYFWLHK	RFKTRPEGSPDFYX				
a663	FYPAWESFSEDAQADAQRMNRFIEERVREHPEQYFWLHK	RFKTRPEGSPDFYX				
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2153>:

g664.seq

```

1 ATGATACATC CGCACCCTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
51 AGAAATTGTT CATCTCCTCA TAGCTGAcgg gCGCACCGG ATGGCGGGTC
101 GGGCCTGCGT CTTCCGGGGA CTGGTTCTGG CGCAGCAGGC GGATGTTCTC
151 GATGCGGCGC ACGGCGCGGC CGGCGCGGTC GCCGGAAC TCTTGGTCGC
201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTTACGCGGT TGCCCGTCCA GTTGTGGAAA TATTCGTGTC CGACCACGGA
301 TTCAATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCGAGGA
351 CGAACTTGGT GTTAAAAATG TTCAAACCTT TGTTTTCCAT CGCGCCCAT
401 TTGAAATCGC CTACGGCGAC GACCATGAaa atatccaagt cataTTCaa
451 cCgaagcgc gtttcgtcCc acttcatcgC gtTTTTTCAA cgaTTCCACG
501 GCAAAGCCGA CCTTGGGTTT GTCCGCTTCG GTGGTGTAAG ACTCGATTTT

```

1056

551 GA

This corresponds to the amino acid sequence &lt;SEQ ID 2154; ORF 664.ng&gt;:

```

g664.pep
1  MIHPHHFRAF  FINGHGVEIV  HLLIADGAHR  MGGRACVFGE  LVLAQQADVL
51  DAAHGAAGAV  AGKLLVAEHG  QPFLQRKLEP  VAAGYAVARP  VVEIFVSDHG
101 FNAFEIGIGG  GAAVGEDELG  VKNVQTLVFH  RAHIEIAYGD  DHENIQVIFQ
151 PEARFVPLHR  VFSTIPRQSR  PWVCPLRWCK  TRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2155>:

```

m664.seq
1  GTGATACATC  CGCACTACTT  CCGCGCCTTT  TTCATAAACG  GTCATGGTGT
51  AGAAATTGTT  CATCTCCTCA  TAGCTGGCGG  GGCGCACCGG  ATGGGCGGTC
101 GGGCCTGCGT  CTTCGGGGAA  CTGGTGCTGG  CGCAGCAGGC  GGATGTTTTC
151 GATCGCGCGC  ACGGCGCGGC  TGGCGCGGTC  GCCGGAAAAT  TCTTGGTCGC
201 GGAACACGGT  CAGCCCTTCC  TTCAGCGAAA  GCTGGAACCA  GTCGCGGCAG
251 GTTACGCGGT  TGCCCGTCCA  GTTGTGAAAA  TACTCGTGTC  CGACCACGGA
301 TTCGATGCCT  TCGAAATCGG  TATCGGTGGC  GGTGCGGCTG  TCGGCAAGGA
351 CGAACTTGGT  GTTAAAGATG  TTCAAACCTT  TGTTTTCCAT  CGCGCCCAT
401 TTGAAATCGC  CCACGGCGAC  GACCATGAAA  ATATCCAAGT  CGTATTCCAA
451 ACCGAAGCGC  GTTTCGTCCC  ATTTTCATCG  GTTTTT.CAA  CGATTCCACG
501 GCAAAGCCGA  CCTTGGGCTT  GTCCGCTTCG  GTGGTGTAAG  ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2156; ORF 664&gt;:

```

m664.pep
1  VIHPHYFRAF  FINGHGVEIV  HLLIAGGAHR  MGGRACVFGE  LVLAQQADVF
51  DAAHGAAGAV  AGKFLVAEHG  QPFLQRKLEP  VAAGYAVARP  VVEILVSDHG
101 FDAFEIGIGG  GAAVGKDELG  VKDVQTLVFH  RAHIEIAHGD  DHENIQVVFQ
151 TEARFVPFHR  VFXTIPRQSR  PWACPLRWCK  TRF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m664/g664 91.8% identity in 183 aa overlap

	10	20	30	40	50	60
m664.pep	VIHPHYFRAFFINGHGVEIVHLLIAGGAHRMGGRACVFGEVLVAQQADVFDAAHGAAGAV					
	:    :					
g664	MIHPHHFRAFFINGHGVEIVHLLIADGAHRMGGRACVFGEVLVAQQADVLDAHGAAGAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m664.pep	AGKFLVAEHGQPFLQRKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGAAVGKDELG					
	:					
g664	AGKLLVAEHGQPFLQRKLEPVAAGYAVARPVVEIFVSDHGFNAFEIGIGGGAAVGEDELG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m664.pep	VKDVQTLVFHRAHIEIAHGDDHENIQVVFQTEARFVPFHRVFXTIPRQSRPWACPLRWCK					
	:					
g664	VKNVQTLVFHRAHIEIAYGDDHENIQVIFQPEARFVPLHRVFSTIPRQSRPWACPLRWCK					
	130	140	150	160	170	180
m664.pep	TRFX					
g664	TRFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2157>:

```

a664.seq
1  GTGATACATC  CGCACCCTT  CCGCGCCTTT  TTCATAAACG  GTCATGGTGT
51  AGAAATTGTT  CATCTCCTCA  TATCGGGCGG  GGCGCACCGG  ATGTGCGGTC
101 GGACCTGCGT  CTTCGGGGAA  CTGGTGCTGG  CGCAGCAGGC  GGATGTTTTC
151 GATACGGCGC  ACGGCGCGGC  TGGCGCGGTC  GCCGGAAAAT  TCTTGGTCGC

```

1057

```

201 GGAACACGGT CAACCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTCACGCGGT TGCCCGTCCA GTTGTGAAA TATTCGTGTC CGACCACGGA
301 TTCGATGCCT TCAAAATCGG TATCGGTGGC GGTACGGCTG TCGGCAAGGA
351 CGAACTTGGT GTTAAAGATG TTCAAACCTT TGTTTCCAT CGCACCATA
401 TTGAAATCGC CCACGCGGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
451 ACCGAAGCGC GTTTCGTCCC ACTTCATTGC GTTTTT.CAG CGATTCCACG
501 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGAAA ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2158; ORF 664.a>:

```

a664.pep
  1 VIHPHHFRAF FINGHGV EIV HLLISGGAHR MCGRTCVEGE LVLAQQADV F
 51 DTAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGHAVARP VVEIFVSDHG
101 FDAFKIGIGG GTAVGKDELG VKDVQTLVFH RTHIEIAHGD DHENIQVVFQ
151 TEARFVPLHC VFXAIPRQSR PWACPLRWCK TRF*

```

m664/a664 92.9% identity in 183 aa overlap

```

              10      20      30      40      50      60
m664.pep      VIHPHYFRAFFINGHGV EIVHLLIAGGAHRMGGRA CVFGE LVLAQQADV F DAAHGAAGAV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a664           VIHPHHFRAFFINGHGV EIVHLLISGGAHRMCGRTC VFGE LVLAQQADV F DTAHGAAGAV
              10      20      30      40      50      60

              70      80      90      100     110     120
m664.pep      AGKFLVAEHGQPFLQRKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGAAVKGDELG
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a664           AGKFLVAEHGQPFLQRKLEPVAAGHAVARPVVEIFVSDHGFDAFKIGIGGGTAVGKDELG
              70      80      90      100     110     120

              130     140     150     160     170     180
m664.pep      VKDVQTLVFHRAHIEIAHGDDHENIQVVFQTEARFVPFHRVEXTIPRQSRPWACPLRWCK
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a664           VKDVQTLVFHRTTHIEIAHGDDHENIQVVFQTEARFVPLHCVFXAIPRQSRPWACPLRWCK
              130     140     150     160     170     180

m664.pep      TRFX
              ||||
a664           TRFX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2159>:

```

g665.seq
  1 atgaagtGg acgaaacgcg cttcgGgttg GAAatgact tggatatTT
 51 CATGGTCGTC GCCGTAGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT TTTTAACACC AAGTTCGTCC TCGCCGACAG CCGCACCGCC
151 ACCGATACCG ATTTCGAAGG CATTGAATCC GTGGTCGGAC ACGAATATTT
201 CCACAAC TGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAGTT TTCCGGCGAC
301 CGCGCCGGCC GCGCCGTGCG CCGCATCGAG AACATCCGCC TGCTGCGCCA
351 GAACCA GTTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCcccg
401 TCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GGGCGCGAAG TGGTGCGGAT GTATCATACC CTGCTCGGCG AAGAGGGCTT
501 CCAAAAAGGC ATGAAGCTAT ATTTCCaacg CCACGACGGA CAGGCAGTGA
551 CCTGCGACGA TTTCCGCGCG GCGatggcgg ATGCGAACGG CATCAATCTC
601 GACCAGTTCG CCTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGGGAAGC
651 CGAAGGCCGT CTGAAAAACA ATGTTTTCTGA GTTAACCATT AAACAAACCG
701 TGCCGCCCAC GCCCGATATG GCGGACAAAC AGCCGATGAT GATTCGCCGC
751 AAAGTCGGGC TTCTGAACCG CAACGGCGAA GCGGTGGCAT TCGATTATCA
801 GGGCAAACGC GCAACCGAAG CCGTGTGCT GATGACCGAA GCCGAACagg
851 CCTTCCCGCT CGAAGGTGTA ACCGAAGCCG TCGTTCCTC GCTGCTGCGC
901 GGGTTCCAGC CGCCAGTGTA TCTGAAC TAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCACG ACAGCGACGC TTTCACGTGC TGGGAAGCCG

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1058

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1001 CCCAAACGCT CTACCGTCGC GCCGTCGCCG CCAACCTTGC CGCGCTTTCA
1051 GACGGCATCG GGTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TGGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCGTC CGAAGCCGAa ctGTGGGACG GCACGAAAAA CATcgaCCCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGtCCG
1251 CttcctgcCG AAATGGCACG AATTGGaccg tcaggcggcg aagCAGgaaa
1301 accaaagtTA CGAATACAGC CCCGAAACCG CCGACTGGCG CACGCTGCGC
1351 AACGTCTGCC GCGCCTcgt cctGCGCGCC GACCCGCGC acatcgAAAC
1401 TGTTGCCGAA Aaatacggcg AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCTGTCT CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACTGCCTG
1501 CTGGCGCAGT TTGCCGAcAA gTtttcAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTCGCT CTTATCGGCT CAAGccggcg cagCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAATTCA GTCTCGAAAA CCCCAACAAA
1651 GCCCGTTTCG TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTTTCACGC
1701 ACAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA cCCGCAggtc gccGCCCGCC TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAAC TTgGTGAAAC AAGAATTGCA
1851 GTGATTTCGG GCGCAGGAAG GATTGTGAA AGacGTGGGC GAaatcgtCG
1901 GCAAGATTTT GGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2160; ORF 665.ng>:

g665.pep

```

1 MKWDETRFGL EYDLDFMVV AVGDFNMGAM ENKGLNIFNT KFVLADSRTA
51 TDTFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RAGRAVRRIE NIRLLRQNOF PEDAGPTAHP VRPVSYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAEGR LKNNVFELTI KQTVPPTPDM ADKQPMPIPV
251 KVGLLNRNGE AVAFDYQGR ATEAVLLMTE AEQAFPLEGV TEAVVPSLLR
301 GFSAPVYLN YPSDDDLLL LAHSDAFTC WEAAQTLYRR AVAANLAALS
351 DGIGLPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGTENIDP
401 LRYHQAREAL LDTLAVRFLP KWHELDRAQA KQENQSYEYS PETADWRTLRL
451 NVCRAFLVLA DPAHIETVAE KYGEMAQNM HEWGILSAVN GNESDTRNCL
501 LAQFADKFSD DALVMDKYFA LIGSSRRSDT LQQVQTALQH PKFSLNPNK
551 ARSLIGFSR NVPHFHAQDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQELQCIR AQEGLSKDVG EIVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2161>:

m665.seq

```

1 ATGAAATGGG ACGAAACGCG CTTCCGTTTG GAATACGACT TGGATATTTT
51 CATGGTCGTC GCCGTGGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGCACCGCC
151 ACCGATACCG ATTTTCAAGG CATCGAATCC GTGGTCGGAC ACGAGTATTT
201 CCACAACCTG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAATT TTCCGGCGAC
301 CGCGCCAGCC GCGCCGTGCG CCGCATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCAAGTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCCCCG
401 CCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GGCGCGGAAG TAGTGCGGAT GTATCACACC CTGCTCGGCG AAGAGGGCTT
501 CCAGAAAGGC ATGAAGCTCT ATTTCCAACG CCACGACGGA CAGGCCGTTA
551 CCTGCGACGA TTTCCGCGCG GCGATGGCGG ACGCGAACGG CATCAATCTC
601 GACCAAGTTC CTTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGGAAGC
651 GGAAGGTCGT CTGAAAAACA ATATTTTCGA GTTGACCGTC AAACAAACCG
701 TGCCGCCCCA GCGCGATATG ACGGATAAAC AGCCGATGAT GATTCCCGTC
751 AAGGTCGGGC TGCTGAACCG CAACGGCGAA GCGGTGGCAT TCGACTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGCTG GCTGACCGAA GCCGAACAGA
851 CTTTCTTGCT CGAAGGCGTA ACCGAAGCCG TCGTTCCCTC GCTGCTCGCG
901 GGGTTCAGCG CGCCGGTGCA TCTGAACTAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCCATG ACAGCGACGC CTTACGCGC TGGGAAGCCG
1001 CCCAAACGCT CTACCGCCGC GCCGTCGCCG CCAACCTTGC CACGCTTTCA
1051 GACGGCGTTG AGCTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TAGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCATC CGAAGCCGAG CTGTGGGACG GCGCAGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGTCCA
1251 CTTCTGCGC AAATGGCACG AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAATACAGC CCCGAAGCCG CCGGCTGGCG CACGCTGCGC

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1059

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1351 AACGTCTGCC GCGCCTTTGT CCTGCGCGCC GACCCCGCGC ACATCGAAAC
1401 CGTTGCCGAA AAATACGGCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCGAACCGC CTTGCAGCAT CCGAAATTCA GCCTCGAAAA CCCCAACAAA
1651 GCCCGTTTCG TCATCGGCAG CTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA CCCGCAGGTC GCCGCCCGCT TAGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTTCG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2162; ORF 665>:

```

m665.pep
  1 MKWDETRFGL EYDLDFIMVV AVGDFNMGM ENKGLNIFNT KFVLADSRTA
 51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPASYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAEGR LKNNIFELTV KQTVPPPTDM TDKQPMIIPV
251 KVGLLNRNGE AVAFDYQGKR ATEAVLLLTE AEQTFLLLEGV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEAAQTLYRR AVAANLATLS
351 DGVELPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDTLAVHFLP KWHELNQAA KQENQSYEYS PEAAGWRTL
451 NVCRAFLVRA DPAHIETVAE KYGEMAQNM HEWGILSAVN GNESDTRNRL
501 LAQFADKFSD DALVMDKYFA LVGSSRRSDT LQQVRTALQH PKFSLENPNK
551 ARSLIGSFSR NVPHFHAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m665/g665 96.1% identity in 637 aa overlap

```

              10      20      30      40      50      60
m665.pep      MKWDETRFGL EYDLDFIMVVAVGDFNMGMENKGLNIFNTKFVLADSRATDTDFEGIES
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g665           MKWDETRFGL EYDLDFIMVVAVGDFNMGMENKGLNIFNTKFVLADSRATDTDFEGIES
              10      20      30      40      50      60

              70      80      90     100     110     120
m665.pep      VVGHEYFHNWTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g665           VVGHEYFHNWTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQNHOF
              70      80      90     100     110     120

              130     140     150     160     170     180
m665.pep      PEDAGPTAHPVRPASYEEMNNFYTMVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDG
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g665           PEDAGPTAHPVRPVSYEEMNNFYTMVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDG
              130     140     150     160     170     180

              190     200     210     220     230     240
m665.pep      QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPPPTDM
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g665           QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTVPPPTDM
              190     200     210     220     230     240

              250     260     270     280     290     300
m665.pep      TDKQPMIIPVKVGLLNRNGEAVAFDYQKRATEAVLLLTEAEQTFLLLEGVTEAVVPSLLR
              : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g665           ADKQPMIIPVKVGLLNRNGEAVAFDYQKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLR
              250     260     270     280     290     300

```

1060

	310	320	330	340	350	360
m665.pep	GFSAPVHLNYPYSDDDLLLHDSDAFTRWEAAQTLYRRVAANLATLSDGVELPKHEK					
g665	GFSAPVYLNYPYSDDDLLLHDSDAFTCWEEAAQTLYRRVAANLAALSDGIGLPKHEK					
	310	320	330	340	350	360
	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
g665	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGTENIDPLRYHQAREALLDTLAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNLRQAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMT					
g665	KWHELDROAAKQENQSYEYSPETADWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVVRTALQH					
g665	HEWGILSAVNGNESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQRTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
g665	PKFSLENPNKARSLIGSFSRNVPHFAQDGSYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQIRAQEGLSKDVGEIVGKILDX					
g665	CNKLEPHRKNLVKQELQCIRAQEGLSKDVGEIVGKILGX					
	610	620	630			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2163>:

```

a665.seq
1  ATGAAGTGGG ACGAAACGCG CTTCGGTTTG GAATACGACT TGGATATTTT
51  CATGTCGTC GCCGTGGGCG ATTTCAATAT GGGTGGCATG GAAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGTACCGCC
151 ACCGATACCG ATTTTGAAGG CATCGAATCC GTGGTCGGAC ACGAATATTT
201 CCACAACCTGG ACGGGCAACC GCGTGACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGTTGACC GTGTTCCGCG ACCAAGAATT TTCCGGCGAC
301 CGCGCCAGCC GCGCCGTGCG CCGTATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCACTTC CCCGAAGACG CAGGTCGGAC CGCACATCCG GTGCGCCCCG
401 CCCGATATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GGCGCGGAAG TGGTGCGGAT GTATCACACC TTGCTCGGCG AAGAGGGCTT
501 CCAAAAAGGT ATGAAGCTCT ATTTCCAACG CCACGACGGA CAGGCTGTTA
551 CCTGCGACGA TTTCCGCGCG GCGATGGTGG ACGCGAACGG CATCAACCTC
601 GACCAATTCG CTTTGTGTA CAGCCAAGCA GGTACGCCGG TTTTAGATGC
651 TCAAGGGCGT CTGAAAAACA ATGTGTTCGA GTTAACCATC AAACAAACCG
701 TGCCGCCAC GCCCGATATG GCGGACAAAC AGCCGATGAT GATTCCCGTC
751 AAAATCGGCG TGCTGAACTG CAACGGCGAA GCGGTGGCAT TTGATTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGCT GCTGACCGAA GCCGAACAGA
851 CCTTCCAGTT CGAAAGCGTA ACCGAAGCCG TCGTTCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCGGTGCA TCTGAACAT CCGTACAGCG ACGACGACCT
951 GCTGCTTCTG CTCGCCCATG ACAGCGACGC CTTACGCGC TGGGAAGCCG
1001 CACAAACGCT CTACCGCCGT GCCGTGCGCG CCAACCTTGC CGCGCTTTCA
1051 GACGGCGTCG AGTTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTCA GACGACTCT TAGACAACGC TTCAAAGCC CTGCTTTTGG
1151 GTGTGCCGTC TGAAGCCGAG CTGTGGGACG GCGCGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATATAC TTGCCGTCCG
1251 CTTTCTGCCG AAATGGCACG AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAGTACAGC CCCGAAGCCG CCGGTTGGCG CACGCTGCGC
1351 AATGTCTGCC GCGCCTTCGT CCTGCGCGCC GATCCGCGC ACATCGAAAC

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1061

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1401 CGTTGCCGAG AAATACGCCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTCGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAGTTCA GCCTCGAAAA TCCCAACAAA
1651 GCCCGCTCGC TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGCG AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTTAA CCCGCAGGTC GCCGCCCGCC TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTCCG GCGCAGGAAG GATTGTGCGA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2164; ORF 665.a>:

```

a665.pep
  1 MKWDETRFGL EYDLDFIMVV AVGDFNMGAM ENKGLNIFNT KEVLADSRTA
 51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPARYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMVDANGINL
201 DQFALWYSQA GTPVLDAQGR LKNNVFELTI KQTPPTPDM ADKQPMIPV
251 KIGLLNCNGE AVAFDYQGKR ATEAVLLLTE AEQTFQFESV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLLL LAHSDAFTR WEAAQTLYRR AVAANLAALS
351 DGVELPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDILAVRFLP KWHELNQAA KQENQSYEYS PEAGWRTLR
451 NVCRAFLRA DPAHIETVAE KYAEMAQNM HEWGILSAVN GNESDTRNRL
501 LAQFADKESD DALVMDKYFA LVGSSRRSDT LQQVQTALQH PKFSLENPNK
551 ARSLIGSFSR NVPFHAEADG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD*

```

m665/a665 97.3% identity in 638 aa overlap

```

              10      20      30      40      50      60
m665.pep      MKWDETRFGL EYDLDFIMVVAVGDFNMGAMENKGLNIFNTKEVLADSRATDTDFEGIES
              |||
a665           MKWDETRFGL EYDLDFIMVVAVGDFNMGAMENKGLNIFNTKEVLADSRATDTDFEGIES
              10      20      30      40      50      60

              70      80      90      100     110     120
m665.pep      VVGHEYFHNW TGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF
              |||
a665           VVGHEYFHNW TGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF
              70      80      90      100     110     120

              130     140     150     160     170     180
m665.pep      PEDAGPTAHPVRPASYEEMN NFYTMTVYEK GAEVVRMYHTLLGEEGFQKGMKLYFQRHDG
              |||
a665           PEDAGPTAHPVRPARYEEMN NFYTMTVYEK GAEVVRMYHTLLGEEGFQKGMKLYFQRHDG
              130     140     150     160     170     180

              190     200     210     220     230     240
m665.pep      QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTPPTPDM
              |||
a665           QAVTCDDFRAAMVDANGINLDQFALWYSQAGTPVLDAQGR LKNNVFELTIKQTPPTPDM
              190     200     210     220     230     240

              250     260     270     280     290     300
m665.pep      TDKQPMIPVKVGLLN RGEAVAFDYQGKRATEAVLLLTEAEQTFLLGEGVTEAVVPSLLR
              :|||
a665           ADKQPMIPVKIGLLNCNGEAVAFDYQGKRATEAVLLLTEAEQTFQFESVTEAVVPSLLR
              250     260     270     280     290     300

              310     320     330     340     350     360
m665.pep      GFSAPVHLNYPYSDDDLLLLLAHSDAFTRWEAAQTLYRR AAVANLATLSDGVELPKHEK
              |||
a665           GFSAPVHLNYPYSDDDLLLLLAHSDAFTRWEAAQTLYRR AAVANLAALS DGVELPKHEK
              310     320     330     340     350     360

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1062

	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
a665	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDILAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNRQAAKQENQSYEYSPEAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMT					
a665	KWHELNRQAAKQENQSYEYSPEAGWRTLNRNVCRAFLRADPAHIETVAEKYAEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
a665	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSF SRNPVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
a665	PKFSLENPNKARSLIGSF SRNPVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQRI RAQEGLSKDVGEIVGKILDX					
a665	CNKLEPHRKNLVKQALQRI RAQEGLSKDVGEIVGKILDX					
	610	620	630			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2165>:

g665-1.seq

```

1  ATGAGCAAAA CCGTCCGTTA TCTGAAAGAT TACCAAACGC CTGCCTACCG
51  CATTCTTGAA ACCGAACTGC ATTCGACAT TGCCGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGGTC GAGCCGCAGA GGGCGGGCGA GCCGCTGGTG
151 TTGGACGGTT CGGCAAAACT CTGTCCGTC AAAATCAACG GCGCGGCGGC
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCAGAG GTACCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAACAAAA
301 TCGCTGATGG GGCTGTATGC TTCCGGCGGC AATCTGTTTA CCCAGTGCAG
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAAAACG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GCGGAGTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTG
551 CTTTGGTCGC GGGCGATTG GCGGTAACGG AAGACCGTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAACC
651 CAAGGTCGGC TTTGCCGTGG AATCGTTGAA AAACGCGATG AAGTGGGACG
701 AAACGCGCTT CGGGTTGGAA TATGACTTGG ATATTTTCAT GGTCGTCGCC
751 GTAGGCCGATT TCAATATGGG CGCGATGGAA AACAAGGGTT TGAACATTTT
801 TAACACCAAG TTCGTCTCTG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT TGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTTCG TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAGTTTTC CGGCGACCGC GCCGGCCGCG
1001 CCGTGCGCCG CATCGAGAAC ATCCGCCTGC TGCGCCAGAA CCAGTTCCCC
1051 GAAGACGCG GCGCGACCGC CCATCCGGTG CGCCCCGTC GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAAAAGGC GCGGAAGTGG
1151 TCGGGATGTA TCATACCTTG CTCGGCGAAG AGGGCTTCCA AAAAGGCATG
1201 AAGCTATATT TCCAACGCCA CGACGGACAG CGAGTGACCT GCGACGATTT
1251 CCGCGCGCG ATGGCGGATG CGAACGCGAT CAATCTCGAC CAGTTTCGCT
1301 TGTGGTACAG CCAGGCGGGC ACGCCCGTTT TGGAAGCCGA AGGCCGTCTG
1351 AAAAAACATG TTTTCGAGTT AACCATTAAA CAAACCGTGC CGCCACGCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAA GTCCGGCTTC
1451 TGAACGCAA CGGCGAAGCG GTGGCATTCT ATTATCAGGG CAAACGCGCA
1501 ACCGAAGCGG TGTGCTGAT GACCGAAGCC GAACAGGCCT TCCCGCTCGA
1551 AGGTGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CAGTGTATCT GAACATCCG TACAGCGACG ACGACCTGCT GCTCTGCTC
1651 GCCCACGACA GCGACGCTT CACGTGCTGG GAAGCCGCC AAACGCTCTA
1701 CCGTCGCGCC GTCGCCGCCA ACCTTGCCG GCTTTCAGAC GGCATCGGGT

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1063

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1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTGG ACAACGCCTT CAAAGCCCTG CTTTGGGGCG TGCCGTCCGA
1851 AGCCGAACTG TGGGACGGCA CGGAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTGT GATACGCTTG CCGTCCGCTT CCTGCCGAAA
1951 TGGCAGCAAT TGGACCGTCA GCGGCGAAG CAGGAAAAAC AAAGTTACGA
2001 ATACAGCCCC GAAACCGCCG ACTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAC CCCGCGCACA TCGAAACTGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CTGCCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTCCGCCCTT
2251 ATCGGCTCAA GCCCGCCGAG CGACACCCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAATTCAGTC TCGAAAAACC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TTCACGCACA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCG GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAAGCTCG
2501 AGCCGCACCG CAAAAACTTG GTGAAACAAG AATTGCAGTG CATTGCGGCG
2551 CAGGAAGGAT TGTGAAAGA CGTGGCGGAA ATCGTCGGCA AGATTTTGGG
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2166; ORF 665-1.ng>:

m665-1.pep

```

1 MSKTVRYLKD YQTPAYRILE TELHFDIAEP QTVVKSRLTV EFQRAGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAD VPSEFTVEV ETEILPAENK
101 SLMLGYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDGRHWV KWEDPFAKPS YLFALVAGDL AVTEDRETTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYDLDFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTDPEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR AGRVRRRIEN IRLLRQNQFP
351 EDAGPTAHPV RVSYSYEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNVFELTIK QTVPPTPDMA DKQPMMPVK VGLLNRRNGEA VAFDYQKRA
501 TEAVLLMTEA EQAFPLEGVT EAVVPSLLRG FSAPVYLNYP YSDDDLLLLL
551 AHDSDAFTCW EAAQTLYRRA VAANLAALSD GIGLPKHEKL LAAVEKVISD
601 DLLDNAFKAL LGGVPSEAEI WGTENIDPL RYHQAREALL DTLAVRFLPK
651 WHELDROAAK QENQSYEYSP ETADWRTLNR VCRAFLVRAD PAHIETVAEK
701 YGEMAQNMTN EWGILSAVNG NESDTRNCLL AQFADKFSDD ALVMDKYFAL
751 IGSSRRSDTL QQVQATLQHP KFSLENPNKA RSLIGSFERN VPHFHAQDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQELQCIRA
851 QEGLSKDVGE IVGKILG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2167>:

m665-1.seq

```

1 ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51 TATTCTCAAA ACCGATTATC ATTTTGATAT TAATGAACCG CAAACCGTCG
101 TGAAGTCCGG TTTGACGGTT GAGCCGCAGA GGGTAGGGGA GCCGCTGGTG
151 TTGGACGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG GGGCGGCGGC
201 GGATTATGTG TTGGAAGGAG AGACGCTGAC GATTGCGGGC GTGCCGTCGG
251 AACGCTTCAC CGTCAAGTG GAAACCGAAA TCCTGCCGGC GGAAAAACAA
301 TCCTGTATGG GGCTGTATGC TTCCGGCGGC AATTGTGTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACATTTTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACCACCACC ATCGTCGCGC AAAAAAACG CTATCCCGTT
451 TTGCTTTTCA ACGGCAACAA AATCGACGGC GGCGAGTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTTC CAAACCGAGC TATCTGTTTG
551 CTTTGGTCGC GGGCGATTG GCGGTAACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGGC TTTGCCGTGG AATCGTTGAA AAACGCGATG AAATGGGACG
701 AAACGCGCTT CGGTTTGGAA TACGACTTGG ATATTTTCAT GGTCGTCGCC
751 GTGGCGGATT TCAATATGGG CGCGATGGAA AACAAGGTT TGAACATCTT
801 TAACACCAAG TTCGTCTTGG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT CGAATCCGTG GTCGGACACG AGTATTTCCA CAACTGGACG
901 GCGCAACCGC TAACCTGCCG CCACTGGTTC CAGCTTTCCG TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
1001 CCGTGCGCCG CATCGAAAAC ATCCGCCTGC TCGCCAGCA CCAGTTCCCC
1051 GAAGACGCGA GCCCGACCGC CCATCCGGTG CGCCCGGCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGA AAAAGGCG GCGGAAGTAG
1151 TGCGGATGTA TCACACCCTG CTCGGCGAAG AGGGCTTCCA GAAAGGCATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCCGTACCT GCGACGATTT
1251 CCGCGCGGCG ATGGCGGACG CGAACGGCAT CAATCTCGAC CAGTTCGCCCT
1301 TTGCGTACAG CAGGCGGGC ACGCCCGTTT TGAAGCGGA AGGTCGCTCG
1351 AAAAACAAAT TTTTCGAGTT GACCGTCAA CAAACCGTGC CGCCACGCC
1401 CGATATGACG GATAAACAGC CGATGATGAT TCCCGTCAAG GTCGGGCTGC
1451 TGAACCGCAA CGCGGAAGCG GTGCATTTCG ACTATCAGGG CAAACGCGCG

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1064

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1501 ACCGAAGCCG TGTTGCTGCT GACCGAAGCC GAACAGACCT TCCTGCTCGA
1551 AGGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CGGTGATCTT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCCATGACA GCGACGCCTT CACGCGCTGG GAAGCCGCCC AAACGCTCTA
1701 CCGCCGCGCC GTCGCCGCCA ACCTTGCCAC GCTTTCAGAC GCGGTTGAGC
1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTAGAC
1801 GACCTCTTAG ACAACGCCTT CAAAGCCCTG CTTTGGGCG TGCCATCCGA
1851 AGCCGAGCTG TGGGACGGCG CAGAAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATACGCTTG CCGTCCACTT CCTGCCGAAA
1951 TGGCACAAGT TGAACCGTCA GCGCGCGAAG CAGGAAAACC AAAGCTACGA
2001 ATACAGCCCC GAAGCCGCCG GCTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTTGTCCT GCGCGCGGAC CCCGCGCACA TCGAAACCGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAATA TTTTGCCCTC
2251 GTCGGCTCAA GCCGCGCAG CGACACCCTG CAACAGGTTT GAACCGCCTT
2301 GCAGCATCCG AAATTCAGCC TCGAAAACCC CAACAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGAGA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCC GCCCGCTTAG TGCAGGCGTT CAACCTCTGC AACAAAGCTCG
2501 AGCCGCACCG CAAAACTTG GTGAAACAAG CATTGCAGCG CATTGCGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGCGGAA ATCGTCGGCA AAATTTTGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2168; ORF 665-1>:

m665-1.pep

```

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTVVKSRLTV EPQRVGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAG VPSERFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDGRHWV KWEDPFKSPS YLFALVAGDL AVTETYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL YLDIFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLLRQHQP
351 EDAGPTAHPV RPASYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDG AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNIFELTVK QTVPTPDMT DKQPMIPVK VGLNLRNGEA VAFDYQKRA
501 TEAVLLLTEA EQTFLLLEGVT EAVVPSLLRG FSAPVHLYNP YSDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLATLSD GVELPKHEKL LAAVEKVISD
601 DLLDNAFKAL LLGVPSEAEI WDGAENIDPL RYHQAREALL DTLAVHFLPK
651 WHELNQAAK QENQSYEYSP EAAGWRTLRLN VCRAFVLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNRL AQAADKFSDD ALVMDKYFAL
751 VGSSRRSDTL QQVRTALQHP KFSLENPNKA RSLIGFSRN VPHFHAEDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQIRIA
851 QEGLSKDVGE IVGKILD*

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m665-1/g665-1 96.1% identity in 866 aa overlap

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10 20 30 40 50 60
m665-1.pep MSKTVHYLKDYQTPAYHILKTDLHFDINEPQTVVKSRLTVEPQRVGEPLVLDGSAKLLSV
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g665-1 MSKTVRYLKDYQTPAYRIETELHFDIAEPQTVVKSRLTVEPQRAEPLVLDGSAKLLSV
10 20 30 40 50 60

70 80 90 100 110 120
m665-1.pep KINGAAADYVLEGETLTIAGVPSERFTVEVETEILPAENKSLMGLYASGGNLFTQCEPEG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g665-1 KINGAAADYVLEGETLTIADVPSEFTVEVETEILPAENKSLMGLYASGGNLFTQCEPEG
70 80 90 100 110 120

130 140 150 160 170 180
m665-1.pep FRKITFYIDRPDVMSKFTTTIVADKKRYPVLLSNGNKIDGGEFSDGRHWVKWEDPFKSPS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g665-1 FRKITFYIDRPDVMSKFTTTIVADKKRYPVLLSNGNKIDGGEFSDGRHWVKWEDPFKSPS
130 140 150 160 170 180

190 200 210 220 230 240
m665-1.pep YLFALVAGDLAVTETYFTTMSGRNVKIEFYTTEADKPKVGFVAVESLKNAMKWDETRFGL
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g665-1 YLFALVAGDLAVTEDRFTTMSGRNVKIEFYTTEADKPKVGFVAVESLKNAMKWDETRFGL
190 200 210 220 230 240

250 260 270 280 290 300
m665-1.pep YLDLIFMVVAVGDFNMGAMENKGLNIFNTKFLVADSRATDTDFEGIESVVGHEYFHNWT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g665-1 YLDLIFMVVAVGDFNMGAMENKGLNIFNTKFLVADSRATDTDFEGIESVVGHEYFHNWT

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	250	260	270	280	290	300
m665-1.pep	310	320	330	340	350	360
g665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQPEDAGPTAHPV					
	310	320	330	340	350	360
m665-1.pep	370	380	390	400	410	420
g665-1	RPASYEEMNNFYMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHGDGQAVTCDDFRAA					
	370	380	390	400	410	420
m665-1.pep	430	440	450	460	470	480
g665-1	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTPPTPDMTDKQPMPIPVK					
	430	440	450	460	470	480
m665-1.pep	490	500	510	520	530	540
g665-1	VGLLNRNGEAVAFDYQGKRATEAVLLLTEAEQTFLLLEGVTEAVVPSLLRGFSAPVHLNYP					
	490	500	510	520	530	540
m665-1.pep	550	560	570	580	590	600
g665-1	YSDDDLLLLLAHDSDAFTRWEEAAQTLYRRAVAANLATLSDGVELPKHEKLLAAVEKVISD					
	550	560	570	580	590	600
m665-1.pep	610	620	630	640	650	660
g665-1	DLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLPKWHELNQRAAK					
	610	620	630	640	650	660
m665-1.pep	670	680	690	700	710	720
g665-1	QENQSYEYSPEAAGWRTLNRVCRAFVLRADPAHIETVAEKYGEMAQNMTHEWGILSAVNG					
	670	680	690	700	710	720
m665-1.pep	730	740	750	760	770	780
g665-1	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVRTALQHPKFSLENPNKA					
	730	740	750	760	770	780
m665-1.pep	790	800	810	820	830	840
g665-1	RSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
	790	800	810	820	830	840
m665-1.pep	850	860				
g665-1	VKQALQIRAQEGLSKDVGEIVGKILDX					
	850	860				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2169>:

a665-1.seq

```

1  ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51  TATTCTCAAA ACCGATTAC ATTTTGATAT TAACGAACCG CAAACCATTG
101 TGAAGTCGCG TTGACGGTC GAGCCGAAGA GGTGGGAGA GCCGTGGTG
151 TTGGACGGTT CGGCGAAACT CTGTCCGTC AAAATCAACG GCGTGGCGGC
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCGGAC GTGCCGTCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAAACAAA
301 TCGCTGATGG GCGTGTATGC GTCCGCCGGT AACCTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA TATCGACCGT CCGGATGTCA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAAAAACG CTATCCCGTT
451 TTGCTCTCCA ACGGCAACAA AATCGACGGC GCGGAGTATT CAGACGGCGC

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1066

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501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTTCG GGGCGATTTC GCGGTACGCG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGGC TTTGCCGTGG AATCGCTGAA AAACGCAATG AAGTGGGACG
701 AAACGCGCTT CGGTTTGGAA TACGACTTGG ATATTTCAT GGTGTCGCGC
751 GTGGGCGATT TCAATATGGG TGCGATGGAA AACAAGGTT TGAACATCTT
801 TAACACCAAG TTCGTCCTTG CCGACAGCCG TACCGCCACC GATACCGATT
851 TTGAAGGCAT CGAATCCGTG GTCGGACACG AATATTCCCA CAACTGGACG
901 TGCAACCGCG TGACCTGCCG CGACTGGTTC CAGCTTTCG TGAAGGAAGG
951 GTTGACCGTG TTCCGCGACC AAGAAATTTT CCGCGACCGC GCCAGCCGCG
1001 CCGTGCGCCG TATCGAAAAC ATCCGCCTGC TCGCCAGCA CCAGTTCCCC
1051 GAAGACGCGAG GTCCGACCGC ACATCCGGTG CGCCCGCCC GATATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGA AAAAGGC GCGGAAGTGG
1151 TGCGGATGTA TCACACCTTG CTCGGCGAAG AGGGCTTCCA AAAAGGTATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCTGTTACCT GCGACGATTT
1251 CCGCGCGGCG ATGGTGGACG CGAACGGCAT CAACCTCGAC CAATTCGCCCT
1301 TGTGTACAG CCAAGCAGGT ACGCCGGTTT TAGATGCTCA AGGGCGTCTG
1351 AAAACAATG TGTTCGAGTT AACCATCAAA CAAACCGTGC CGCCACGCGC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAAA ATCGGGCTGC
1451 TGAAGTCAA CGGCGAAGCG GTGGCATTTC ATTATCAGGG CAAACGCGCG
1501 ACCGAAGCCG TGTGCTGCT GACCGAAGCC GAACAGACCT TCCAGTTCGA
1551 AAGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGG TTCAGCGCGC
1601 CCGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTTCTGCTC
1651 GCCCATGACA GCGACGCCTT CACGCGCTGG GAAGCCGCAC AAACGCTCTA
1701 CCGCCGTGCC GTCGCCGCCA ACCTTGCCGC GCTTTCAGAC GCGTCTGAGT
1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTCAGAC
1801 GACCTCTTAG ACAACGCTTT CAAAGCCCTG CTTTGGGTG TGCCGTCTGA
1851 AGCCGAGCTG TGGGACGGCG CGGAAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATATACTTG CCGTCCGCTT TCTGCCGAAA
1951 TGGCACAAT TGAACCGTCA GCGGCGAAG CAGGAAAACC AAAGCTACGA
2001 GTACAGCCCC GAAGCCGCCG GTTGGCGCAC GCTGCGCAAT GTCTGCCGCG
2051 CCTTCGTCTT CCGCGCCGAT CCCGCGCACA TCGAAACCGT TGCCGAGAAA
2101 TACGCCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTCGCCCTC
2251 GTCGGCTCAA GCGCGCGCAG CGACACCCGT CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAGTTCAGCC TCGAAAATCC CAACAAAGCC CGCTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGCAGA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCAT GAAATCGACC GCTTTAACCC
2451 GCAGGTCGCC GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAAAGTCTG
2501 AGCGGCACCG CAAAAACTTG GTGAAACAAG CATTCGAGCG CATTCGGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGGCGAA ATCGTCCGCA AAATTTTGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2170; ORF 665-1.a>:

a665-1.pep

```

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV
51 LDGSAKLLSV KINGVAADYV LEGETLTIA DVPSEFTVEV ETEILPAENK
101 SLMLGYASAG NLFQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEYS DGRHWV KWEDPFAKPS YLFALVAGDL AVTEDYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYDLDFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRTAT DTDFEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLLRQHQP
351 EDAGPTAHPV RPARYEEMNN FYTMTVYEG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MVDANGINLD QFALWYSQAG TPVLDAQGRL
451 KNNVFELTIK QTVPTPDMA DKQPMIPIVK IGLNLCNGEA VAFDYQGKRA
501 TEAVLLLTEA EQTFQFESVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAFTWR EAAQTLYRRA VAANLAALSD GVLPKHEKL LAAVEKVISD
601 DLLDNAFKAL LLGVPSEAE LWDGAENIDPL RYHQAREALL DILAVRFLPK
651 WHELNQAQAK QENQSYEYSP EAAGWRTLRL VCRFVLRAD PAHIETVAEK
701 YAEMAQNMT HEGWILSAVNG NESDTRNRL AQAADKFSDD ALVMDKYFAL
751 VGSSRRSDTL QQVQTALQHP KFSLENPNKA RSLIGSFSRN VPHFHAEDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQRIRA
851 QEGLSKDVGE IVGKILD*

```

a665-1/m665-1 97.2% identity in 867 aa overlap

```

          10      20      30      40      50      60
a665-1.pep MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV LDGSAKLLSV
          |||
m665-1      MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV LDGSAKLLSV
          10      20      30      40      50      60
          70      80      90     100     110     120

```

1067

a665-1.pep	KINGVAADYVLEGETLTIADVPSEFTVEVETEILPAENKSLMGLYASAGNLFTQCEPEG
m665-1	KINGAAADYVLEGETLTIAGVPSEFTVEVETEILPAENKSLMGLYASGGNLFTQCEPEG
	70 80 90 100 110 120
a665-1.pep	130 140 150 160 170 180
m665-1	FRKITFYIDRPDVMSKFTTTIVADKKRYPVLLSNGNKIDGGEYS DGRHWVKWEDPFAKPS
	130 140 150 160 170 180
a665-1.pep	190 200 210 220 230 240
m665-1	YLFALVAGDLAVTEDYFTTMSGRNVKIEFYTTEADKPKVGF AVESLKNAMKWDETRFGLE
	190 200 210 220 230 240
a665-1.pep	250 260 270 280 290 300
m665-1	YDLDFIMVVAVGDFNMGAMENKGLNIFNTKFVLADSR TATDTDFEGIESVVGHEYFHNWT
	250 260 270 280 290 300
a665-1.pep	310 320 330 340 350 360
m665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQH QFPEDAGPTAHPV
	310 320 330 340 350 360
a665-1.pep	370 380 390 400 410 420
m665-1	RPARYEEMNFFYTM TVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRH DQAVTCDDFRAA
	370 380 390 400 410 420
a665-1.pep	430 440 450 460 470 480
m665-1	MVDANGINLDQFALWYSQAGTPVLDAQGR LKNNVFELTIKQTVPPTPDMADKQPMMPVK
	430 440 450 460 470 480
a665-1.pep	490 500 510 520 530 540
m665-1	IGLLNCNGEAVAFDYQ GKRATEAVLLLTEAEQTFQFESVTEAVVPSLLRGFSAPVHLNYP
	490 500 510 520 530 540
a665-1.pep	550 560 570 580 590 600
m665-1	YSDDDLLLLLAHDSDAFTRWEAAQ TLYRRAVAANLAALSDGVLPKHEKLLAAVEKVISD
	550 560 570 580 590 600
a665-1.pep	610 620 630 640 650 660
m665-1	DLLDNAFKALLGVPSEAELWDGAENIDPLRYHQAREALLDILAVRFLPKWHELN RQAAK
	610 620 630 640 650 660
a665-1.pep	670 680 690 700 710 720
m665-1	QENQSYEYSPEAAGWRTL RNVCR AFLVLRADPAHIETVAEKYAEMAQNMTHEWGILSAVNG
	670 680 690 700 710 720
a665-1.pep	730 740 750 760 770 780
m665-1	NESDTRNRLLAQFADKFSD DALVMDKYFALVGSSRRSDTLQQVQTALQHPKFSLENPNKA
	730 740 750 760 770 780
a665-1.pep	790 800 810 820 830 840
m665-1	RSLIGSFSRNVPHFHAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL
	790 800 810 820 830 840

	790	800	810	820	830	840
	850	860				
a665-1.pep	VKQALQRIRAEGLSKDVGEIVGKILD	X				
m665-1	VKQALQRIRAEGLSKDVGEIVGKILD	X				
	850	860				

g666.seq

1	ATGCTTTGTA	TGAATTATCA	ATCAAACCTCA	GGCGAAGGAG	TGCTTGTAGC
51	TAAAAACATAT	TTATTGACTG	CATTGATAAT	GTCTATGGTA	ATCTCCGGAT
101	GTCAAGTCAT	CCATGCCAAT	CAAGGTAAGG	TTAATACTAA	TTCTGCTGTC
151	ATCGCAGGTG	CAGACGCTCA	CACGCGTGAA	CATGTAACGG	GACTGACCCA
201	ACAAAAGCAG	TGATTGCAA	GTGATTTTAT	AGTAGCGTCA	GCCAATCCAT
251	TAGCAACACA	AGCTGGCTAT	GATATCTTAA	AGCAAGGCGG	TAGCGCTGCA
301	GATGCGATGG	TGGCGGTGCA	GACGACACTA	AGCTTGGTAG	AGCCACAGTC
351	GTCAGGCTTG	GGCGGTGGTG	CATTTGTGTT	GTATTGGGAC	AATACCGCCA
401	AAACATTGAC	CACATTTGAT	GGGCGTGAGA	CGGCACCGAT	GCGTGCGACG
451	CCAGAATTAT	TTTTGGATAA	AGATGGTTAA	CGATTGAAAT	TTATGGAAGC
501	GGTGGTCGCT	CGGTAGGTAC	GCCTGCTATC	CCTAAACTGA	

g666.pep

1	MLCMNYQSNS	GEGVLVAKTY	<u>LLTALIMSMV</u>	<u>ISGCQVIHAN</u>	QGVNTNSAV
51	IAGADAHTPE	HVTGLTEQKQ	<u>VIASDFIVAS</u>	<u>ANPLATQAGY</u>	DILKQGGSA
101	DAMVAVQTTL	SLVEPQSSGL	GGGAFVLYWD	NTAKTLTTFD	GRETAPMRAT
151	PELFLLDKDGX	PLKFMEAVVA	RXVRLLSLN*		

```
m666.seq
1  ATGCCTTGTA  TGAATCATCA  ATCAAACCTCA  GGCGAAGGAG  TGCTTGTGGC
51  TAAAACATAT  TTATTGACTG  CATTGATAAT  GTCTATGACA  ATCTCTGGAT
101  GTC AAGTCAT  CCATGCCAAT  CAAGGTAAGG  TTAATACTCA  TTCTGCTGTC
151  ATCACAGGTG  CAGACGCTCA  CACGCCTGAA  CATGCAACGG  GACTGACCCA
201  ACAAAAAGCAG  GTGATTGCAA  GTGATTTTAT  GGTAGCGTCA  GCCAATCCAT
251  TAGCAACACA  AGCTGGCTAT  GATATCTTAA  AGCAAGGCGG  TAGCGCTGCA
301  GATGCGATGG  TGGCGGTGCA  GACGACACTA  AGCTTGGTAG  AGCCACAGTC
351  GTCAGGCTTG  GGC GGTGGTG  CATTTGTGTT  GTATTGGGAT  AATACCGCCA
401  AAACATTGAC  CACATTTGAT  GGGCGTGAGA  CGGCACCGAT  GCGTGCGACG
451  CCGGAATTAT  TTTTGGATAA  AGATGGTCAA  CCATTGAAAT  TTATGGAAGC
501  GGTGGTCTGTG  GTCGCTCGGT  GGGTACGCCT  GCTATCCCTA  AACTGA
```

m666.pep

1	MPCMNHQSNS	GEGVLVAKTY	<u>LLTALIMSMT</u>	<u>ISGCQVIHAN</u>	QGKVNTHSAV
51	ITGADAHTPE	HATGLTEQKQ	<u>VIASDFMVAS</u>	<u>ANPLATQAGY</u>	DILKQGGSA
101	DAMVAVQTTL	SLVEPQSSGL	GGGAFVLWYD	NTAKLTTFD	GRETAPMRAT
151	PELFLDKDGO	PLKFMEAVVU	VARVWRLLSL	N*	

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m666.pep	MPCMNHQSNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE					
	:                             :                 :					
g666	MLCMNYQSNSGEGVLVAKTYLLTALIMSMVISGCQVIHANQGKVNTHSAVIAGADAHTPE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m666.pep	HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVOTTLSLVEPOSSGL					

```
a666.seq
1  ATGCCTTGTA TGAATCATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTTGGC
51  TAAAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCAAGTCAT CCATGCCAAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGTG CAGACGCTCA CACGCTGAA CATGCAACGG GACTGACCGA
201 ACAAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GGCAGTGGTG CATTGTGTT GTATTGGGAT AATACCGCCA
401 AAACATTGAC CACATTGTAT GGGCGTGAGA CGGCACCGAT CCGTGCGACG
451 CCGGAATTAT TTTTGGATAA AGATGGTCAA CCATTGAAAT TGTGGAAGC
501 GGTGGTCGTG GTCGCTCGGT GGGTACGCCT GCTATCCCTA AACTGA
```

a666.pep

1	MPCMNHQSNS	GEGVLVAKTY	<u>LLTALIMSMT</u>	<u>ISGCQVIHAN</u>	QGKVNTHSAV
51	ITGADAHTPE	HATGLTEQKQ	<u>VIASDFMVAS</u>	<u>ANPLATQAGY</u>	DILKQGGSA
101	DAMVAVQTTL	SLVPEQSSGL	<u>GGAFAVLWD</u>	<u>NTAKLTTFD</u>	GRETAPMRAT
151	PELFLDKDGQ	PLKFMEAVVV	<u>VARVRLLSL</u>	N*	

		10	20	30	40	50	60
m666.pep		MPCMNHQSN	SGEGLVAKTYLL	TALIMSMTIS	GCQVIHANQ	GKVNTHSA	VITGADAHTPE
a666		MPCMNHQSN	SGEGLVAKTYLL	TALIMSMTIS	GCQVIHANQ	GKVNTHSA	VITGADAHTPE
		10	20	30	40	50	60
		70	80	90	100	110	120
m666.pep		HATGLTEQKQ	VIASDFMVASAN	PLATQAGYDIL	KQGGSAADAM	VAVQTTL	SLVEPQSSGL
a666		HATGLTEQKQ	VIASDFMVASAN	PLATQAGYDIL	KQGGSAADAM	VAVQTTL	SLVEPQSSGL
		70	80	90	100	110	120
		130	140	150	160	170	180
m666.pep		GGGAFVLYWD	NTAKTLTTFD	GRETAPMRAT	PELFLDKDG	QPLKFMEAV	VVVVARWVRLLSL
a666		GGGAFVLYWD	NTAKTLTTFD	GRETAPMRAT	PELFLDKDG	QPLKFMEAV	VVVVARWVRLLSL
		130	140	150	160	170	180
m666.pep	NX						
a666	NX						



The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2177>:

```
g667.seq
1   atgcgggtttg tcttctgttt gggcgGAGAG ATAGttttctg atccgtgtga
51  tttccAtttg gtattcgtcc gcgtcgaaac tgccgctgAc CAGAcagaaa
101 cgCAGataca tCaaatacgt attcacggca tcggtttcgc aatAAAttgcg
151 GAtttccttc agcgtgcccgc cgtgGAacgc ttcccacact ttgctgccgt
201 ccataCCCAg ctTGCCCGGA AAGCCGCACA GTTTCgcCat atcgctccagC
251 GGCACATTcg ccctcggtG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCActtg AAATCGCGGC
351 tgtcgccgAA ATCGccgTCG CCCGTATCCC AATAGCGCGC GGCGTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGGTCGA AACCGCCGCC
451 GTTCCAGCTG ACCAGTTGCG GCGTATGTTT TTCAACCAAT TCGAAAAACT
501 TGGCAATCAC GACTTCTTCG CCATCGTCCA TCTCGCCGAT GGTGCCGACA
551 TGAACCTTGT CCTGCCCCCA GCGCATACAG CAGGAAACCG CCACAACCTG
601 ATGGAGGTGG TGCTGCATAA AATCGCCGCC GGTCTGTGCG CGGCGTTTCT
651 GCTGCGCGAA CAGCACCCT TCGTCATCCG GCAGGGAAGA CGGCAAGTCA
701 TACAACGTAC GGATACCCTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTA TTCATGGCAg tACCTTGCAT tcaAAAACAG ActTGCGCCT
801 ATTgTgtcat TAA
```

This corresponds to the amino acid sequence <SEQ ID 2178; ORF 667.ng>:

```
g667.pep
1   MRFVFLGGE IVSDPCDFHL VFVRVESAAD QTETQIHQIR IHGIGFAIIA
51  DFLQARVER FPHFAAVHTQ LARKAAQFRH IVQRHIRPRL VKREQIHQIA
101 VALVITADV VPLEIAAVAE IAVARIPIAR GVDVYQGA V MQYQVETAA
151 VPADQLRRMF FNQFEKLG NH DFFAIVHLAD GADMNVLPP AHTAGNRHNL
201 MEVVLHKIAA GLCAAFLLRE QHNFVIRQGR RQVIQRTDTL HIGYGFNIES
251 QNRHGSTLH SKTDLRLLC H *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2179>:

```
m667.seq (PARTIAL)
1   ATGCGGCTTT TCCCCGGCTT GTGCGGACAG GTAATTCCGC ATCCGTTTGA
51  TTTCCATTTT GTATTCTGTC GCATCCAGCC TGCCGCTGAC CAGACAGAAA
101 CGCAGGTACA TCAGATAAGT GTTTGCCGCG TCGGTTTCGC AATAATTGCG
151 GATTTCCTTC AGCCTGCCCG TATGGAATGC CTCCCAAACC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAGC
251 GGCACGTTTG CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTGCGCGAA ATCGCCGTCG CCCATATCCC AATAGCGCGC GGCGTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGATCGA AACCGCCGCC
451 GTTCCAATG ACCAGTTGCG GCGTATGTTT TTCAATCAAT TCGAAAAATT
501 TAGCAATGAC CACTTCCTCG CCGTCATCCA TCTCGCCGAT GGTGCCGACA
551 TGTACTTTAT CCTGCCCCCA ACGCATGCAG CACGAAATCG CCACAACCTG
601 ATGAAGATGA TGCTGCATAA AATCGCCGCC CGTCTGAGCA CGGCGTTTGT
651 GCTGGGCAAT CAGCACCCT TG...
```

This corresponds to the amino acid sequence <SEQ ID 2180; ORF 667>:

```
m667.pep (partial)
1   MRLFPGLCGQ VIPHPDFHF VFVRIQPAAD QTETQVHQIS VCRVGFALIA
51  DFLQPARMEC LPNLAAVHTQ LARKTAQFRH IVQRHVCPR L VKREQIHQIA
101 VALVITADV VPLEIAAVAE IAVAHIPIAR GVDVYQGA V MQYQIETAA
151 VPTDQLRRMF FNQFEKFSND HFLAVIHLAD GADMYFILPP THAARNRHL
201 MKMMLHKIAA RLSTAFVLGN QHHL...
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m667/g667 75.0% identity in 224 aa overlap

```

              10      20      30      40      50      60
m667.pep    MRLFPGLCGQVIPHPDFHFVFVRIQPAADQTETQVHQISVCRVGFALIIADFLQPARMEC
              ||:  | |::: | ||:||||:| |||||:| | | : | ||||| | | | |

```

g667	MRFVFCLGGEIVSDPCDFHLVFVRVESAADQTETQIHQIRIHGIGFAIIADFLQRARVER 10                20                30                40                50                60
m667.pep	LPNLAAVHTQLARKTAQFRHIVQRHVCPRLVKREIQIHQIAVALVITADVVPLEIAAAVE 70                80                90                100                110                120
g667	: ::       :  :       :       :       :       :       : FPHFAAVHTQLARKAAQFRHIVQRHIRPRLVKREIQIHQIAVALVITADVVPLEIAAAVE 70                80                90                100                110                120
m667.pep	IAVAHIPIARGVDNAVYQGAVMQYGQIETAAVPTDQLRRMFFNQFEKFSNDHFLAVIHLAD 130                140                150                160                170                180
g667	:       :       :       :       :       :     : :  IAVARIPARGVDNAVYQGAVMQYGVETAAVPADQLRRMFFNQFEKLGNHDFFAIVHLAD 130                140                150                160                170                180
m667.pep	GADMYFILPPTHAARNRHNLMKMMLHKIAARLSTAFVLGNQHLL 190                200                210                220
g667	:   :     :     :     :     :     :     : GADMNLVLPPTHAGNRHNLMENVLHKIAAGLCAAFLLREQHHFVIROGRRQVIQRTDTL 190                200                210                220                230                240
g667	HIGYGFNIESQNRIHGSTLHSKTDLRLLCHX 250                260                270

```
a667.seq
1  ATGCGGTTTG TCTTCTGTTT GGGCGGAGAG ATAGTTTCTG ATCCGCTTGA
51  TTTCCATTTC GTATTCGTCT GCGTCGAATC TGCGGCTGAC CAGACAGAAA
101 CGCAGATACA TACAGATAGT ATTTACCGCA TCCGTTTCGC AATAATTGCG
151 GATTTCCTTC AGCCTGCCCG CGTGGAACGC CTCCACACC TTGCTGCCGT
201 CCATACCAG CTGCCCCGGA AAACCGCACA GTTCGCCAT ATCGTCCAAC
251 GGCACATTGC CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAAATCGCA
301 ATGACGTGG TGGTAGCGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTGCGCGAA ATCGCCGTCG CCGATATCCC AATAGCGCGC GCGGTTGATG
401 CCGTGTAGCA GCGAACGGTA ATGCAGAAC GGCAGGTCGA AACCGCCGCC
451 GTTCCAAC TG ACCAGTTGCG GCGTATGTTT TTCAATCAAC TCGAAAAATT
501 TGGCGATAAC CACTTCTCTG CCGTCATCCA TCTCGCCGAT TGTACCGGCA
551 TGGACTTTAT C TGCTGCATAA AATCCCCACC CGTCTGAGCA CGGCGTTTTT
601 ATGAAGATGA TGCTGCATAA AATCCCCACC CGTCTGAGCA CGGCGTTTTT
651 GCTGGGCAA CAGCACCAC TCATCGTCGG GCAGCGAGGA CGGCAAGTCA
701 TACACGCTAC GGATACACTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTG GTCATGACAG CACCTTGAT TTAATAA.CAG ACTTGCGCCT
801 ATTGTCAT TAA
```

a667.pep

1	MRFVFCLGGE	IVSDPLDFHF	VFVCVESAAD	QTETQIHQIG	IYRIGFAIIA
51	DFLQPARVER	LPHLAAVHTQ	LARKTAQFRH	IVQRHIRPRL	VKREQIHQIA
101	MTLVAADV	VPLEIAAVAE	IATAHIPIAR	GVDAV*QRTV	MQNRQVETAA
151	VPTDQLRRMF	FNQLEKFGDN	HFLAVIHLAD	CTDMDFILPP	THAARNRHNH
201	MKMMMLHKIPT	RLSTAFLLGK	QHHFIVGQRG	RQVIQRDSDL	HIGYGFNIIES
251	ONRGHDSSTLY	LKXDLRLHCH	*		

	10	20	30	40	50	60
m667.pep	MRLFPGLCGQVIPHFPDFHFVVFVRIQPAADQTETQVHQISVCRVGF	FAIIADFLQPARM				
	:	::	:	:	:	: :
a667	MRFVFC	LGGEIVSDPLDFHFVFCV	ESAADQTETQIHQIGIYRIG	FAIIADFLQP	ARVER	
	10	20	30	40	50	60
	70	80	90	100	110	120
m667.pep	LPNLA	AVHTQLARKTAQFRHIVQRHVC	PRLVKREQIHQIA	VALVITADV	VVPLEIA	AAVAE
	: :	:	:	:	:	:
a667	LPHLA	AVHTQLARKTAQFRHIVQRH	IRPLVKREQIHQIA	MTLVVAADV	VVPLEIA	AAVAE

1072

	70	80	90	100	110	120
m667.pep	130	140	150	160	170	180
	IAVAHIPIARGVDAVYQGAVMQYQIETAAVPTDQLRRMFFNQFEKFSNDHFLAVIHLAD					
a667	IAVAHIPIARGVDAVXQRTVMQNRQVETAAVPTDQLRRMFFNQLEKFGDNHFLAVIHLAD					
	130	140	150	160	170	180
m667.pep	190	200	210	220		
	GADMYFILPPTHAARNRHNLMKMMLHKIAARLSTAFVLGNQHHL					
a667	CTDMDFILPPTHAARNRHNLMKMMLHKIPTRLSTAFLLGKQHHFIVGQRGRQVIQRTDTL					
	190	200	210	220	230	240
a667	HIGYGFNIESQNRGHDSTLYLKXDLRLLLCHX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2183>:

```

g669.seq
1   ATGCGCCGCA TCGTTAAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AGCGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2184; ORF 669.ng>:

```

g669.pep
1   MRRIVKKHQV VNAPHIVLEI RIMKLHRAV FLGRKRPHHH DRSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ SGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2185>:

```

m669.seq
1   ATGCGCCGCA TCATTAAAAA ACACCAGCCC ATAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACAGCAGCC TTCGGCGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2186; ORF 669>:

```

m669.pep
1   MRRIIKKHQV INAPHIVLEI RIMKLHRAV FLGRKRPHHH DSSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m669/g669 96.2% identity in 106 aa overlap

	10	20	30	40	50	60
m669.pep	MRRIIKKHQVINAPHIVLEIRIMKLHRAVFLGRKRPHHH DSSLRRQHGI EGMGFDFKQI					
	:     :     :     :     :     :     :     :     :     :					
g669	MRRIVKKHQPVNAPHIVLEIRIMKLHRAVFLGRKRPHHH DRSLRRQHGI EGMGFDFKQI					
	10	20	30	40	50	60
	70	80	90	100		

1073

```

m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||
g669        FRHVQSSNRQSGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2187>:

```

a669.seq
1  ATGCGCCGCA TCATTA AAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51 TTTGGA AATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGAATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTG TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2188; ORF 669.a>:

```

a669.pep
1  MRRIKKHQP VNAPHIVLEI RIMKLHRA FV FLGRKRPHHH DRSLRRQHGI
51 EGMGFDFKQI FRHVQSSNRQ NGRQPVCTK PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

m669/a669 98.1% identity in 106 aa overlap

```

              10      20      30      40      50      60
m669.pep    MRRIKKHQPINAPHIVLEIRIMKLHRA FV FLGRKRPHHH DSSLRRQHGI EGMGFDFKQI
             |||||
a669        MRRIKKHQPVNAPHIVLEIRIMKLHRA FV FLGRKRPHHH DRSLRRQHGI EGMGFDFKQI
              10      20      30      40      50      60

              70      80      90      100
m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||
a669        FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2189>:

```

g670.seq
1  ATGACTTGTT GCAGGAACTG CTTGGCGCGT TCGTGTTTCG GGTTGGTGAA
51 AAACGCTTCC GGCGTTTCGT CTTCAAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCTGT GGTTACGCAC
151 ATCATCGTCA TGCCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAAGT CGGCTCGTCA AACAGCATCA
251 CGCGCGGCTC CATCGCCAGC CCGCGCGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGA AA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGGTGATGT TGTCCAACAC GGTCAGGTGC
451 GG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2190; ORF 670.ng>:

```

g670.pep
1  MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
51 IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NSITRGSIAS PRAIATRC CW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMLSNTVRC
151 G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2191>:

```

m670.seq
1  ATGACCTGTT GCAGGAACTG CTTGGCGCGT TCGTGTTTCG GGTTGGTAAA
51 AAACGCTTCC GGCGTTTCGT CTTGAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCTGT GGTTACGCAC
151 ATCATCGTCA TGCCGCTTTC TGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAGGT CGGTTCTGTC AACAAACATTA

```

1074

```

251 CGCGCGGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAG GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGTAATGT TTCCAACAC GGTCAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2192; ORF 670>:

```

m670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
 51 IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMFSNTVRC
151 G*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m670/g670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
              |||||||
g670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
              10      20      30      40      50      60

              70      80      90     100     110     120
m670.pep      FITFNTSPTISGSSAEVGSSNNITRGSIAKPRAIATRCCWPPESWEGKASFLCASPTRSK
              |||||||:|||||:|||||
g670           FITFNTSPTISGSSAEVGSSNSITRGSIASPRAIATRCCWPPESWEGKASFLCASPTRSK
              70      80      90     100     110     120

              130     140     150
m670.pep      SSIAFFSACS AFCPLTFIGARVMFSNTVRCGX
              |||||||:|||||
g670           SSIAFFSACS AFCPLTFIGARVMLSNTVRCGX
              130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2193>:

```

a670.seq
  1 ATGACCTGTT GCAGGAACTG CTTGGCGCGT TCGTGTTTCG GGTGGTAAA
 51 AAACGCTTCC GGCCTTTCGT CTTCGAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATGGTCA TACCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAGGT CGGTTCTGCA AACAACTTA
251 CGCGCGGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAG GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGTTCCATCG CTTTTTCTC TGCCTGTTCC GCATTTTGAC
401 CTTTAACCTT CATCGGTGCG AGGTAATGT TTCCAACAC GGTCAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2194; ORF 670.a>:

```

a670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
 51 IMVIPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AF*PLTFIGA RVMFSNTVRC
151 G*

```

m670/a670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
              |||||||
a670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIMVIPLSAKS
              10      20      30      40      50      60

```

1075

	70	80	90	100	110	120
m670.pep	FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPEWEGKASFLCASPTRSK					
a670	FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPEWEGKASFLCASPTRSK					
	70	80	90	100	110	120
	130	140	150			
m670.pep	SSIAFFSACSAFCPLTFIGARVMFSNTVRCGX					
a670	SSIAFFSACSAFXPLTFIGARVMFSNTVRCGX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2195>:

```

g671.seq
1  ATGATCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACACC
51  GCCCAAATG CGGTTGGCAA AGCCCAGACC GACCGCCGAA ACTGCGCCGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAATG ACAGagccaa TGCAAACAgg cggggTTGGA ACGaggCAAA
201 GGCGAGGTcg gcgaaggGTG CGGCaaAGAG TTTggcaaAA AAGAaggAAA
251 ccaccCATGC cACCATCgaa ccTGCTTCCG CAATCACGCC GCGCATCGTG
301 GAAATGACGA TGCAGGCGGC GATGACGGcg gAGGCGAGGA GGTCGGCAAT
351 GGGGAGGCTA TTCATTCTGT ACCTGGCCGG CGATGCCGTG CACGCGCAGT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2196; ORF 671.ng>:

```

g671.pep
1  MISRVTIKTP FNApNTppKM RLAKPRPTAE TAPVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKGAakSLAK KkETTHATIE PASAITPRIV
101 EMTMQAAMTA EARRSAMGRL FIRYLAGDAV HAQFVQIAFG IPCVFIVA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2197>:

```

m671.seq
1  ATGACCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAATG CGGTTGGCAA AGCCCAAACC GACCGCCGAA ACTGCGCTGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTGGA ACGAGGCAAA
201 GGCGAGGTcG GCGAAGGAGG CGGCAaAGAG TTTGGCGAAA AAGAAGGAAA
251 CCACCCATGC CGCCATTGAG CCTGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCACGA TGCAGGCGGC GATGACGGCG GAGACGAGGA GGTCGGCAAT
351 GGGGAGGCTA TTCATTCTGT ACCTGACCGG CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2198; ORF 671>:

```

m671.pep
1  MTSRVTIKTP FNApNTppKM RLAKPKPTAE TALVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKEAAkSLAK KkETTHAAIE PASAITPRIA
101 DSTMQAAMTA ETRRSAMGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

**m671/g671** 91.9% identity in 148 aa overlap

	10	20	30	40	50	60
m671.pep	MTSRVTIKTPFNAPNTppKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR					
g671	MISRVTIKTPFNAPNTppKMRLAKPRPTAETAPVSSERSIFWIRQAMTNREMNDRANANR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m671.pep	RGWNEAKARSAKEAAkSLAKKkETTHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL					

	:             :             :
g671	RGWNEAKARSAKGAAKSLAKKKETTHATIEPASAITPRIVEMTMQAAMTAEARRSAMGRL
	70               80               90              100            110           120
m671.pep	130               140              149 FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
	:       :
g671	FIRYLAGDAVHAQFVQIAFGIPCVFIVAX
	130               140

```
a671.seq
1  ATGACCAGCA GGGTAATAAT CAAAATGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAAATG CGGTGTGGCAA AGCCCAAACC GACCCCGCAAT ACTGCCCCGG
101 TCAGCAGCGA CGGTGAGTATT TTCTGGATCA CAGAGGCAAT ACGGAATAGG
151 GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTTGGA GCGATGCAAA
201 GGCATGTCTG GCGAAGGGTG CGGCAAAGAG TTTGGCGAAA AAAAAGGCAA
251 CCACCCATGC CGCCATTGAG CCAGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCAGCA TGCAGGCGGC GATGATGGCG GAGACAGGGA GGTCGGCAAC
351 GGGGAGGTTA TTCATTCTGT ACCTGACCGG CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTTCGGC ATCCCTTGCG TTTTATAGT TACTTGA
```

```
a671.pep
  1  MTSRVIIKMP  FNAPNTPPKM  RLAKPKPTAE  TAPVSSERSI  FWIRQAMTNR
 51  EMNDRANANR  RGWNDAKAMS  AKGAAKSLAK  KKATTHAAIE  PASAITPRIA
101  DSTMQAAMMA  ETRRSATGRL  FIRYLTGDTV  YAQFVQIAFG  IPCVFIVA*
```

		10	20	30	40	50	60
m671.pep		MTSRVTIKTFPNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR					
a671		MTSRVIIKMPFNAPNTPPKMRLAKPKPTAETAPVSSERSIFWIRQAMTNREMNDRANANR					
		10	20	30	40	50	60
		70	80	90	100	110	120
m671.pep		RGWNEAKARSAKEAAKSLAKKKETTHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL					
		:					
a671		RGWNDAKAMSAGAAKSLAKKKATTHAAIEPASAITPRIADSTMQAAMMAETRRSATGRL					
		70	80	90	100	110	120
		130	140	149			
m671.pep		FIRYLTGDTVYAQFVQIAFGIPCVFIVAX					
a671		FIRYLTGDTVYAQFVQIAFGIPCVFIVAX					
		130	140				

g672.seq

1	ATGAGGAAAA	TCCGCACCAA	AATCTGCGGC	ATCACCACAC	CGGAAGACGC
51	ACTGTATGCC	GCCCACGCCG	GCGCAGACGC	ATTGGGACTG	GTTTTTTACC
101	CCCAAAGCCC	CCGCGCTATC	GACATCATT	AAGCAAAAA	AATCGCCGCC
151	GCACTGCCGC	CGTTTGTCAG	CGTTGTGCGC	CTTTTCGTCA	ACGAAAGCGC
201	GCAAAACATC	CGCCGCATCC	TTGCCGAAGT	GCCGATACAC	ATCATCCAAT
251	TCCACGGCGA	CGAAGACGAT	GCATTCTGCC	GGCAGTTCGA	CGCCCCCTAT
301	ATTAAAGCCA	TTCGTGTTCA	CACGGCATCA	GACATCCGAA	ACGCCGCCAC
351	GCGCTTCCCC	AACGCTCAGG	CGCTGCTGTT	GCGATGCTAT	CACCCCTTCG
401	AATACGGCGG	CACCGGACAC	CGCTTCGact	GGacgctgtt	ggcggAATAT
451	TCGGGCAAGC	CGTGGGTGCT	TGCCGGCGGG	CTGACCCCTG	AAAACGTCGG
501	CGAAGCCGTC	CGCATCACCG	GAGCGGAAGC	GGTCGACGTA	TCCGGCGGCG
551	TGGAAGCGTC	TAAAGGCAAA	AAAGACCCCG	CCAAAGTCGC	CGCCTTTATC
601	GCAACCGCCA	ACCGCCATATC	CCGTTAA		

This corresponds to the amino acid sequence <SEQ ID 2202; ORF 672.ng>:

```
g672.pep
  1 MRKIRTKICG ITTPEDALYA AHAGADALGL VFYQSPRAI DIIKAQKIAA
 51 ALPPFVSVVA LFVNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFDRPY
101 IKAIRVQTAS DIRNAATRF P NAQALLFDAY HPSEYGGTGH RFDWTLLAEY
151 SGKPWVLAGG LTPENVGEAV RITGAEAVDV SGGVEASKGK KDKPAKVAAFI
201 ATANRLSR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2203>:

```
m672.seq
  1 ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
 51 AGCTGCCGCC GCAGCGGCAG GTGCGGATGC CGTCGGGCTG GTCTTTTTC
101 AAGGCAGCAG CCGGGCCGTC GATATTGCCG GCGCCAAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTCAG CGTTGTCGCC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT GCCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCTAT
301 ATCAAAGCCA TTCGTGTTCG GACGGCATCA GACATCCGAA ACGCCGCCAC
351 GCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGAAAC CGCTTCGACT GGACGCTGCT GGCGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGG
501 CGAAGCCGTC CGCATACCGG GAGCGGAATC GGTCGATGTA TCCGGCGGTG
551 TGAAGCGTTC TAAAGGCAAA AAAGATGCCG CCAAAGTCGC CGCCTTTATC
601 GCAACGCCCA ACCGCCTATC CCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2204; ORF 672>:

```
m672.pep
  1 MRKIRTKICG ITTPEDAAAA AAAGADAVGL VFFQGSSRAV DIARAKKITA
 51 ALPPFVSVVA LFVNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAATRF P DAQALLFDAY HPSEYGGTGN RFDWTLLAEY
151 SGKPWVLAGG LTPENVGEAV RITGAESVDV SGGVEASKGK KDKAAKVAAFI
201 ATANRLSR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m672/g672 91.3% identity in 208 aa overlap

	10	20	30	40	50	60
m672.pep	MRKIRTKICG	ITTPEDAAAA	AAAGADAVGL	VFFQGSSRAV	DIARAKKITA	ALPPFVSVVA
g672	MRKIRTKICG	ITTPEDALYA	AHAGADALGL	VFYQSPRAID	IKAQKIAA	ALPPFVSVVA
	70	80	90	100	110	120
m672.pep	LFVNESAQNI	RRILAEVPIH	IIQFHGDEDD	AFCRQFHRPY	IKAIRVQTAS	DIRNAATRF
g672	LFVNESAQNI	RRILAEVPIH	IIQFHGDEDD	AFCRQFDRPY	IKAIRVQTAS	DIRNAATRF
	130	140	150	160	170	180
m672.pep	DAQALLFDAY	HPSEYGGTGN	RFDWTLLAEY	SGKPWVLAGG	LTPENVGEAV	RITGAESVDV
g672	NAQALLFDAY	HPSEYGGTGH	RFDWTLLAEY	SGKPWVLAGG	LTPENVGEAV	RITGAEAVDV
	190	200	209			
m672.pep	SGGVEASKGK	KDKAAKVAAFI	ATANRLSRX			
g672	SGGVEASKGK	KDKPAKVAAFI	ATANRLSRX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2205>:

a672.seq



1	ATGAGGAAAA	TCCGCACCAA	AATCTGCGGC	ATCACCACAC	CGGAAGACGC
51	ACTGTATGCC	GCCCCAGCCG	GCGCAGACCA	ATTGGGACTG	GTTTTTTACC
101	CCCCAAGCCG	CCGCGTGTCT	GACATCATTA	AAGCAACAAA	AATCACCCGC
151	GCACTGCGCG	CGTTTGTCTAG	CGTTGTCTGC	CTTTTCGTCA	ACGAAAGCGC
201	GCAAAACATC	CGCCGCATCC	TTGCCGAAGT	ACCGATACAC	ATCATCCAAT
251	TCCACGGCCA	CGAAGACGAC	GCATTCTGCG	GCCAGTCCA	CCGCCCTAT
301	ATCAAGGCCA	TTCTGTGTTA	GACGGCATCA	GACATCCGAA	ACGCCGCCGA
351	CCGCTTCCCC	GACGCTCAGG	CACGTGTGTT	CGATGCCTAC	CATCCTTCGG
401	AATACGGCGG	CACCGGACAC	CGCTTCGACT	GGACGCTGTT	GGCGGAATAT
451	TCGGGGCAAC	CGTGGGTGCT	TGCCGCGGG	CTGACCCCTG	AAAACGTCGA
501	CGAAGCCATC	CGCATACCCG	GAGCGGGAAG	GGTCGATGTA	TCCGGCGGCG
551	TGGAAGCGTC	TAAAGGCAAA	AAAGACCCAG	CCAAAGTTGC	CGCCTTTATC
601	GCAACCGCCA	ACCGCTATTC	CCGTAA		

a672.pcp

1	MRKIRTKICG	ITTPEDALYA	AHAGADALGL	VFYPQSPRAV	DIIKAQKITA
51	ALPPFVSVA	LFVNESAQNI	RRILAEVPIH	IIQFHGDEDD	AFCRQFHRPY
101	IKAIRVQTAS	DIRNAADRFP	DAQALLFDAY	HPSEYGGTGH	RFDWTLIAEY
151	SGKPWVLRAG	LTPENVDEAI	RITGAEAVDV	SGGVEASKGK	KDPAKVAAFI
201	ATANRWL*				

		10	20	30	40	50	60
m672.pep		MRKIRTKICGITT	PEDAAAAAAGAD	AVGLVFFQGS	RAVDIARAKK	ITAALPPFV	SVVA
					:   :		
a672		MRKIRTKICGITT	PEDALYAAHAGAD	ALGLVFYQSPRA	VDIIKAQKITA	ALPPFVSVVA	
		10	20	30	40	50	60
		70	80	90	100	110	120
m672.pep		LFVNESAQNIRRI	LAEVPIHIIQFH	GDEDDAFCRQ	FHRPYIKAIRV	QTASDIRNAAT	RFP
a672		LFVNESAQNIRRI	LAEVPIHIIQFH	GDEDDAFCRQ	FHRPYIKAIRV	QTASDIRNAAD	RFP
		70	80	90	100	110	120
		130	140	150	160	170	180
m672.pep		DAQALLFDAYHP	SEYGGTGNRFD	WTLLEAYESGK	PWVLAGGLTP	ENVGEAVRIT	GAESVDV
				:		:	
a672		DAQALLFDAYHP	SEYGGTGHRFD	WTLLEAYESGK	PWVLAGGLTP	ENVDEAIRIT	GAEAVDV
		130	140	150	160	170	180
		190	200	209			
m672.pep		SGGVEASKGKKD	AAKVAAFIAT	ANRLSRX			
a672		SGGVEASKGKKD	PAKVAAFIAT	ANRLSRX			
		190	200				

g673.seq

1	ATGGATATTG	AAACCTTCCT	TGCAGGGGAA	CGCGCCGCCG	GCGGATACCG
51	TTGCGGCTTC	GTGGCGATTG	TCGTCTGTCC	GAAGCTGGGC	AAATCAACGC
101	TGATGAACCA	TCTCATCGGT	CAGAAAAATCA	GTATTACCAG	CAAAAAGGCG
151	CAGACGACGC	GCAACCCGCGT	AACGGGGATT	TATTCCGACG	TATCCGCGCA
201	GTTCGTGTTT	GTCGATACGC	CGGGCTTTCA	AACCGACCAC	CGCAACGCGC
251	TCAACGAGAG	GCTGAATCAA	AATGTTACCG	AGGCGCTCGG	CGGTGTGGAT
301	TGGGTGGGTT	TCGTCTGTGA	GGCGATCGCG	CTTACCGATG	CCGACCCGCGT
351	CGTGTTGAAA	CAACTGCCCA	AGCACACGCC	GGCTCATTTTA	GTGATCAACA
401	AAATCGACAA	GGACAAGGCG	AAAGACCGTT	AGCGCTGGA	GGCGTTTGTT
451	GCCCAAGTGC	GCGCGGAATT	TGAATTTGCG	GCGGCGGAGG	CGGTCAGTGC
501	GAACACAGGT	TTGCGGATTG	CCAACCTGTT	GGAGCTGCTC	AAGCCGATATC
551	TGCCCGAAAG	CGTACCGATG	TATCCCCAAG	ACATGGTTAC	GGCAAAATCG
601	GCGCGTTTTT	TGGCGATGGA	AATCGTGCGT	GAAAAACCTCT	TCGCTATTTT

1079

```

651 GGGCGAGGAG CTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGGAGACGG TTTGAACCGC ATCTACatcg cCGTTTTGGT CGACAAAGAA
751 AGCCAAAAGG CGATTTTGAT CGGTAAAGGC GGGGAGCGTT TGAAAAAAT
801 TTCCACCGAA GCGCGGCTGG ATATGGAAAA ACTGTTTGAT AACAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCAGA CGACATTCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2208; ORF 673.ng>:

```

g673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR LTDADRVLK QLPKHTPVIL VINKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEVSAKHG LRIANLLELL KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFRLGEE LPYAMNVEVE QFEEGDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD NKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2209>:

```

m673.seq
1 ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CCGGCTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGCGTGGAT
301 GTGGTGTTT TCGTCGTGGA GGCGATGCGC TTTACCGATG CCGACCGCGT
351 CGTGTTGAAA CAACTGCCCA AGCACACGCC GGTCAATTTA GTGGTCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GGCCTTTGTT
451 GCCCAAGTGC GCGCCGAATT TGAATTGCG GCGGCGGAGG CCGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
751 AGCCAAAAGG CAATTTTAAT CGGTAAAGGC GGAGAACGTT TGAAGAAAAT
801 TTCCACCGAA GCGCGTTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2210; ORF 673>:

```

m673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR FTDADRVLK QLPKHTPVIL VVINKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEVSAKHG LRIANLLELI KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFRLGEE LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD TKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m673/g673 98.4% identity in 307 aa overlap

```

          10      20      30      40      50      60
m673.pep MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
          |||
g673      MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
          10      20      30      40      50      60

          70      80      90     100     110     120
m673.pep YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVLK
          |||

```

1080

```

g673      YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRLTDADRVVLK
              70      80      90      100     110     120

              130     140     150     160     170     180
m673.pep  QLPKHTPVILVVKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI
          |||||
g673      QLPKHTPVILVINKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELL
              130     140     150     160     170     180

              190     200     210     220     230     240
m673.pep  KPYPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
          |||||
g673      KPYPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
              190     200     210     220     230     240

              250     260     270     280     290     300
m673.pep  IYIAVLVDKESQKAILIGKGGERLKKISTEARLDMEKLFDTKVFLKVWVKVKS GWADDIR
          |||||
g673      IYIAVLVDKESQKAILIGKGGERLKKISTEARLDMEKLFDNKVFLKVWVKVKS GWADDIR
              250     260     270     280     290     300

m673.pep  FLRELGLX
          |||||
g673      FLRELGLX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2211>:

```

a673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG ACGGATACCG
51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAATCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTTGTGTTT GTCGATACGC CCGGTTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACCG TTTGAATCAA AACGTTACCG AGGCACTCGG CGGCGTGGAT
301 GTGGTGGTTT TCGTCGTGGA AGCGATGCGT TTTACCGATG CCGACCGCGT
351 CGTGTGTGAAA CAACTGCCCA AGCACACGCC GGTCATTTTA GTGGTCAACA
401 AAATCGATAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTTGT
451 GCCCAGGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CCGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCCGAAAG CGTGCCGATG TATCCCAGAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TAGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
751 AGCCAAAAGG CGATTTTAAT CGGCAAAGGC GGGGAGCGTT TGAAGAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2212; ORF 673.a>:

```

a673.pep
1  MDIETFLAGE RAADGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVVFVVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFRYLGE ELPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFDT KVFVKVWVK VKSGWADDIR
301 FLRELGL*

```

m673/a673 99.7% identity in 307 aa overlap

```

              10      20      30      40      50      60
m673.pep  MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
          |||||
a673      MDIETFLAGERAADGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
              10      20      30      40      50      60

```

1081

	70	80	90	100	110	120
m673.pep	YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK					
a673	YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m673.pep	QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
a673	QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m673.pep	KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR					
a673	KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m673.pep	IYIAVLVDKESQKAILIGKGGERLKKISTEARLDMEKLFDTKVFLKVWVKVSGWADDIR					
a673	IYIAVLVDKESQKAILIGKGGERLKKISTEARLDMEKLFDTKVFLKVWVKVSGWADDIR					
	250	260	270	280	290	300
m673.pep	FLRELGLX					
a673	FLRELGLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2213>:

g674.seq

1	ATGAAAACAG	CCCGCCGCCG	TTCCCGCGAG	CTTGCCGTAC	AAGCCGTTTA
51	CCAATCCCTT	ATCAACCGCA	CCGCCGCGCC	CGAAATTGCT	AAAAACATCC
101	GCGAAATGTC	CGACTTTGCC	AAAGCGGACG	AAGAATTGTT	CAACAACTC
151	TTCTTCGGCA	CACAAACCAA	TGCAGCGGAC	TACATCCAAA	AAATCCGCCC
201	GCTGCTCGAC	AGGGACGAAA	AAGACCTCAA	CCCCATCGAA	CGCGCCGTTT
251	TGCTGACCGC	CTGCCACGAG	CTTCCGCTA	TGCCCCGAAAC	GCCCTACCCC
301	GTCATTATCA	ACGAAGCCAT	CGAAGTTACC	AAAACCTTCG	GCGGCACGGA
351	CGGGCACAAA	TTCTGCAACG	GCATCCTCGA	CAAACCTGCC	GCCCCAATCC
401	GCCCAGACGA	GCCCCAACGC	CGTTGA		

This corresponds to the amino acid sequence <SEQ ID 2214; ORF 674.ng>:

g674.pep

1	MKTARRRSRE	LAVQAVYQSL	INRTAAPEIA	KNIREMSDFA	KADEELFNKL
51	FFGTQTNAAD	YIQKIRPLLD	RDEKDLNPIE	RAVLLTACHE	LSAMPETYP
101	VIINEAIEVT	KTFGGTDGHK	FVNGILDKLA	AQIRPDEPKR	R*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2215>:

m674.seq

1	ATGAAAACAG	CCCGCCGCCG	TTCCCGCGAG	CTTGCCGTAC	AAGCCGTTTA
51	CCAATCCCTT	ATCAACCGCA	CCGCCGCGCC	CGAAATTGCT	AAAAACATCC
101	GCGAAATGTC	CGACTTTGCC	AAGGCAGACG	AAGAATTGTT	CAACAACTT
151	TTCTTCGGCA	CGCAAACCAA	TGCGGCAGAG	TATATCCGAC	AAATCCGCCC
201	GCTACTTGAC	AGGGACGAAA	AAGACCTCAA	CCCCATCGAA	CGCGCCGTTT
251	TGCTGACCGC	CTGCCACGAG	CTGTCCGCCA	TGCCCCGAAAC	GCCCTACCCC
301	GTCATTATCA	ACGAAGCCAT	CGAAGTTACC	AAAACCTTCG	GCGGCACGGA
351	CGGGCACAAA	TTCTGCAACG	GCATCCTCGA	CAAACCTGCC	GCCCCAATCC
401	GCCCCGACGA	GCCCCAACGC	CGTTGA		

This corresponds to the amino acid sequence <SEQ ID 2216; ORF 674>:

m674.pep

1	MKTARRRSRE	LAVQAVYQSL	INRTAAPEIA	KNIREMSDFA	KADEELFNKL
---	------------	------------	------------	------------	------------

1082

51 FFGTQTNAAE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP  
 101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R\*

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m674/g674 97.9% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAE					
g674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLDRDEKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	::					
g674	YIQKIRPLDRDEKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
g674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2217>:

a674.seq

1	ATGAAAACAG	CCCGCCGCCG	TTCCCGCGAG	CTTGCCGTAC	AAGCCGTTTA
51	CCAATCCCTT	ATCAACCGCA	CCGCCGCGCC	CGAGATTGCT	AAAAACATCC
101	GCGAAATGCC	CGACTTTGCC	AAGGCAGACG	AAGAATTGTT	CAACAACTT
151	TTCTTCGGCA	CGCAAACCAA	TGCGGCAGAG	TACATCCGAC	AAATCCGCC
201	CCTGCTCGAC	CGCGACGAAA	AAGACCTCAA	CCCCATCGAA	CGCGCCGTCC
251	TGCTGACCGC	CTGCCACGAG	CTGTCCGCCA	TGCCCCGAAAC	GCCCTACCCC
301	GTCATCATCA	ACGAAGCCAT	CGAAGTAACC	AAAACCTTCG	GCGGCACGGA
351	CGGGCACAAA	TTCGTCAACG	GCATCCTCGA	CAAACCTCGC	GCCCAAATCC
401	GTCCCGACGA	GCCCAAACGC	CGTTGA		

This corresponds to the amino acid sequence <SEQ ID 2218; ORF 674.a>:

a674.pep

1	MKTARRRSRE	LAVQAVYQSL	INRTAAPEIA	KNIREMPDFA	KADEELFNKL
51	FFGTQTNAAE	YIRQIRPLLD	RDEKDLNPIE	RAVLLTACHE	LSAMPETPYP
101	VIINEAIEVT	KTFGGTDGHK	FVNGILDKLA	AQIRPDEPKR	R*

m674/a674 99.3% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAE					
a674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMPDFAKADEELFNKLFFGTQTNAAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLDRDEKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
a674	YIRQIRPLDRDEKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
a674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2219>:

```
g675.seq
  1  ATGAACACCA TCGCCCCcaa cctcgacgGC AAACACCTCC GCATCGGCAT
 51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCCAAATG CTCAAAGTCT
101  GCTGCCGCAC CCTCCAAGAA TTGGGCGTAG CAGACGAAAa catcacgctc
151  gCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
201  CTCTTCCGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251  GCGAAACCTA CCATTTTCGAG CTGGTTGCCA ACGAATCCGG CGCAGGGATC
301  GGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAACG CCGTCCTGAC
351  CACCGAAAAC GACGCGCAGG CAATTGAACG GATTGGAGAA AAAGCCTCGG
401  ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTTCTGCTC
451  GAAGAACAGT TTGAAGACGA AGAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2220; ORF 675.ng>:

g675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSQM LKVCCRTLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVANESGAGI
101 GRVALDYNIP IANAVLTEN DAQAIERIGE KASDAAKVAV ECANLVNLLL
151 EEQFEDEE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2221>:

m675.seq

```

1  ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
201 CTCTTCCGAA AAGTTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGCGTC
301 AGCCGCGTCG CACTCGACTA CAATATCCCG ATTGCCAATG CCGTCCTAAC
351 CACCGAAAAC GACGCGCAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCGGTC GAATGCGCCA ACCTCGTCAA CCTGCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2222; ORF 675>:

m675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCRTLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV
101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAAKVAV ECANLVNLLL
151 EEQFEDEE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m675/g675 96.8% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCRTLQELGVADENITVATVPGALEIP					
g675	MNTIAPNLDGKHLRIGIVQARFTNEIGSQMLKVCCRTLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
g675	IALMNFASSEKFDALIAIGVVIRGETYHFELVANESGAGIGRVALDYNIPIANAVLTEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
g675	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2223>:

a675.seq

```

1  ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
201 CTCTTCTGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTTATCCGTG
251 GCGAAACCTA CCATTTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGGGTC
301 AGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAATG CCGTCCTGAC
351 CACGGAAAAC GACGCACAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCGGTA GAATGCGCCA ACCTCGTCAA CCTCCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2224; ORF 675.a>:

a675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCRTLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV

```

1085

101 SRVALDYNIP IANAVLT TEN DAQAIERIEE KASDAAKVAV ECANLVNLLL  
 151 EEQFEDEE\*

m675/a675 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCTRLQELGVADENITVATVPGALEIP					
a675	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCTRLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLT TEN					
a675	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLT TEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLL EEQFEDEE X					
a675	DAQAIERIEEKASDAAKVAVECANLVNLLL EEQFEDEE X					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2225>:

g677.seq  
 1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTtg  
 51 ggAAACGGTG CGCTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT  
 101 TTGATGTATT CGACAGAAAG GATTTC AATT TCCTCACGGC CTCCGGCGT  
 151 GTTCAAAACC ACTTCGTGCG CTTCGCGCGC TTTAATCAGG CAACCGGCCA  
 201 ACGGCGAAAT CCAAGAAATT TTGTTTGGCG CGGTATCGAT TTCATCGACG  
 251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGCGCGCA ACAGACCGAC  
 301 GGTGCGCGCG AAAAATACTT GGTGCGTGC TCGCGCAAT TCGGGATCGA  
 351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTGCG  
 401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTCGCTGCG  
 451 GTCGCGGTTG CCTGCCGCC AGTTGACGAT TTGGACGATT TCGGGGCGTT  
 501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG  
 551 GGCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2226; ORF 677.ng>:

g677.pep  
 1 MPQILVRIFL IRYSEFIWETV RLCRFRRHSR SVDFDVDRK DFNFLTAFR  
 51 VQNHVFAFAR FNQATRQRRN PRNFVLRGID FIDADDFDGL LAPVAAQQT  
 101 GRAEKYLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA  
 151 VAVACRPVDD LDDFGAFFID QLIKLVFQCL PSGGRNVVFG FGTHIVCG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2227>:

m677.seq  
 1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTG  
 51 GGAAACGGCG CGCTTTTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT  
 101 TTGATGTATT CGACAGAAAG GATTTC AATT TCCTCACGCC CTTCGGCGT  
 151 GTTCAAAACC ACTTCGTGCG CTTCGCGCGC TTTAATCAGA CAACGAGCCA  
 201 GCGGCGAAAT CCAAGAAATT TTGTTTGGCG CGGTATCGAT TTCATCGATG  
 251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGTCGCGCA ACAGTCCGAC  
 301 CGTCGCGCGG AAAAACACTT GGTGCGTGC TCGCGCAAT TCGGGATCGA  
 351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTGCG  
 401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTCGCTGCG  
 451 GTCGCGGTTG CCTGCCGCC AGTTGACGAT TTGGACGATT TCGGGGCGTT  
 501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG  
 551 GGCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2228; ORF 677>:

m677.pep  
 1 MPQILVRIFL IRYSEFIWETA RLCRFRRHSR SVDFDVDRK DFNFLTPFR



1086

51 VQNHFAFAR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVVAQQSD  
 101 RRAEKHLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA  
 151 VAVACRPVDD LDDFGAFFVD QLIKLVFQCL PSGGRNVVFG FGTHIVCG\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m677/g677 94.9% identity in 198 aa overlap

	10	20	30	40	50	60
m677.pep	MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDRKDFNFLT	PFRRVQNHFAFAR				
g677	MPQILVRIFLIRYSFIWETVRLCRFRHRSVDFDVFDRKDFNFLT	AFRRVQNHFAFAR				
	10	20	30	40	50	60
	70	80	90	100	110	120
m677.pep	FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGR	FAQFGIDDDG				
g677	FNQATRQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQT	DGRAEKYLVGRFAQFGIDDDG				
	70	80	90	100	110	120
	130	140	150	160	170	180
m677.pep	SLQTFGQETDAAVDFAHTAF	FAVKIVAVFAAVAVACRPVDDLDDFGAFFVDQLIKLVFQCL				
g677	SLQTFGQETDAAVDFAHTAF	FAVKIVAVFAAVAVACRPVDDLDDFGAFFIDQLIKLVFQCL				
	130	140	150	160	170	180
	190	199				
m677.pep	PSGGRNVVFGFGTHIVCGX					
g677	PSGGRNVVFGFGTHIVCGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2229>:

a677.seq

1	ATGCCGCAGA	TTTTGGTGCG	GATTTTCCTC	ATTCGGTATT	CCTTTATTTG
51	GGAAACGGCG	CGTTTGTGCC	GTTTCAGACG	GCATTCCCGA	TCAGTCGATT
101	TTGATGTATT	CGACAGAAAG	GATTTCAATT	TCCTCACGCC	CTTCCGGCGT
151	GTTTAAAC	ACTTCGTCGC	CTTCACGCGC	TTAATCAGA	CAACGAGCCA
201	GCGGCGAAAT	CCAAGAAATT	TTGTTTTCGC	CGGTATCGAT	TTCATCGATG
251	CCGACGATTT	TGACGGTTTG	CTCGCGCCCG	TCGCCGCGCA	ACAGACCGAC
301	GGTCGCGCCG	AAAAACACTT	GGTCGCTCGC	TTCGCGCAAT	TCGGGATCAA
351	CGACGACGGC	GGCTTCCAAA	CGCTTGGTCA	GGAAACGGAT	GCGGCGGTGC
401	ATTTCGCGCA	TACGGCGTTT	GCCGTAAAGG	TAGTCGCCGT	TTTCGCTGCG
451	GTCGCCGTTG	CCTGCCGCCC	AGTTGACGAT	TTGGACGATT	TCGGGGCGTT
501	CTTTATTAAAC	CAGTTGATAA	AGCTCGTCTT	TCAATGCCTG	CCATCCGGCG
551	GCGGTAATGT	AGTTTTTGGT	TTCGGTACTC	ATATTGTGTG	CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2230; ORF 677.a>:

a677.pep

1	MPQILVRIFL	IRYSFIWETA	RLCRFRHRSR	SVDFDVFDRK	DFNFLT	PFRR
51	V*NHFVAFTR	FNQTSQRRN	PRNFVLRGID	FIDADDFDGL	LAPVAAQQT	D
101	GRAEKHLVGR	FAQFGINDDG	GFQTLGQETD	AAVDFAHTAF	AVKVVAVFAA	
151	VAVACRPVDD	LDDFGAFFIN	QLIKLVFQCL	PSGGRNVVFG	FGTHIVCG*	

m677/a677 93.4% identity in 198 aa overlap

	10	20	30	40	50	60
m677.pep	MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDRKDFNFLT	PFRRVQNHFAFAR				
a677	MPQILVRIFLIRYSFIWETARLCRFRHRSVDFDVFDRKDFNFLT	PFRRVXNHFAFTR				
	10	20	30	40	50	60
	70	80	90	100	110	120

```

m677.pep  FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG
a677       FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTGGRRAEKHLVGRFAQFGINDDG
           70      80      90      100     110     120

           130     140     150     160     170     180
m677.pep  SLQTFGQETDAAVDFAHTAFVAVFAAVAVACRPVDDLDDFGAFFVDQLIKLVFQCL
a677       GFQTLGQETDAAVDFAHTAFVAVFAAVAVACRPVDDLDDFGAFFINQLIKLVFQCL
           130     140     150     160     170     180

           190     199
m677.pep  PSGGRNVVFGFGTHIVCGX
a677       PSGGRNVVFGFGTHIVCGX
           190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2231>:

```

g678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GCCTccgCCG TCATCGCCGC
51 CTGCATCGTC ATTTCCACGA TCGCGGCGGT GATTGCGGAA GCAggttcGA
101 TGGTgGCATG ggtggTTTcc tTCTTTTttg ccAAACTCTt tGCCGCACcc
151 ttcgcccACC TCGCCTTTGc ctCGTTCCAA ccccgccTGT TTGCAttggc
201 tCTGTCATTc ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTCGCT GCTGACCGGC GCAGTTTCGG CGGTCGGTCT GGGCTTTGCC
301 AACCGCATTT TGGGCGGTGT ATTCGGTGCA TTGAAAGGCG TTTTGATTGT
351 TACCCTGCTG ATCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCAACA GTCCTATACC GTACCGTTTT TCGTATCGCT TTCCGAAGCG
451 GTGTTAAACC atacggaCAA CGCaccgaa tCCctcgacg acgactaa

```

This corresponds to the amino acid sequence <SEQ ID 2232; ORF 678.ng>:

```

g678.pep
1  MNSLPIADLL ASAVIAACIV ISTMRGVIAE AGSMVAWVVS FFFAKLFAAP
51 FADLAFASFO PRLFALALSF ISLFVIACLI QKMLRSLLTG AVSAVGLGFA
101 NRILGGVFGE LKGVLIIVTLL IMLASKTDLP DTEEWQSYT VPFFVSLSEA
151 VLNHTDNAPE SLDDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2233>:

```

m678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GTCTCCGCCG TCATCGCCGC
51 CTGCATCGTG CTATCCGCGA TCGCGGCGGT GATTGCGGAG GCAGGCTCAA
101 TGGCGGCATG GGTGTTTCC TTCTTTTCG CCAAACTCTT TGCCGCCTCC
151 TTCGCCGACC TCGCCTTTGC CTCGTTCCAA CCCCgcCTGT TTGCATTGGC
201 TCTGTGCTTC ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTCGCT GCTGACCAGC GCAGTTTCGG CGGTCGGTTT GGGCTTTGCC
301 AACCGCATTT TGGGCGGCGT ATTCGGTGCA TTGAAAGGCG TTTTGATTGT
351 TACCCTGCTG GTCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2234; ORF 678>:

```

m678.pep
1  MNSLPIADLL VSAVIAACIV LSAMRGVIAE AGSMAAWVVS FFFAKLFAAS
51 FADLAFASFO PRLFALALSF ISLFVIACLI QKMLRSLTTS AVSAVGLGFA
101 NRILGGVFGE LKGVLIIVTLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m678/g678 89.7% identity in 165 aa overlap

1088

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ					
g678	MNSLPIADLLASAVIAACIVISTMRGVIAEAGSMVAWVVSFFFAKLFAAPFADLAFASFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFISLFVIACLIQKMLRSLLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
g678	PRLFALALSFISLFVIACLIQKMLRSLLTGAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
g678	IMLASKTDLPDTEEWQSYTVPFFVSLSEAVLNHTDNAPESLDDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2235>:

```

a678.seq
1  ATGAATAACC TCCCGTTGCG CGACCTCCTC GTCTCCGCCA TCATCGCCGC
51  CTGCATCGTG CTATCCGCGA TGCGCGGCGT GATTGCGGAG GCTGGCTCAA
101 TGGCGGCATG GGTGGTTGCC TTTTTCCTCG CCAAACCTCTT TGCCGCACCC
151 TTCGCCGACA TCGCCTTTGC ATCGTTCCAA CCCCCTGTGT TTGCATTGGC
201 TCTGTCGTTT ATTTCCCTAT TCGTCATTGC CTGTCTGATC CAGAAAATAC
251 TCCGCTCGCT GCTGACCGGG GCACTTCGGG CCGTCGGTTT GGGCTTTGCC
301 AACC GCATTT TGGGCGGCGT ATTCGGTGCA TTGAAAGGCA TTTTGATTAT
351 TACCCTGCTG GTCATGCTCG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGCGGAA ACTCCGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2236; ORF 678.a>:

```

a678.pep
1  MNNLPVADLL VSAIIAACIV LSAMRGVIAE AGSMAAWVVA FFFAKLFAAP
51  FADIAFASFQ PRLFALALSF ISLFVIACLI QKILRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGILIIITLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

m678/a678 93.9% identity in 165 aa overlap

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ					
a678	MNNLPVADLLVSAIIAACIVLSAMRGVIAEAGSMAAWVVAFFFAKLFAAPFADIAFASFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFISLFVIACLIQKMLRSLLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
a678	PRLFALALSFISLFVIACLIQKILRSLLTGAVSAVGLGFANRILGGVFGALKGILIIITLL					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
a678	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2237>:

```

g680.seq
1  ATGACGAAGG GCAGTTCGGC GATGTCCAGC CCACGCGCGG CGATATCGGT
51  GGCGACGAGG ACGCGCAGGC TGCCGTCTTT GAAGGCGTTG AGTGTTCGTA
101 GCCTGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG

```

```

151 CGGCGCACCA GTTCGCGCGT TACGCGGTCTG ACGCTTTGTT TGGTtttgCA
201 AAAGACGATA ACTTGGTTCA TATGCAGATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT TTGGAAGGTA TCGACGGCGA TGATGTgttg ttcGACGTTG
301 GCGTTGGTGG TGTTTTGGGC GGCAACCTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGTGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAAAC CCATATCCAA CATGCGGTCT GCTTCGTCCA GAACGACGAT
501 TTCGGCTTTG TTTAAACTGA TGTTTTTCTG TTTACATGG TCGAGCAGCC
551 GTCCGACGGT GGCGACGACT ATTTTCGAGC CGGCACGCAG GTCGGCGGTT
601 TGTTTGTTCA TGTTGACACC GCCGAAGAGG ACGGTATGCC GCAGCGGCAG
651 GTTTTTAATg tag

```

This corresponds to the amino acid sequence <SEQ ID 2238; ORF 680.ng>:

```

g680.pep
  1 MTKGSSAMSS PRAAISVATR TRRLPSLKAL SVSSLLCWER SPCACADRL
 51 RRTSSRVTRS TLCLVLQKTI TWFICRSTIS RSSRLRFWKV STAMMCCSTL
101 ALVVFWAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151 SINPISNMRS ASSRTTISAL FKLMMFFCTW SSSRPTVATT ISQPARRSAV
201 CLSMLTTPKR TVCRSGRFLM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2239>:

```

m680.seq
  1 ATGACGAAGG GCAGTTCGGC AATGTCCAGC CCGCGCGCGG CGATGTCGGT
 51 GGCGACGAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CGGCGCACCA GTTCGCGCGT TACGCGGTCTG ACGCTTTGTT TGGTTTTGCA
201 GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 GCGTTGGTGG TGTTTTGGCG GGCAGCTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAAAC CCATATCCAG CACACGGTCG GCTTCGTCCA AAACGACGAT
501 TTCCACTTTG TTCAAATGGA TGTTTTTCTG TTTACAGTGG TCGAGCAGCC
551 GTCCGACGGT GGCGACGACG ATTTTCGAGC CGGCACGCAG GTCGGCGGTC
601 TGTTTGTTCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTTGATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2240; ORF 680>:

```

m680.pep
  1 MTKGSSAMSS PRAAMSVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
 51 RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVVFCAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFFCTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPPKN TVWRSGRFLM *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

**m680/g680** 90.9% identity in 220 aa overlap

```

          10      20      30      40      50      60
m680.pep  MTKGSSAMSSPRAAMSVATRTRRLPSLKALS SVSSRLCWERSPCACADRLRRTSSRVTRS
          |||
g680       MTKGSSAMSSPRAAISVATRTRRLPSLKALS SVSSLLCWERSPCACADRLRRTSSRVTRS
          10      20      30      40      50      60

          70      80      90      100     110     120
m680.pep  TLCLVLQNTMTWFICKSTISRSSRLRF*MXVSTAMMCCSTLALVVFWCAATSTVSGAFMKSC
          |||
g680       TLCLVLQKTITWFICRSTISRSSRLRFWKVSTAMMCCSTLALVVFWAATSTVSGAFMKSC
          70      80      90      100     110     120

          130     140     150     160     170     180
m680.pep  ASLRIGAEKVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCTW

```

```

g680      |||||
          ASLRIGAEKVAEKSRVWRWRGSGICMILRMSSINPISNMRSASSRTTISALFKLMFFCFTW
          130      140      150      160      170      180

          190      200      210      220
m680.pep  SSSRPTVATTISQPARRSAVCLSIFIPPNKTVWRSGRFLMX
          |||||
g680      SSSRPTVATTISQPARRSAVCLSM LTPPKRTVCRSGRFLMX
          190      200      210      220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2241>:

```
a680.seq
1  ATGACGAAGG  GCAGTTCGGC  AATATCCAGC  CCCCGCGCGG  CGATATCGGT
51  GGCAGCAGAG  ACGCGCAGGT  TGCCGTCTTT  GAAGCGCGTG  AGTGTTTCCA
101  CCGCGCTTTG  TTGGGAACGG  TCGCCGTGTA  TCGCCTGTGC  GGACAGGTTG
151  CGGCGCACCA  GTTCGCGCGT  TACGCGGTCT  ACGCTTTGTT  TGGTTTTGCA
201  GAACACGATG  ACCTGGTTCA  TATGCAAATC  GACAATCAGC  CGTTCGAGCA
251  GGTTCGCGCT  CTGAATGGTA  TCGACGGCGA  TGATGTGCTG  CTCGACGTTG
301  CGGTTGGTGG  TGTCTTGGCG  GGCAGCTTCG  ACGGTTTCGG  GCGCGTTTCA
351  GAAGTCTTGC  GCCAGTTTGC  GTATCGGGGC  GGAGAAGTTG  GCGGAAAAGA
401  GCAGGGTTTG  CGCTTGGCGG  GGCAGCATCT  GCATGATTTT  CGGGATGTCT
451  TCGATAAAAC  CCATATCCAG  CATACGGTCT  GCTCGTCCA  AAACAGCAGT
501  TTCGACTTTG  TTCAAATGGA  TGTTTTTCTG  TTTCACGTGG  TCGAGCAGCC
551  GTCCGACGGT  GGCAGCAGCG  ATTTTCGCAG  CGGCACGCAG  GTCGGCGGTC
601  TGTTTGTCCT  TATTCATACC  GCCGAACAAG  ACGGTGTGGC  GCAGCGGCAG
651  GTTTTGTATG  TAG
```

This corresponds to the amino acid sequence <SEQ ID 2242; ORF 680.a>:

```
a680.pep
1  MTKGSSAISS PRAAISVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
51  RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSRLRF*MV STAMMCSTL
101 ALVVSCAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASKTKTISTL FKWMFFCFTW SSSRPTVAT ISQPARSAV
201 CLSIFIPPNK TVWRSGRFLM *
```

m680/a680 98.6% identity in 220 aa overlap

	10	20	30	40	50	60
m680.pep	MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS					
	::   :					
a680	MTKGSSAISSPRAAISVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m680.pep	TLCLVLQNTMTWFICKSTISRSSLRFRXVMVSTAMMCCSTLALVVFCAATSTVSGAFMKSC					
a680	TLCLVLQNTMTWFICKSTISRSSLRFRXVMVSTAMMCCSTLALVVSAAATSTVSGAFMKSC					
	70	80	90	100	110	120
	130	140	150	160	170	180
m680.pep	ASLRIGA EKVAEKSRVWRWRSICMILRMSSIKPISSIRASSKTTISTLFKWMFFCFTW					
a680	ASLRIGA EKVAEKSRVWRWRSICMILRMSSIKPISSIRASSKTTISTLFKWMFFCFTW					
	130	140	150	160	170	180
	190	200	210	220		
m680.pep	SSSRPTVATTISQPARRSAVCLSIFIPPNKTVWRSGRFLMX					
a680	SSSRPTVATTISQPARRSAVCLSIFIPPNKTVWRSGRFLMX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2243>:

g681.seq  
1 ATGACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCGG AAGAGGCAAA  
51 GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGcgacqq

```

101  tgatgtTTTC GTCTGCTACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151  TTGAGCATTT GGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201  GATGCCGAGG TGTTCGCGT cgaggttgGG GCGCATGGTG TTCATTGGGT
251  GTCCTTTGGT ATTCGGGGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301  CGGCTGCCAG TCGGCAACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351  ACGCGCTGCC TTCGGGTTGG GAAAGCAGTG CGGCGGTTTC AGGGTTGGTT
401  TTGGTGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GGTCTCGGT
451  GTATTCGTCG GTTTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501  CAAAAACGGG GGCTTCGCGG TAAAGGAAGC CGACGGGCCG GTTTTGTTTG
551  GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601  TGCAAATGCG TTCATTGCGG GAATACGTTG GGGGGGGGGA AACTTGCGGA
651  TTTTACCACG ATTCCCGCGT TGTCGCGAGA CGGCGGCGGT TTGGTGGTAC
701  AATGTGCGCC GTTTCGAGCC TTAAGGTGTT TCTGTATTTT TGGAGTATGG
751  AAACGCATTC GGGCTGTTTT TTGCGGAAGA CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2244; ORF 681>:

**g681.pep**

```

1  MTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVNGGLEC AVFGKLPRAA FGLGKQCGGF RVGFGDVGEA DDAEVVGVVG
151 VFVGLVAAEE TPAAVVFKNG GFAVKEADGP VLFGDGVGGD AAVECRGKCL
201 CKCVHCGNTL GGGKLADFTT IPALSADGGG LVVQCAPFAA LRCFCIFGVW
251 KRIRAVFCGR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2245>:

**m681.seq**

```

1  ATGACGACGC CGATGGCAAT CAGTGCGTCA AACTTTTCGG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTT GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCCGAGG TGTTTGCCGT CGAGGTTGGG GCGCATGGTG TTCATTGGGT
251 GTCCTTTGGT ATTCGGAGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301 CGGCTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351 ATGCGCTGCC TTCGGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGCGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GATCGTCGGT
451 GTATTGCTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCCG GTTTTGTTTG
551 GCGACGGTGT TGGTGGCGAT ACAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTACGG GAATACGTTG GGGG.AAAAC TTACGGATT
651 TACCACGATT CGTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGAAA
751 CGCATTCGGG CTGTTTTTTG CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2246; ORF 681>:

**m681.pep**

```

1  MTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVNGGLEC AVFGKLPRAA FGLGKQCGGF RVGFGDVGEA DDAEVVVRIVG
151 VFVGLVAAEE TPAAVVFKNG GFAVEEADGP VLFGDGVGGD TAVECRGKCL
201 CKCVHYGNTL GXKLDTFTT RALSADGGGL VVQCAPFAAL RCFCIFGVW
251 RIRAVFCGR *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 681 shows 94.6% identity over a 261 aa overlap with a predicted ORF (ORF681.a) from *N. gonorrhoeae*:

**m681/g681**

```

m681.pep      10      20      30      40      50      60
               MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV
               |||
g681          10      20      30      40      50      60
               MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSIWLPISLV

```

	70	80	90	100	110	120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVGDGLECAVFGKLPCAA					
g681	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVGNGLCAVFGKLPRAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGFVDVGEADDAEVVRIVGVFVGLVAAEETPAAVVFKNGGFAVEEADGP					
g681	FGLGKQCGGFRVGFVDVGEADDAEVVGIVGVFVGFVAAEETPAAVVFKNGGFAVKEADGP					
	130	140	150	160	170	180
	190	200	210	220	230	239
m681.pep	VLFGDGVGGDTAVECRGKCLCKCVHYGNTLGX-KLTDFTTIRALSADGGGLVVQCAPFAA					
g681	VLFGDGVGGDAAVECRGKCLCKCVHCGNTLGGGKLADFTTIPALSADGGGLVVQCAPFAA					
	190	200	210	220	230	240
	240	250	260			
m681.pep	LRCFCIFGVWKRIRAVFCGRRX					
g681	LRCFCIFGVWKRIRAVFCGRRX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2247>:

```

a681.seq
1  ATAACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCAG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTC GTCTGCCACG CCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTG CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTGGG GCGATGGTG TTCATTGAGT
251 GTCCTTTGGT ATTCGGAGGT TTCGGAATGC CGTCTGAAGG GTCAGTCCTT
301 AGGTTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCT GCCAATTCCC
351 ACGCGCTGCC TTCAGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGTGATAT CCGCGAGGCT GACGATGCTG AAGTTGTCCG GGTCGTCGGT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCTG GTTTTGTGTTG
551 GCGACGGTGT TGGTGCGCAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTGCGG GAATACGTT. GGGGAAAAC TTGCGGATTT
651 TACCACGATT CTTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCGGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAA
751 CGCATTCGGG CTGTTTTTTG CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2248; ORF 681.a>:

```

a681.pep
1  ITPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSISLPISLV KRACTMPMRR CLPSRLGAMV FIECPLVFGG FGMPSEGSVL
101 RLPVGDGLEC AVFCQFPRAA FRLGEQCGGF RVGFGDIGEA DDAEVVRVVG
151 VFVGLVAAEE TPAAVVFKNV GFAVEEADGL VLFGDGVGGD AAVECRGKCL
201 CKCVHCGNTX GGKLADFTTI LALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGRR *

```

m681/a681 90.8% identity in 260 aa overlap

	10	20	30	40	50	60
m681.pep	MTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV					
a681	ITTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVGDGLECAVFGKLPCAA					
a681	KRACTMPMRRCLPSRLGAMVFIECPLVFGGFGMPSEGSVLRLPVGDGLECAVFCQFPRAA					
	70	80	90	100	110	120

	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGF	GDVGEADDAEVVR	IVGVFVGLVAAEET	PAAVVFKN	GGFAVEEADGP	
a681	FRLGEQCGGFRVGF	DIGEADDAEVVRV	GVFVGLVAAEET	PAAVVFKN	GGFAVEEADGL	
	130	140	150	160	170	180
	190	200	210	220	230	240
m681.pep	VLFGDGVGGDTAVE	CRGKCLCKCVHY	GNLTGKXKLTDF	TTIRALSADGG	GLVVQCAPFAAL	
a681	VLFGDGVGGDAAVE	CRGKCLCKCVHC	GNLTGKXKLTDF	TTIRALSADGG	GLVVQCAPFAAL	
	190	200	210	220	230	240
	250	260				
m681.pep	RCFCIFGVWKRIR	AVFCGRRX				
a681	RCFCIFGVWKRIR	AVFCGRRX				
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2249>:

**g682.seq**

```

1  ATGCGCGATT TCGCCGTATG GGTGCCTTAC GGGGAACGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCC CGCACCTTAT TCGCCTGAGC CCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCC ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTATATTTGT GTGAATGATG AAATAAAAAAT GCCGCTCTGAA CCCGATTGGA
251 TTCAGACGGC ATTTTGTATG GCAGGATTTA TTCGCTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCAGTC AGGCGTTGTT CGGATTTTCG CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2250; ORF 682>:

**g682.pep**

```

1  MRDFAVWPY GERRKNWDIR YCLPHLIRLS PTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDYIC VNDEIKMPSE PDWIQTAFCM AGFIRFPTDR
101 PILTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2251>:

**m682.seq**

```

1  ATGCGTGATT TCACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCC ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTAT..... GAAA TGGCAATGCC GTCTGAACCC GATTGGATTG
251 AGACGGCATT TTGTATGGCG TACGGATTTA TTCGCTTTCC AACTGACCGA
301 CCCATTCGGA CAAGGCAGTC AGGCGTTGTT CGGATTTTCG CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2252; ORF 682>:

**m682.pep**

```

1  MRDFTVWVSY GKWRKNWDIR YCLLHLIHLs STRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDY.. EMAMPSEP DWIQTAFDMA YGFIRFPTDR
101 PIRTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 682 shows 88.1% identity over a 134 aa overlap with a predicted ORF (ORF682.a) from *N. gonorrhoeae*:

**m682/g682**





1094

```

                                10      20      30      40      50      60
m682.pep    MRDFTVWVSYGKWRKNWDI RYCLHLHLHSSTRLRKCGRILSGICEPFLITPDLTMHYC
            |||||:||| :| ||||||||| |||:| | ||||||||||||| |||||||||
g682         MRDFAVWPYPGERRKNWDI RYCLPHLIRLSPTRLRKCGRILSGICEPFLITPDLTMHYC
                        10      20      30      40      50      60

                                70      80      90     100     110
m682.pep    PILILIDY-----EMAMPSEPDWIQTAFCMAYGFIRFPTDRPIRTQSGVVRI SPRTGFR
            ||||| |||   |: ||||||||||||| ||||||||| ||||||||| |||||||||
g682         PILILIDYICVNDEIKMPSEPDWIQTAF-CMA-GFIRFPTDRPILTRQSGVVRI SPRTGFR
                        70      80      90     100     110

                                120     130
m682.pep    YPTRSLPKSKKAYGX
            ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g682         YPTRSLPKSKKAYGX
                120       130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2253>:

```
a682.seq
  1  ATGCGCGATT TTACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
 51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101  TGAGAAAGTG TGGCGGAATA TTAAGCGGTA TCTGCGAACC TTTTGTCTG
151  ATTACGCCCC ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201  ATAT.....
251  .....TATA TTCGGTTTCC AACTGACCGA
301  CCCATTCTGA CAAGGCCGAC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351  TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401  GA
```

This corresponds to the amino acid sequence <SEQ ID 2254; ORF 682.a>:

```
a682.pep
  1 MRDFTVWVS Y GKWRKNWDIR YCLLHLIHL S STRLRKCGRI LSGICEPFCL
 51 ITPDLTMHYC PILILIEY. . . . . . . . . . . . . . . . . .YIRFPTDR
101 PILTRPTGVV RISPRTGFRY PTRSLPKSKK AYG*
```

m682/a682      80.6% identity in 129 aa overlap

```

                                10          20          30          40          50          60
m682.pep  MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          |||||||
a682      MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
                                10          20          30          40          50          60

                                70          80          90          100         110         120
m682.pep  PILILIDYEMAMPSEPDWIIQTAFCMAYGFIRFPTDRPIRTRQSGVVRISPRTGFRYPTRS
          |||||:|
a682      PILILIEY-----YIRFPTDRPILTRPTGVVRISPRTGFRYPTRS
                                70          80          90          100

                                130
m682.pep  LPKSKKAYGX
          |||||||
a682      LPKSKKAYGX
                                110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2255>

```

g683.seq
1  ATGATTAAGG  AAACCCCTAAT  GCGCCCAATC  TTCTATCTT  TCGTTTTACT
51  CCTATTTTG  ATAACGCGCT  CGAGCACACC  GGACAAGTCT  GCGCGATGGG
101 AAAATATCGG  CACAATCTCA  AACGGCAATA  TTCATACATA  TATTAATAAA
151 GACAGTGTGA  GAAAAACGG  AAATCTGATG  ATTTTCCAA  GATAAAAAAG
201 TGTTACCAAT  CTGAAACAAG  AAGCTTTTGC  CAACACCCCG  GCATACAAGA
251 CTGCCATTGC  CGAGTGGGAA  ATCCACTGCA  ACAACAAAAC  ATACCGCTTA
301 AGTTTCGTAT  AGTTATTTGA  TACAAAAAAC  ACGGAAATTT  GGCACAAAA
351 CTACACAGCC  TCTTCCCTCC  GCCCGATGAG  CATCTGTCT  GGCATATTA

```

401 CTGAAAAACA ATATGAAACC GTATGCGGGA AAAA ACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2256; ORF 683 >:

g683.pep

```

1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMISLS GTLTEKQYET VCGKKL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2257>:

m683.seq.

```

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
201 TGTTACCAAT CTAAAACAAG AACGTTTTCG CAACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AGTTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAA ACTCTG A
```

This corresponds to the amino acid sequence <SEQ ID 2258; ORF 683>:

m683.pep.

```

1 MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMISLS GTLTEKQYET VCGKKL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 683 shows 99.3% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. gonorrhoeae*:

m683/g683 99.3% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPI	FLSFVLPIL	ITACSTPDKS	ARWENIGTIS	NGNIHTYINK	DSVRKNGNLM
g683	MIKETLMRPI	FLSFVLPIL	ITACSTPDKS	ARWENIGTIS	NGNIHTYINK	DSVRKNGNLM
	10	20	30	40	50	60
	70	80	90	100	110	120
m683.pep	IFQDKKVVVN	TLKQERFANT	PAYKTAIAEWE	IHCNNKTYRL	SSLQLFDTKN	TEISTQNYTA
g683	IFQDKKVVVN	TLKQERFANT	PAYKTAIAEWE	IHCNNKTYRL	SSLQLFDTKN	TEISTQNYTA
	70	80	90	100	110	120
	130	140				
m683.pep	SSLRPMISLS	GTLTEKQYET	VCGKKLX			
g683	SSLRPMISLS	GTLTEKQYET	VCGKKLX			
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2259>

a683.seq

```

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCNAG ATAAAAAAGT
201 TGTTACCAAT CTAAAACAAG AACGTTTTCG CNACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AATTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
351 NTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAA ACTCTG A
```

This corresponds to the amino acid sequence <SEQ ID 2260; ORF 683.a>:

a683.pep

```

1 MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFXDKKVVVN LKQERFAXTP AYKTAIAEWE IHCNNKTYRL
```

101 SSLQLFDTKN TEISTQXYTA SSLRPMSILS GTLTEKQYET VCGKKL\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 683 shows 97.9% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. meningitidis*:

m683/a683 97.9% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPILFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
a683	MIKETLMRPILFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m683.pep	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
a683	IFXDKKVVTNLKQERFAXTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQXYTA					
	70	80	90	100	110	120
	130	140				
m683.pep	SSLRPMSILSGLTTEKQYETVCGKKLX					
a683	SSLRPMSILSGLTTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2261>

g684.seq

1	ATGCGCCTTT	TCCCCATCGC	CGCCGCCCTG	ACGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACCGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCATCAACAC
201	CGCACAAAAC	CATGTTTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAC	CTTTGTTCCCT
301	GCCTCACGCA	GCGGCAGTAC	CGACAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CGATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2262; ORF 684>:

g684.pep

1	MRLFPIAAL	TLAACGTVQS	TQYFVLPDSR	YIRPATQGGG	TAVEVRLAEP
51	LKRGGVLVQT	DPYRINTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRTFVP
101	ASRSGSTDKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD
151	GYAAMTAAL	QGLKQAAQGM	VE*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2263>:

m684.seq

1	ATGCGCCTTT	TCCCGATTGC	CGCCGCCCTG	TCGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACTGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCCTCAACAC
201	CGCACAAAAC	CACGTCTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAT	CTTTGTTCCCT
301	GCCTCACGCA	GCGGCAGTAC	CGAAAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CGATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2264; ORF 684>:

m684.pep

1	MRLFPIAAL	SLAACGTVQS	TQYFVLPDSR	YIRPATQGGG	TAVEVRLAEP
51	LKRGGVLVQT	DPYRLNTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRIFVP
101	ASRSGSTDKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD

Computer analysis of this amino acid sequence gave the following results:

ORF 684 shows 97.7% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m684 .pep	MRLFFIAAALS	LAACGT	VQSTQYF	VLDPDS	RYIRPAT	QGGETAVEVRLAEPLKRGGLVYQT
g684	MRLFFIAAALT	LAACGT	VQSTQYF	VLDPDS	RYIRPAT	QGGETAVEVRLAEPLKRGGLVYQT
	10	20	30	40	50	60
	70	80	90	100	110	120
m684 .pep	DPYRLNTAQN	HVWADT	LDDMLEA	ALSNAF	NRLDSTR	IFVPASRSGST
g684	DPYRLNTAQN	HVWADT	LDDMLEA	ALSNAF	NRLDSTR	IFVPASRSGST
	70	80	90	100	110	120
	130	140	150	160	170	
m684 .pep	YTGKTLISG	YAVLPD	GTNRPF	HIETE	QQGDGYA	AMTAALEQGLKQAAQOMVEX
g684	YTGKTLISG	YAVLPD	GTNRPF	HIETE	QQGDGYA	AMTAALEQGLKQAAQOMVEX
	130	140	150	160	170	

a684.seq

```
1 ATGCGCCTCT TCCCGATTGC CGCCGCCCTG ACGCTTGCCG CTTGCGGTAC
51 TGTGCAAAAG ACACAATATT TCTGTGTGCC CGACACGCCG TACATCCCGT
101 CTGCACACGA AGCGGCGGAA ACGTCCGTCG AAGTCCGTCT TCGCGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCCTCAACAC
201 CGCACAAAAC CACGTCCTGG GACAGACCTT GGACGATATG CTTGCAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGGACA GCACACGCAT CTTTGTTCCT
301 GCCTCACGCA GCGGCGAGTAC GCAAAAATGG ACGGTCTATG TCACAGCAT
351 CCAAGGCAGC TACACGGGCA AAACCCTCAT CAGCGGCTAC GCCGTCCTAC
401 CCGACGGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
451 GGCTACGCCG CCATGACCCG CGCATCCGAA CAGGGACTGA AACAGGCGGC
501 GCAACAGATG GTCAGATAA
```

```
a684.pep
1  MRLFPIAAAL TLAACGTVQS TQYFVLPDSR YIRPATQGGE TAVEVRLAEP
51  LKRGGLVYQT DPYRLNTAQN HVWADTLDDM LEAALSNAFN RLDSTRIFVP
101 ASRSGSTEKW TVYIDAFQGS YTGKTLISGY AVLPGDGNRP FHIETEQQGD
151 GYAAMTAALE QGLKQAAQOM VE*
```

ORF 684 shows 99.4% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. meningitidis*

	10	20	30	40	50	60
m684.pep	MRLFP	IAAALS	LAACGTVQSTQYFVLPDSRYIRPATQGGETA	VEVRLAEPLKRGGLV	YQT	
a684	MRLFP	IAAALT	LAACGTVQSTQYFVLPDSRYIRPATQGGETA	VEVRLAEPLKRGGLV	YQT	
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRLNTAQN	HVWADTLD	DDMLEAALSNAFNR	LDSTRI	FVPASRSGSTE	KWTVYIDAFQGS
a684	DPYRLNTAQN	HVWADTLD	DDMLEAALSNAFNR	LDSTRI	FVPASRSGSTE	KWTVYIDAFQGS
	70	80	90	100	110	120
	130	140	150	160	170	

```

m684 . pep      YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQQMVEX
                  |||||
a684            YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQQMVEX
                  130      140      150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2267>

```

g685 . seq
1   TTGTTTGGCC GTATCGGGAA TTTTGCGTTT TGCGGCGTGG TTTCTGCAGG
51  TTGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGcct GCGCCGTCCT GCCGGCCGCC
151 TGTTCCGCCG AACCTGCCGC CGAAAAAACT GTATccgCCG CATCCCAAGC
201 CGCATCCACA CCTGTCGCCA CGCTGACCGT GCCGACCGCG CGGGGCGATG
251 CCGTTGTGCC GAAGAATCCC GAACgcgctg ccgtgtAcga CtggGCGGCG
301 TtggATACGC TGACCGAGCC GGGCGTGAAT GTGGGCGCAA CCACCGCGCC
351 GGTGCGCGTG GACTATTTCG AGCCTGCATT TGACAAGGCG GCAACGGTGG
401 GGACGCTGTT TGAGCCCGAT TGCGAATCCC TGCACCGCCA CAATCCGCAG
451 TTTGTCATTA CCGGCGGGCC GGGTGCGGAA GCGTATGAAC AGTTGGCGAA
501 AAACCGCGACC ACCATAGATT TGACGGTGGG CAACGGCAAT ATCCGCACCA
551 GCGGCGAGAA GCAGATGGAG ACCCTGTCGC GGATTTTCGG TAAGGAAGCG
601 CGCGTGGCGG AATTGAATGC GCAGATTGAC GCGCTGTTCC CCCAAAAGCG
651 CGAAGCCGCC AAAGGCAAAAG GACGCGGGCT GGTGCTGTGC GTTACAGGCA
701 ACAAGGTGTC CGCCTTCGGC ACGCAATCGC GGTGCGCAAG TTGGATACAC
751 GCGGACATCG GCCTGCCGCC CGTGGACGAA TCTTTACGCA ACGAAGGCGA
801 CCGGCAGCCC GTTTCCTTCG AATACATCAA AGAGAAAAAC CCCGGCTGGA
851 TTTTCATCAT CGACCGCACC GCCGCCATCG GGCAGGAAGG GCCGGCTGCC
901 GTGGAAGTGT TGGATAACGC GCTGGTATGC GGCACGAACG CTGGAAGCG
951 CAAGCAAATC ATCGTCATGC CTGCCGCGAA CTACATTGTC GCGGGCGGCG
1001 CCGGGCAGTT GATACAGGCG GCGGAACAGT TGAAGGCGGC GTTTGAAAAA
1051 GCAGAACCCG TTGCGGCGCA GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2268; ORF 685 >:

```

g685 . pep
1   LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLPAA
51  CSPEPAAEKT VSAASQAAST PVATLTVPTA RGDVAVPKNP ERVAVYDWAA
101 LDTLTEPGVN VGATTAPVRV DYLPAPFDKA ATVTGLFEPD CESLHRHNPO
151 FVITGGPGAE AYEQLAKNAT TIDLTVDNGN IRTSGEKQME TLSRIFGKEA
201 RVAELNAQID ALFAQKREAA KGKGRGLVLS VTGNKVSAGF TQSRLASWIH
251 GDIGLPPVDE SLRNEGHGQP VSFEYIKEKN PGWIFIIDRT AATGQEGPAA
301 VEVLNDAVLC GTNAWKRKQI IVMPAANYIV AGGARQLIQA AEQLKAFAFEK
351 AEPVAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2269>:

```

m685 . seq
1   TTGTTTGGCC GTATCGGGAA TTTTGCGTTT TGCGGCGTGG TTTCTGCAGG
51  TTGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCCT GCTGACCGCC
151 TGTTCCGCCG AACCTGCCGC CGAAAAAACT GTATCCGCCG CATCCGCATC
201 TGCCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG TGCAGCTGGA
351 TTATTTGCAG CCTGCATTTG ACAAGGCGGC AACGGTGGGG ACGCTGTTCG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTATTACC
451 GCGGGGCGCG GCGCGGAAGC GTATGAACAG TTAGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GCGGAAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCGCC CAAACGCGCG AAGCCGCCAA
651 AGGCAAAGGA CGCGGGCTGG TGCTGTCGGT TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAG GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGCG
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG
851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGAAGCGCA AGCAAATCAT
951 CGTCATGCCT GCCGCGAAGT ACATTGTCGC GGGCGGCGCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGCGGCGT TTAATAAGGC AGAACCCGTT
1051 GCGGCGGGGA AAAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2270; ORF 685>:

m685 . pep

```

1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51 CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLO PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPGEAEAYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGKG RGLVLSVTGN KVSAGFTQSR LASWIHGDIG
251 LPPVDESLRN EHGQPVVSFE YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGA RQLIQAAEQL KAAFKAEPV
351 AAGKK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 685 shows 94.4% identity over a 356 aa overlap with a predicted ORF (ORF 685) from *N. gonorrhoeae*:

m685/g685 94.4% identity in 356 aa overlap

```

              10      20      30      40      50      60
m685.pep      LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPPEAAEKT
              10      20      30      40      50      60
g685           LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLPAACSPPEAAEKT

              70      80      90      100     110
m685.pep      VSAASASA----ATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRV
              70      80      90      100     110
g685           VSAASQAASTPVATLTVPTARGDAVVPKNPERVAVYDWAALDTLTEPGVNVGATTAPVRV

              120     130     140     150     160     170
m685.pep      DYLPAPFDKAATVGTLEFEPDYEALHRYNPQLVITGGPGAEAYEQAKNATTIDLTVDNGN
              120     130     140     150     160     170
g685           DYLPAPFDKAATVGTLEFEPDCESLHRHNPQFVITGGPGAEAYEQAKNATTIDLTVDNGN

              180     190     200     210     220     230
m685.pep      IRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKGRGLVLSVTGNKVSAGF
              180     190     200     210     220     230
g685           IRTSGEKQMETLSRIFGKEARVAELNAQIDALFAQKREAAKGKGRGLVLSVTGNKVSAGF

              240     250     260     270     280     290
m685.pep      TQSRLASWIHGDIGLPPVDESLRNEHGQPVVSFEYIKEKNPDWIFIIDRTAAIGQEGPAA
              240     250     260     270     280     290
g685           TQSRLASWIHGDIGLPPVDESLRNEHGQPVVSFEYIKEKNPDWIFIIDRTAAIGQEGPAA

              300     310     320     330     340     350
m685.pep      VEVLNLAALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKAEPVAAAGKKX
              300     310     320     330     340     350
g685           VEVLNLAALVCGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFEKAEPVAAQX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2271>

```

a685.seq
1  TTGTTTGGCC GTATCGGGAA TTTTGCCTTT TGCGGCGTGG TTTCTGCAGG
51 TTGTTTGGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTATAT TGGGCAGCCT GCGCCGTCTT GCTGACCGCC
151 TGTTCCGCCCG AACCTGCCGC CGAAAAAAGT GTATCCGCCG CATCCGCATC
201 TGCCGCCACA CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GTGTGAATGT GGGCGCAACC ACCGCGCCGG TGCGCGTGGA
351 TTATTGTCAG CCTGCATTG ACAAGCGCGC AACGGTGGGG ACGCTGTTCTG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCTCAGCT TGTCATTACC
451 GCGCGGCCCG GCGCGGAAGC GTATGAACAG TTGGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GCGGAAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCCGC CAAACGCGCG AAGCCGCCAA
651 AGGCAAAGGA CGCGGGCTGG TGCTGTCGGT TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG

```

1100

```

851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGGAGCGCA AGCAAATCAT
951 CGTCATGCCT GCCGCGAACT ACATTGTCGC GGGCGGCTCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGAGGCGT TTGAAAAGGC AGAACCCGTT
1051 GCGGCGGGGA AAGAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2272; ORF 685.a>:

a685.pep

```

1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51  CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPAGAEAYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKKGK RGLVLSVTGN KVSFAGTQSR LASWIHGDIG
251 LPPVDES LRN EGHGQPV SFE YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGS RQLIQAAEQL KEAFEKAEPV
351 AAGKE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 685 shows 98.9% identity over a 355 aa overlap with a predicted ORF (ORF 685) from *N. meningitidis*:

m685/a685 98.9% identity in 355 aa overlap

	10	20	30	40	50	60
m685.pep	LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT					
a685	LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m685.pep	VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ					
a685	VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m685.pep	PAFDKAATVGTLFEPDYEALHRYNPQLVITGGPGAEAYEQLAKNATTIDLTVDNGNIRTS					
a685	PAFDKAATVGTLFEPDYEALHRYNPQLVITGGPGAEAYEQLAKNATTIDLTVDNGNIRTS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m685.pep	GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKKGKRGVLVSTGNKVSFAGTQSR					
a685	GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKKGKRGVLVSTGNKVSFAGTQSR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m685.pep	LASWIHGDIGLPPVDES LRN EGHGQPV SFE YIKEKNPDWIFIIDRTAAIGQEGPAAVEVL					
a685	LASWIHGDIGLPPVDES LRN EGHGQPV SFE YIKEKNPDWIFIIDRTAAIGQEGPAAVEVL					
	250	260	270	280	290	300
	310	320	330	340	350	
m685.pep	DNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEFVAAGKKX					
a685	DNALVRGTNAWKRKQIIVMPAANYIVAGGSRLIQAAEQLKEAFEKAEPVAAGKEX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2273>

g686.seq (partial)

```

1  ..AATTTCTCCT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
51  TGAAGGCTTC ggcgcgCATTC CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TGCCTCAGCA TAGCGCCGGC
151 ATTGTGGAAA CGGTCGGCAA GCCGTTGTCC GGTGCTCGCG TTGTCGGTCA
201 GGTGAGGCGC GATATTTTGG GCAACGCCCTT TTATGTCGTA GCTGTATATA
251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGGCG GGATGGTGTG CGTATCCGTC CCAATGGATG CGGTAAAGGC
351 TGAATCCGTC AACGGGACTA CCGGCTTCGT CAGAATCGGA ATGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2274; ORF 686 >:

g686.pep (partial)

```

1  ..NFSCRADDVF DDICSAVEGF GGIARSVQLG AVSGGAFESV AYSLRQHSAG
51  IVETVGKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
101 AVGGMVFVSV PMDAVKAESV NGTTGFVRIG M*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2275>:

m686.seq..

```

1  ATGATGTTGA AAAAATTCGT ACTCGGCGGT ATTGCCGCAT TGGTTTGGC
51  GGCCTGCGGC GGTTCGGAAG GCGGCAGCGG AGCGNNNNNN NNNNNNAATT
101 TCTCCTGCAG CGCCGATGAT GTTTTAAACG ATATCTGCAG TGCCGTTGAA
151 GGCTTCGGCG GCATTGCCCG ATCTGTCCAG CTCGGGGCTG TATCGGGTGG
201 CGCGTTTGAA TCCGTCGCCT ACTCCTTGGC TCAGCATACT ACCGGCATTG
251 TGGAACCGGT CGGCAAGCCG TTGTCCGGTG CTGCGGTTGT CGGTCAGGTT
301 GAGGCGGATA TTTTGGGCAA CGCCTTTTAT GTCGTAGCTG TATATATCCC
351 TCGCGCCTTT GGGAGCGGGA TAGCCGCCGC CCTGTGGCCC GTCATAGCCG
401 TCGGCGGGAT GGTGTTCGTA TCCGTCCCAA TGGATGCGGT AAAGGCTAAA
451 TCCGTCAACG GGAATACCGG CTTATCAGA ATCGGAATGT GA

```

This corresponds to the amino acid sequence <SEQ ID 2276; ORF 686>:

m686.pep

```

1  MMLKKFVLGG IAALVLAACG GSEGGSGAXX XXNFSCSADD VFNDICSAVE
51  GFGGIARSVQ LGAVSGGAFE SVAYSLRQHT TGIVETVGKP LSGAAVVGQV
101 EADILGNAFY VVAVYIPRAF GSGIAAALWP VIAVGGMVFV SVPMDAVKAK
151 SVNGTTGFIR IGM*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 686 shows 95.4% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. gonorrhoeae*

g686/m686 95.4% identity in 131 aa overlap

```

                                     10      20      30
g686.pep                             NFSCRADDVFDDICSAVEGFGGIARSVQLG
                                     ||| ||||:|||||||
m686      LKKFVLGGIAALVLAACGGSEGGSGAXXXNFSCSADDVFNDICSAVEGFGGIARSVQLG
               10      20      30      40      50      60

               40      50      60      70      80      90
g686.pep      AVSGGAFESVAYSLRQHSAGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
               |||||:|||||||
m686      AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
               70      80      90      100     110     120

               100     110     120     130
g686.pep      GIAAALWPVIAVGGMVFVSVPMDAVKAESVNGTTGFVRIGMX
               |||||:|||||||
m686      GIAAALWPVIAVGGMVFVSVPMDAVKAESVNGTTGFIRIGMX
               130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2277>

a686.seq (partial)

```

1  ..AATTCTCCT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
51  TGAAAGCTTC GCGGCGATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TGCGTCAGCA TACTACCGGT
151 ATTTGGGAAA CGGTCGACAA GCCGTTGTCC GGTGCTGCGG TTGTGGGTCA
201 GGTGTAGGCG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGGCG GGATGGTGTG CGTATCCGTC CCAATGGATG CGGTAAAGGC
351 TGAATCCGTC AACGGGACTA CCGGCTTCAT CAGAATCGGA ATGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2278; ORF 686.a>:

a686.pep (partial)





1 ..NFSCRADDVF DDICSAVESF GGIARSVQLG AVSGGAFESV AYSLRQHTTG  
51 IVETVDKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI  
101 AVGGMVFVSV PMDAVKAESV NGTTGFIRIG M\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 686 shows 96.2% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N meningitidis*:

m686/a686 96.2% identity in 131 aa overlap

```

      10          20          30          40          50          60
m686.pep    LKKFVLGGIAALVLAACGGSEGGSGAXXXXNFSCSADDFNDICSAVEGFGGIARSVQLG
              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a686         NFSCRADDVFDDICSAVESFGGIARSVQLG
                  10          20          30

      70          80          90          100         110         120
m686.pep    AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a686         AVSGGAFESVAYSLRQHTTGIVETVDKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
                   40          50          60          70          80          90

      130         140         150         160
m686.pep    GIAAALWPVIAVGGMVFSVPMDAVKAKSVNGTTGFIRIGMX
              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a686         GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFIRIGMX
                   100         110        120        130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2279>

```

g687.seq
1  ATGAAATCCA  GACACCTCGC  CCTCGCCCTC  GGGCTTGCCG  CCCTGTTCCG
51  CTTTGCCCGG  TCGGACAGCA  AAGTCCAAC  CAGCGTCCCC  CGGCAGTCGC
101 CGCCTGCCGC  TTCGGCAGCC  GCCGCCCCGG  CAGGACTGGT  CGAAGGGCAA
151 AACTACACCG  TCCTTGCCAA  CCCGATTCCC  CAACACAGCG  CAGGCAAGCT
201 TGAAGTGCTT  GAGTTTTTCG  GCTATTTTGT  TCCGCACATG  GCCCGCCTcg
251 AACCTGTTTT  GAGCAAAAC  GCCAAGTCTT  TTAAGACGA  TATGTACCTG
301 CGTACCGAAC  ACGTCGCTGT  GCAGAAAGAA  ATGCTGCCGC  TGGCAGCGct
351 cGCCGCCGCC  TCGCATATGG  CTGCCGCCGA  AAGCAAAGAT  GTGGCGAACA
401 GCCATATTTT  CGATCGCATG  GTCACCAAAA  AAATCAAGCT  CGAAGAGCCG
451 GAAGTCTCTA  AAAAATGGCT  GGGCGAACAa  ACgcctTTG  ACGGCAAAAA
501 AGTCCTTGCC  GCCTACGAAT  CCCCCGAAAG  TCAGGCGCGC  CGcggGAAAT
551 TGCAGGAGCT  GACCGAAACC  TTCCAAATCG  ACGGTACGCG  CACggTTATC
601 GTCGGCGGCA  AATATAAAGT  CGAATTTGCC  GACTGGGAGT  CCGGTATGAA
651 CACCATCGAC  CTTTGGCGG  ACAAGTAGC  TGAAGAACAA  AAAGCCCGCG
701 AGTAG

```

This corresponds to the amino acid sequence <2280 ID 724; ORF 687>:

```
g687.ppep
1  MKSRHLALAL  GVAALFALAA  CDSKVQTSVP  ADSAPAAASA  AAPAGLVEGQ
51  NYTVLANPFP  QQAGKVEVL  EFFGYFCPHC  ARLEPVLSKH  AKSKFDDMYL
101 RTEHVVVQKE  MLPLARLAAA  VDMAAASKD  VANSIFDAM  VNQIKLQEP
151 EVLKKWLGEQ  TAFDGKKVLA  AYAPESQAR  AGKMQLTET  FQIDGTPTVI
201 VGGKYKVEFA  DWESGNTID  LLADKRVREO  KAAQ*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2281>:

```
m687.seq
1  ATGAAATCCA  GACACCTTGC  CCTCgGCGTT  GCCGCCCTGT  TCGCCCTTGC
51  CGCGTGCAC  AGCAAAGTCC  AAACACAGCT  CCCCgCCGAG  AGCGCGCCTG
101 CGCGTTCGGC  AGCGCGCGCC  CGCGCAGGGC  TGGTCGAAGG  CAAAACTAT
151 ACCGTCTCTG  CCAACCCGAT  TCCCAACAG  CAGGCAGGCA  AAGTCGAAGT
201 CTTTGAGTTT  TTCGGCTATT  TCTGTCCGCA  CTGCGCCAC  CTGGAACCTG
251 TTTTAAGCAA  ACACGCCAAG  TCTTTAAAG  ACGATATGTA  CTTCCGTACC
301 GAACACGTCG  TCTGGCAGAA  AGAAATGCTG  ACGCTGGCAG  GCCTCGCCGC
351 CGCCCTCGAT  ATGGCTGCCG  CCGACAGATCA  AGATGTGGCG  AACAGCCATA
401 TTTTCGATGC  GATGGTCAAC  CAAAAAATCA  AGCTGCAAAA  TCCGGAAGTC
451 CTCAAAAAAT  GGCTGGGCGA  ACAAACCGCC  TTTGACGGCA  AAAAAGTCCT
```

м687.рер

Computer analysis of this amino acid sequence gave the following results:

ORF 687 shows 97.0% identity over a 234 aa overlap with a predicted ORF (ORF 687) from *N. gonorrhoeae*:

		10	20	30	40	50
m687.pep		MKSRHLAL--GVAALFALAACDSKVQTSVPADSAPAASAAAAPAGLVEGQNYTVLANPIP				
g687		MKSRHLALALGVAALFALAACDSKVQTSVPADSAPAASAAAAPAGLVEGQNYTVLANPIP				
		10	20	30	40	50
						60
		60	70	80	90	100
m687.pep		QQQAGKVEVLEFFGYFCPHCAHLEPVLKSHAKSFKDDMYLRTHEVWVWQKEMLTARLAAA				110
g687		QQQAGKVEVLEFFGYFCPHCARLEPVLKSHAKSFKDDMYLRTHEVWVWQKEMLTARLAAA				
		70	80	90	100	110
						120
		120	130	140	150	160
m687.pep		VDMAAADSKDVANSHIFDAMVNQIKLQNPVLKKWLGEQTAFDGKKVLAAYESPESQAR				170
g687		VDMAAASKDVANSHIFDAMVNQIKLQNPVLKKWLGEQTAFDGKKVLAAYESPESQAR				
		130	140	150	160	170
						180
		180	190	200	210	220
m687.pep		ADKMQELTETETQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVVREEQKAAQX				230
g687		AGKMQELTETETQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVVREEQKAAQX				
		190	200	210	220	230

a687.seq

This corresponds to the amino acid sequence <SEQ ID 2284; ORF 687.a>:

a687.pwp

1	MKSKHLALGV	AALFALAACD	SKVQTSVPAD	SAPAASAAAA	PAGLVEGQNY
51	TVLANPIPQQ	QAGKVEVLEF	FGYFCPHCAH	LEPVLSKHAK	SFKDDMYLRT
101	EHVVWQKEML	TLARLAAAVD	MAAADSKDVA	NSHIFDAMVN	QKIKLQPEEV
151	LKKWLGEQTA	FDGKKVLAAV	ESPESKARDV	KMQELTETFQ	IDGTPTVIVG
201	GKYKVEFADT	ESGMNTIDLL	ADKVREEOKA	AH*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 687 shows 98.7% identity over a 232 aa overlap with a predicted ORF (ORF 687) from *N meningitidis*:

m687/a687 98.7% identity in 232 aa overlap

	10	20	30	40	50	60
m687.pep	MKSRLHALGVAALFALAACDSKVQTSVPADSAPAAASAAAAPAGLVEGQNYTVLANPIPQQ					
a687	MKSRLHALGVAALFALAACDSKVQTSVPADSAPAAASAAAAPAGLVEGQNYTVLANPIPQQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m687.pep	QAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTEHVVWQKEMLTARLAAAVD					
a687	QAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTEHVVWQKEMLTARLAAAVD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m687.pep	MAAADSKDVANSHIFDAMVNQIKIKLQNPVLKKWLGEQTAFDGKKVLAAYESPESQARAD					
a687	MAAADSKDVANSHIFDAMVNQIKIKLQNPVLKKWLGEQTAFDGKKVLAAYESPESQARAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m687.pep	KMQELTETFTQIDGTPVIVGGKYKVEFADWESGMNTIDLLADKVVREEQKAAQX					
a687	KMQELTETFTQIDGTPVIVGGKYKVEFADWESGMNTIDLLADKVVREEQKAAHX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2285>

g688.seq

```

1 GTGCTACACT AGACATCCCG ATTTGCACAG AAAGGTTCTC CCGTGAACAA
51 AACCCCTCATC CTCGCCCTTT CCGCCCTGTT CAGCCTGACC GCGTGCAGCG
101 TCGAACGCGT CTCGCTGTTT CCTCCTACA AACTCAAAT CATCCAAGGC
151 AACGAACTCG AACCGCGCGC CGTTGCCGCC CTGCGCCCCG GCATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCTTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCGCAA CGGCATCATC
301 AAAGAACGCA GCAACCTGAC CGTCTATTTT GAAAACGGCG TACTCGTCCG
351 CACCGAAGGC GACGCCCTCC AAAATGCCGC CGAAGCCCTC CGCGCGAAAC
401 AAAACGCAGA CAAACAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2286; ORF 688 >:

g688.pep

```

1 VLH*TSRFAQ KGSPVNKTLI LALSALFSLT ACSVERVSLF PSYKLKIIQG
51 NELEPRVAA LRPGMTKDQV LLLGSPILR DAFHTDRWDY TFNTRNGII
101 KERSNLTVYF ENGLVLRTEG DALQNAEAL RAKQNADKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2287>:

m688.seq

```

1 GTGTACACT ACCCATCCCG ATTTGCACAG AAAGGCATTT CCGTGAACAA
51 AACCCCTCATC CTCGCCCTTT CCGCCCTCCT CGGCCTTGCC GCGTGCAGTG
101 CCGAACGCGT TTAAGTGTTC CCTCGTACA AACTCAAAT CATACAGGGC
151 AACGAACTCG AACCGCGCGC CGTTGCCGCC CTCCGCCCCG GCATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCTTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCGCAA CGGCATCATC
301 AAAGAACGCA GCAATCTGAC CGTCTATTTT GAAAACGGCG TACTCGTCCG
351 CACCGAAGGC GACGCTCTGC AAAACGCTGC CGAAGCCCTC AAAGACCGCC
401 AAAACACAGA CAAACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2288; ORF 688>:

m688.pep

```

1 VLHYPSTRFAQ KGISVNKTLI LALSALLGLA ACSAERVSLF PSYKLKIIQG
51 NELEPRVAA LRPGMTKDQV LLLGSPILR DAFHTDRWDY TFNTRNGII
101 KERSNLTVYF ENGLVLRTEG DVLQNAEAL KDRQNTDKP*

```

1105

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 688 shows 90.6% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. gonorrhoeae*:

m688/g688 90.6% identity in 138 aa overlap

```

              10      20      30      40      50      60
m688.pep    VLHYPSRFAQKGISVNKTLILALSALLGLAACSVERVSLFSPYKLIKIIQGNELEPRVAA
            ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g688        VLHXTSRFAQKGSPVNKTLILALSALFSLTACSVVERVSLFSPYKLIKIIQGNELEPRVAA
              10      20      30      40      50      60

              70      80      90      100     110     120
m688.pep    LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
            ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g688        LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
              70      80      90      100     110     120

              130     140
m688.pep    DVLQNAAEALKDRQNTDKPX
            |:||||| |:|:|
g688        DALQNAAEALRAKQNAKQX
              130     140

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2289>

```

a688.seq
1  GTGTACTACT ACCCATCCCG ATTTGCACAG AAAGGCATTT CCGTGAACAA
51 AACCCCTCATC CTCGCCCTTT CCGCCCTCCT CGGCCTTGCC GCGTGCAGCG
101 TCGAACGCGT TTCACTGTTC CCCTCGTACA AACTCAAAAT CATACAGGGC
151 AACGAACTCG AACCTCGCGC CGTCGCCTCC CTCGCCCCG GTATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCATTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCCGCAA CGGCATCATC
301 AAAGACCGAA GCAATCTGAC CGTCTATTTT GAAACGCGC TGCTCGTCCG
351 CACCGAAGGC AACGCCCTGC AAAATGCCGC CGAAGCCCTC CGCGTAAAC
401 AAAACGCAGA CAAACAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2290; ORF 688.a>:

```

a688.pep
1  VLHYPSRFAQ KGISVNKTLI LALSALLGLA ACSVERVSLF PSYKLIKIIQG
51 NELEPRAVAS LRPGMTKDQV LLLLGSPILR DAFHTDRWDY TFNTSRNGII
101 KDRSNLT VYF ENGVLVRTEG NALQNAAEAL RVKQNAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 688 shows 93.5% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. meningitidis*

m688/a688 93.5% identity in 138 aa overlap

```

              10      20      30      40      50      60
m688.pep    VLHYPSRFAQKGISVNKTLILALSALLGLAACSVERVSLFSPYKLIKIIQGNELEPRVAA
            ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a688        VLHYPSRFAQKGISVNKTLILALSALLGLAACSVERVSLFSPYKLIKIIQGNELEPRAVAS
              10      20      30      40      50      60

              70      80      90      100     110     120
m688.pep    LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
            ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a688        LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKDRSNLT VYFENGVLVRTEG
              70      80      90      100     110     120

              130     140
m688.pep    DVLQNAAEALKDRQNTDKPX
            |:||||| |:|:|
a688        NALQNAAEALRVKQNAKQX
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2291>

**g689.seq (partial)**

```

1  ..TCTCCGCCCC TTCCTCCGAT GAGCGGAAAA CTGATGGCGG TTTTGATGGC
51  GGTACTGGTC GCGCTGATGC CGTTTTCCAT CGATGCCTAC CTGCCCGCGA
101 TTCCCGAAAT GGCGCAGCCG CTGAACGCGG ATATCCACCG TATCGAATAG
151 AGTCTGAGTT TGTATTATGTT CGGCACGGCG TTCGGGCAAG TGGCCGGCGG
201 CGCGGTGTCC GACATCAAAG GGCGCAAACC CGTCGCCCTG ACCGGTTTGA
251 TTGTATATTG CCTTGCCGTT GCCGCCATCG TATTTGCTTC GAGTACCGAA
301 CAGCTCCTTA ACCTGCGTGC GGTACAGGCG TTCGGCGCAG GCATGGCTGT
351 AGTCATCGTC ggtgcatgg tgccgatgta TTATCCGGA CGCAAAGCCG
401 cgcAGATGTT TGCCCTTATC GGCATCATTG TGATGGTTGT GCCGCTGGCC
451 GCACCATAGG TCGGCGCATT GTTGCGAGGA TTGGGCGGAT GGCGGGCGAT
501 TTTTCGTTTT ttggcGgctt ATTCGCCGGT GCTGCCCGGT TTGGTACAGT
551 ATTTCTTGCC CAATCCCGCC GTCGGCGGCA AAATCGGCAG GGATGTGTTC
601 GGGCTGGTGG CGGGGCGGTT CAAGCGCGTA TTGAAAACCC GTGCCCGCAT
651 GGGTtatCTG TTTTTTCAGG CATTAGCTT CGGTTTCGATG TTCGCCTTTC
701 TGACCGAATC TTCCTTCGTG TACCGGCAGC TCTACCACGT TACGCCGCAC
751 CGGTACGCAT GGGTGTTCG ACTCAACATC ATCAGCATGA TGTTTTTCAG
801 CCGCGTTACC GCGTGGCGGC TTAACACCGG CGCGCATCCG CAAAGCATCC
851 TGCTGCGGGG GATTGTCTGC CAATTGCGC CCAACCCGTC CCAACTCGCC
901 GCCGTGCTGT TTTTCGGGTT GCCCCCGTTT TGGCTGCCGG TCGCGTGCCT
951 GATGTTTTTC GTCCGTACGC AGGGCCTGGT CCGTGCGGAC ACGCAGGCAT
1001 GCTTTATGTC TTATTCAAA GAAGAGGGCG GCAGCGCGAA CGCCGTGTTC
1051 GGTGTATTCC GGTCTTAAT CGGCGCGGGC GTGGTCATGG CGGCAACCGT
1101 GATGGCGGCA ACCATGACCG CGTCCGCCTC TTGCGGCATT GCGCTTTTGT
1151 GGCTCTGCTC GCACAAGGCG TGAAGGAAA ACGAAAAAA GCGAATACTT

```

This corresponds to the amino acid sequence <SEQ ID 2292; ORF 689 >:

**g689.pep (partial)**

```

1  ..SPPLPMSGK LMAVLMAVLV ALMPFSIDAY LPAIPEMAQP LNADIHRIE*
51  SLSLFMFETA FGQVAGGAVS DIKGRKPVAL TGLIVYCLAV AAIVFASSTE
101 QLLNLRAVQA FGAGMAVVIV GAMVRDYYSG RKAQMFAFI GIILMVVPLA
151 APMVGALLQG LGGWRAIFVF LAAYSPVLPG LVQYFLPNPA VGGKIGRDVF
201 GLVAGRFKRV LKTRAAMGYL FFQAFSFGSM FAFLTESSFV YRQLYHVTPH
251 RYAWVFALNI ITMMFFSRVT AWRLKTGAHP QSILLRGIVV QFAANPSQLA
301 AVLFFGLPPF WLPVACVMFS VGTQGLVGAD TQACFMSYFK EEGGSANAVS
351 GVFRSLIGAG VVMAATVMAA TMTASASCGI ALLWLCSHKA WKENEKRIL

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2293>:

**m689.seq**

```

1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51  GTTGCCGCTT GTTGTGCGG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGGCG GTTTGTTTGC GAATCGGACG AGAATTTATG
151 CTTCTGCCCC ATTATCTGA AATGAGCGAA AAATGATGG CGGTTTTGAT
201 GCGGATGCTG GTTACGCTGA TGCCGTTTTC CATCGATGCC TACCTGCCCC
251 CGATTCCCGA AATGGCGCAA TCCTGAACG CGGATGTTC CCGCATCGAA
301 CAGAGTTTGA GTTTGTTTAT GTTCGGCAGC GCGTTCGGAC AGGTGGTCGG
351 CCGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCC CTGACCGGTT
401 TGATTGTATA TTGCCTTGCC GTTGCCGCCA TCGTATTGTT TCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTCCGTG CGGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGCGCGA TTATTATTCC GGACGCAAAG
551 CCGCCAGAT GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTTGTT TTCTGGCGG CGTATTGCTT GGTGCTGCTC GGTGTTGTAC
701 AGTATTTTCT GCCCAAGCCC GCCGTCGGCG GCAAAATCGG ACGGGACGTG
751 TTCGGGCTGG TGGCGGGGCG GTTCAAGCGC GTATTGAAA CCCGTGCTGC
801 GATGGGTTAT CTGTTTTTTC AGGCATTGAG CTTCGGTTTC ATGTTCCGCT
851 TTCTGACCGA ATCTTCTTTC GTGTACGAG AGCTCTACCG TGTTACGCCT
901 CATCAATACG CTTGGGCGTT TGCACTCAAC ATCATCAGT TGATGTTTTT
951 CAACCGCGTT ACCGCGTGGC GGCTCAAAAC CGGCGTGAT CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCAAACCT GTCCCAACTC
1051 GCCGCCGTGC TGTTTTTCGG GTTGCCCGCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGGCTT GGTCGGTGCA AACACGAGG
1151 CGTGTTTTAT TCCTATTTC AAAGAAGAGG GCGGACGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTTCTTGACG GACGGTTCGG CAACCGTGAT GCGGCGAACG ATGACCGCGT
1301 CCACCTCTTG CGGCATTGCG CTCTGTGGC TCTGCTCGCA TCGTGCGTGG

```

1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA

This corresponds to the amino acid sequence &lt;SEQ ID 2294; ORF 689&gt;:

m689.pep  
 1 LLIHIVPVR PVLPGLLP VPAGVLKFSV SAYCVFRRRA VCLRIGREFM  
 51 PSAHYPEMSE KLMAVLMAML VTLMPFSIDA YLPAIPEMAQ SLNADVHRIE  
 101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLIVYCLA VAAIVFVSSA  
 151 EQLNLNRVVQ AFGAGMTVVI VGAMVRDYYS GRKAAQMFAL IGIILMVVPL  
 201 VAPMVGALLQ GLGGWQAI FV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV  
 251 FGLVAGRFKR VLKTRAAMGY LFFQAFSFGS MFAFLTESSV VYQQLYRVTP  
 301 HQYAWAFALN IITMMFFNRV TAWRLKTGVH PQSILLWGIV VQFAANLSQL  
 351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV  
 401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW  
 451 KENGQSEYL\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 689 shows 88.0% identity over a 408 aa overlap with a predicted ORF (ORF 689) from *N. gonorrhoeae*:

m689/a689 88.0% identity in 408 aa overlap

	30	40	50	60	70	80
m689.pep	CAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSEKLMAVLMAMLVTLMPFSIDAY					
g689	SPPLPPMSGKLMMAVLMVVALMPFSIDAY					
	10	20	30			
	90	100	110	120	130	140
m689.pep	LPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSVSDIKGRKPVALTGLIVYCLAV					
g689	LPAIPEMAQPLNADIHRIEXSLSLFMFGTAFGQVAGGAVSDIKGRKPVALTGLIVYCLAV					
	40	50	60	70	80	90
	150	160	170	180	190	200
m689.pep	AAIVFVSSAEQLNLNRVVQAFGAGMTVVI VGAMVRDYYSGRKAAQMFALIGIILMVVPLV					
g689	AAIVFASSTEQLNLNRVVQAFGAGMAVVIVGAMVRDYYSGRKAAQMFALIGIILMVVPLA					
	100	110	120	130	140	150
	210	220	230	240	250	260
m689.pep	APMVGALLQGLGGWQAI FV FLAAYSLVLLGLVQYFLPKPAVGGKIGRDVFGVLVAGRFKRV					
g689	APMVGALLQGLGGWRAIFVFLAAYS PVLPGLVQYFLPNPAVGGKIGRDVFGVLVAGRFKRV					
	160	170	180	190	200	210
	270	280	290	300	310	320
m689.pep	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTPHQYAWAFALNIITMMFFNRVT					
g689	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYRQLYHVT PHRYAWVFALNIITMMFFSRVT					
	220	230	240	250	260	270
	330	340	350	360	370	380
m689.pep	AWRLKTGVHPQSILLWGIVVQFAANLSQLAAVLFFGLPPFWLLVACVMF SVGTQGLVGAN					
g689	AWRLKTGAHPQSILLRGIVVQFAANPSQLAAVLFFGLPPFWLPVACVMF SVGTQGLVGAD					
	280	290	300	310	320	330
	390	400	410	420	430	440
m689.pep	TQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLHDGSATVMAATMTASTSCGIAL					
g689	TQACFMSYFKEEGGSANAVSGVFRSLIGAGVMAAT-----VMAATMTASASCIAL					
	340	350	360	370	380	
	450	460				
m689.pep	LWLCSHRAWKENGQSEYLX					
g689	LWLCSHKAWKENEKKRIL					
	390	400				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2295>

```
a689.seq
1   TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51  GTTGCCGCCT GTTTGTGCCG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGGCG GTTTGTTTGC GAATCGGACG AGAATTTATG
151 CCTTCTGCCC ATTATCCTGA AATGAGCGAA AAACGTATGG CGGTTTTGAT
201 GGCATGCTG GTTACGCTGA TCCGTTTTTC CATCGATGCC TACCTGCCCC
251 CGATTCCCCA AATGGCGCAG TCGCTGAACG CGGATGTCCA CCGCATCGAA
301 CAGAGCCTGA GTTTGTTTAT GTTCGGCAGC GCGTTCGGAC AGGTGGTCGG
351 CGTTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCG CTGACCGGAC
401 TGCCCGTCTA CTGCCTTGCC GTTGCCGCCA TCGTATTTGC TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGACG GCATTCGGTG CGGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGC GCGA TTATTATTCC GGACGCAAAG
551 CCGCCCAGAT GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGGCG ATTGTTGACG GGCTTGGGTG GCTGGCAGGC
651 GATTTTTGTT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGTGAC
701 AGTATTTTCT GCCCAAGCCC GCCGTGCGCG GCAAAATCGG CAGGGATGTG
751 TTCGGGCTGG TGGCTGGGCG GTTCAAACGC GTATTGAAAA CCGGTGCCGC
801 GATGGGTTAT CTGTTTTTTC AGGCATTACG CTTGCGTTTCG ATGTTGCGCT
851 TTCTGACCGA ATCTTCCTTC GTGTACCAGC AGCTCTACCA CGTTACGCCG
901 CACCACTACG CTTGGGCGTT TGCACCAAC ATCATCACGA TGATGTTTTT
951 CAACCGTATT ACCGCGTGGC GGCTCAAAC CCGCGTGCA TCCGAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCAACCT GTCCCAACTC
1051 GC CGCGCTGC GTTTTTTCGG GTTGCCCCCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTGCGTA CGCAGGGCTT GGTGCGTGCA AACACGCAGG
1151 CTGTGTTTTT GTCTATTTC AAAGAAGAGG GCGGCAGCGC AACGCCGTA
1201 TTGGGTGTAT TCCAATCTT AATCGGCGCG GGGGTGGGTA TGGCGCGGAC
1251 CTTCTTGCAC GACGGTTCGG CAACCGTGAT GGGGCAACC ATGACCGCGT
1301 CTACCTCTTG CCGCATTGCG CTTTGTGGC TCTGCTCGCA TCGTGCCTGG
1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2296; ORF 689.a>:

```
a689.pep
1   LLIHYIVPVR PVLPGLLLPP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
51  PSAHYPEMSE KLMAVLMAML VTLMPFSIDA YLPAIPEMAQ SLNADVHRIE
101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLAVYCLA VAAIVFASSA
151 EQLLNLRVVO AFGAGMTVVI VGAMVRDYS GRKAAQMFAL IGIILMVVPL
201 VAPMVGALLQ GLGGWQAIFV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
251 FGLVAGRFRK VLKTRAAMGY LFFQAFSEFS MFAFLTESSV VYQQLYHVP
301 HQYAWAFALN IITMMFFNRI TAWRLKTGVH PQSILLWGIV VQFAANLSQL
351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW
451 KENGQSEYL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 689 shows 99.1% identity over a 459 aa overlap with a predicted ORF (ORF 689) from *N. meningitidis*:

```
m689/a689    99.1% identity in 459 aa overlap

m689.pep      10      20      30      40      50      60
                LLIHYIVPVRPVLPGLLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE
a689          10      20      30      40      50      60
                LLIHYIVPVRPVLPGLLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE

m689.pep      70      80      90      100     110     120
                KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV
a689          70      80      90      100     110     120
                KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV

m689.pep     130     140     150     160     170     180
                SDIKGRKPVALTGLIVYCLAVAAIVFSSAEQLLNLRVVQAFGAGMTVVIVGAMVRDYS
a689         130     140     150     160     170     180
                SDIKGRKPVALTGLAVYCLAVAAIVFSSAEQLLNLRVVQAFGAGMTVVIVGAMVRDYS

m689.pep     190     200     210     220     230     240
                GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAIFVFLAAYSLVLLGLVQYFLPKP
```

1109

```

|||||
a689      GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAI FVFLAAYSLVLLGLVQYFLPKP
          190      200      210      220      230      240

          250      260      270      280      290      300
m689.pep  AVGGKIGRDVFLVAGRFKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTP
          |||||
a689      AVGGKIGRDVFLVAGRFKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYHVT
          250      260      270      280      290      300

          310      320      330      340      350      360
m689.pep  HQYAWAFALNIITMMFFNRVTAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLF FGLPP
          |||||
a689      HQYAWAFALNIITMMFFNRITAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLF FGLPP
          310      320      330      340      350      360

          370      380      390      400      410      420
m689.pep  FWLLVACVMF SVGTQGLVGANTQACFMSYFKEEGGSANAVLVGFQSLIGAGVGM AATFLH
          |||||
a689      FWLLVACVMF SVGTQGLVGANTQACFMSYFKEEGGSANAVLVGFQSLIGAGVGM AATFLH
          370      380      390      400      410      420

          430      440      450      460
m689.pep  DGSATVMAATMTASTSCGIALLWLC SHRAWKENGQSEY LX
          |||||
a689      DGSATVMAATMTASTSCGIALLWLC SHRAWKENGQSEY LX
          430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2297>

g690.seq (partial)

```

1  ATGAAAAACA AAACGTCATC ACTTCCCTTA TGGCTTGCCG CAATCATGCT
51  GGCCGCGCGT TCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTTC GTCTTCCGCG TCATCGGCTT CTCCCAAAC CGATTGCAA
151 CCGGCCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCACT
201 GTGAAATGCG ACCGGCCTGC ACCCGCCGCG CGGCATTGGC GATCTCATA
251 AGCAAATCGC CGAACACATC GACTCGGACT GTCTGTTTGC CCTTCCCAT
301 AACGAACTGG AAACCCGTTT CGGCTTACCC GCGCGCGGCT ATGACAACAT
351 ACAGCGGctG CTgtttCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAATCAT GCTGGCAATC GAAGACTTGC GTTACGGAAC GCGCACCATC
451 AGccgGCAGG CACAAGATGC CATAATGGAA CAGGAACGCC gcctccGaGa
501 agCGACGCTG ATGCTGACAC AGGCGAGTCA AAAAACCCGC GGaCAAGGCG
551 AGGAACCGAA ACGCGCACGT TATTTTGAAG TTTCGGCAAC ATctgCctat
601 TgaaccgGc ACAaacaacGG ACTTggcgGc AATTTCcAAT ACATCGGcCA
651 ATTGCCCGGC TATCTGAAAA TGCACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTtagAC
751 ATCCATTTTG ACGAAAATGG CAAAATCACG CGTATTGTGc TTTACGAAAA
801 AAATATCTAT...

```

This corresponds to the amino acid sequence <SEQ ID 2298; ORF 690>:

g690.pep (partial)

```

1  MKNKTSSLPL WLAAIMLAAR SPSKEDKtKE NGASAASSSA SSASSQTDLQ
51  PAASAPDNVK QAESAPL*NC TGLHPAAGIG DLIQQIAEHI DSDCLFALSH
101 NELETRFGLP GGGYDNIQRL LFPDIRPEDP DYHQIMLAI EDLRYGTRTI
151 SRQAQDAIME QERRLREATL MLTQGSQKTR GQGEEPKRAR YFEVSATSAY
201 LNRHNNGLGG NFQYIGQLPG YLKMHGEMLE NQSLFRLSNR ERNPDkPFLD
251 IHFDENGKIT RIVVYEKNiY ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2299>:

m690.seq..

```

1  ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTACCG CAATCATGCT
51  GACCGCGTGT TCTCCGAGCA AAGACGATAA AACCAAAGAA GTCGGTGCAT
101 CCGCTGCTTC GTCTTCCGCG TCATCAGCTC CTCCCAAAC CGATTGCAA
151 CCGACCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCGCC
201 GTCAAATGCG ACCAGCCTGC ACCCGCCGCG CGGCATTGAC GATCTCATGC
251 AGCAAATCGC CGAACACATT GACTCGGACT GTCTGTTTGC CCTTCCCAT
301 CACGAACTGG AAACCCGTTT CGGCTTACCC GACGGTGGCT ATGACAACAT
351 ACAGCGGCTG CTGTTTCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAATCAT ACTGGCAATT GAAGACTTGC GTTACGGAAC GCGCACGATC
451 AGCCGGCAGG CAAAAATGC CTTGATGGAA CAGGAACGCC GCCTCCGAGA
501 AGCGACGCTG TTGCTGATAC AGGCGAGTCA AGAAACCCGC GGACAAGGCG

```



1110

```

551 AGGAGCCGAA ACGCACGCGT TATTTTGAAG TTTCGGCAAC CCCTGCCTAT
601 TCGAGCCGGC ACAACAACGG ACTTGGCGGC AATTTCGAAT ACATCAGCCA
651 ATTGCCCGGC TATCTGAAAA TACACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTGTAGAC
751 ATCCATTTTG ACGAAAAATGG CAAAATCACG CGTATTGTCG TTTACGAAAA
801 AAACATCTAC TTCAATCCAA ACACGGGGCG AATATAA

```

This corresponds to the amino acid sequence <SEQ ID 2300; ORF 690>:

```

m690.pep
  1 MKNKTSSLLL WLTAIMLTAC SPSKDDKTKE VGASAASSA SSAPSQTDLQ
 51 PTASAPDNVK QAESAPPSNC TSLHPATGID DLMQQIAEHI DSDCLFALSH
101 HELETRFGLP DGGYDNIQRL LFPDIRPEDP DYHQKIILAI EDLRYGKRTI
151 SRQAQNALME QERRLREATL LLIQGSQETR GQGEEPKRTR YFEVSATPAY
201 SSRHNNGLGG NFQYISQLPG YLKIHGEMLE NQSLFRLSNR ERNPDKPFLLD
251 IHFDENGKIT RIVVYEKNIY FNPNTGRI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 690 shows 89.3% identity over a 408 aa overlap with a predicted ORF (ORF 690) from *N. gonorrhoeae*:

```

m690/g690      89.3% identity in 408 aa overlap

      10      20      30      40      50      60
m690.pep      MKNKTSSLLLWLTAIMLTACSPSKDDKTKEVGASAASSASSAPSQTDLQPTASAPDNVK
      ||||| ||||| ||||| ||||| ||||| |||||
g690           MKNKTSSLPWLAAIMLAARSPSKEDKTKENGASAASSASSASSQTDLQPAASAPDNVK
      10      20      30      40      50      60

      70      80      90      100     110     120
m690.pep      QAESAPPSNCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNIQRL
      ||||| ||||| ||||| ||||| ||||| |||||
g690           QAESAPLXNCTGLHPAAGIGDLIQQIAEHIDSDCLFALSHNELETRFGLPGGGYDNIQRL
      70      80      90      100     110     120

      130     140     150     160     170     180
m690.pep      LFPDIRPEDPDYHQKIILAIEDLRYGKRTISRQAQNALMEQERRLREATL LLIQGSQETR
      ||||| ||||| ||||| ||||| ||||| |||||
g690           LFPDIRPEDPDYHQKIMLAIEDLRYGTRTISRQAQDAIMEQERRLREATLMLTQGSQKTR
      130     140     150     160     170     180

      190     200     210     220     230     240
m690.pep      GQGEEPKRTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGYLKIHGEMLENQSLFRLSNR
      ||||| ||||| ||||| ||||| ||||| |||||
g690           GQGEEPKRARYFEVSATSAYLNRHNNGLGGNFQYIGQLPGYLMKHGEMLENQSLFRLSNR
      190     200     210     220     230     240

      250     260     270     279
m690.pep      ERNPDKPFLLDIHFDENGKITRIVVYEKNIYFNPNTGRIX
      ||||| ||||| ||||| ||||| ||||| |||||
g690           ERNPDKPFLLDIHFDENGKITRIVVYEKNIY
      250     260     270

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2301>

```

a690.seq
  1 ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTGCCG CAATGATGCT
 51 GACCGCGTGT TCCCGGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTTC GTCCACGGCA TCCGCGGCTT CGTCTTCGCG GCCCAAACCC
151 GATTTGCAAC CGGCCGCATC CGCCCTGAT AACGTCAAGC AGGCAGAAAG
201 CGTGCCGCGC TCAAATTGCA CCGACCTGCA CCGCGCCACC GGCAATTGACG
251 ATCTCATGCA GCAAATCGCC GAACACATTG ACTCGGACTG TCTGTTTGCC
301 CTTTCCCATC ACGAACTGGA AACCCGTTTC GGCTTACCCG CGCGCGGCTA
351 TGACAAACATA CAGCGGCTGC TGTTCCTCGA CATCCGCCCT GAAGATCCCG
401 ACTACCATCA GAAAATCATA CTGGCAATTG AAGACTTGCG TTACGGAAG
451 CGCACGATCA GCCGGCAGGC ACAAGATGCC TTGATGGAAC AGGAACGCCG
501 CCTCCGAGAA GCGACGCTGT TGCTGATACA GGGCAGTCAA GAAACCCGCG
551 GACAAGGCGA GGAGCCGAAA CGCACGCGTT ATTTTGAAGT TTCGGCAACC
601 CCTGCCCTATT CGAGCCGGCA CAACAACGGA CTTGGCGGCA ATTTCCAATA
651 CATCGGCCAA TTGCCCGGCT ATCTGAAAAT ACACGGAGAA ATGCTTGAAA

```

1111

701 ACCAATCACT CTTCCGGCTG TCCAACCGTG AACGCAATCC CGACAAACCG  
 751 TTTTTAGACA TCCATTTTGA CGAAAATGGC AAAATCACGC GTATTGTCGT  
 801 TTACGAAAAA AACATCTACT TCAATCCAAA CTTGGGGCGA AGATAA

This corresponds to the amino acid sequence <SEQ ID 2302; ORF 690.a>:

a690.pep  
 1 MKNKTSSLLL WLAAMMLTAC SPSKEDKKE NGASAASSTA SAASSSAPQT  
 51 DLQPAASAPD NVKQAESVPP SNCTDLHPAT GIDDLMQQIA EHIDSDCLFA  
 101 LSHHELETRF GLPGGGYDNI QRLFPDIRP EDPDYHQKII LAIEDLRYGK  
 151 RTISRQAQDA LMEQERRLRE ATLLLIQGSQ ETRQGQEEP RTRYFEVSAT  
 201 PAYSSRHNN LGGNFQYIGQ LPGYLKIHGE MLENQSLFRL SNRERNPDKP  
 251 FLDIHFDENG KITRIVVYEK NIYFNPNLGR R\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 690 shows 93.9% identity over a 280 aa overlap with a predicted ORF (ORF 690) from *N. meningitidis*:

m690/a690 93.9% identity in 280 aa overlap

m690.pep	10	20	30	40	50
a690	10	20	30	40	50
m690.pep	60	70	80	90	100
a690	60	70	80	90	100
m690.pep	120	130	140	150	160
a690	120	130	140	150	160
m690.pep	180	190	200	210	220
a690	180	190	200	210	220
m690.pep	240	250	260	270	279
a690	240	250	260	270	280

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2303>

g691.seq  
 1 GTGCCGCTGC CTGCTCCCTG CCGTTTTGCC AAACCTGCCG CCTCTTTTTT  
 51 AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCGGCC ACGGCTTATA  
 101 TCCCCCGGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGGCTG  
 151 ACACAGGGTC AGCACAATGA GCTGCGTAA ATCCGCGCCG CCTTCAAAAT  
 201 GCGCGGCGAC AGGGCGCGTT TGAAGGTAT GCATTCCGAA CACAGCCGCC  
 251 GCCGCTCTGT CGTCGAAATC ATTTCTTCGG ATGTTTTTAA TCGGAACGAG  
 301 GCGCGCGATT ATGTCGAAAG CCGCTACCAC TCCAGCATGG ATTTTGCGGT  
 351 GGACGAATTG GAAATCCAAC ACCGCTTCTT CCATATTCTC ACACCGCAAC  
 401 AGCAGCAAAT GTGGCTTTCT TCCTGCCTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2304; ORF 691 >:

g691.pep  
 1 VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL  
 51 TQGHNELRK IRAAFKMAGD RARLKVHSE HSRRSVVEI ISSDVFNRE  
 101 ARDYVESRYH SSMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2305>:

```
m691.seq
1  GTGCCACTGC CTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GTCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCGGAA CGATTTTCAA CCGAACTGCG ACATACGCCG ACTCGGGCTG
151 ACCCAAAGTC AGCACAATGA GCTGCGTAAA ATCCGCACCG CCTTCAAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC
251 GCCGGTCTGT CGTCGAAATC ATTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTCTT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2306; ORF 691>:

```
m691.pep
1  VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
51  TQSQHNELRK IRTAFKMAGD RARLKMVHSE HSRRRSVVEI ISSDVFNENE
101 ARDYVESRYL SGMDFAVDEL EIQHRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. gonorrhoeae*:

```
m691/g691    97.2% identity in 144 aa overlap

          10      20      30      40      50      60
m691.pep    VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFO PNCDIRRLGLTQSQHNELRK
g691         VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFO PNCDIRRLGLTQSQHNELRK
          10      20      30      40      50      60

          70      80      90     100     110     120
m691.pep    IRTAFKMAGDRARLKMVHSEHSRRRSVVEI ISSDVFNENE ARDYVESRYLSGMDFAVDEL
g691         IRTAFKMAGDRARLKMVHSEHSRRRSVVEI ISSDVFNENE ARDYVESRYLSGMDFAVDEL
          70      80      90     100     110     120

          130     140
m691.pep    EIQHRFFHILTPQQQMWLS SCLKX
g691         EIQHRFFHILTPQQQMWLS SCLKX
          130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2307>

```
a691.seq
1  GTGCCACTGC NTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCTGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGACTG
151 ACACAGGGTC AGCACAATGA ACTGCGTAAA ATCCGCACCG CCTTCAAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC
251 GTCGGTCTGT CGTCGAAATC ATTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTCTT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2308; ORF 691.a>:

```
a691.pep
1  VPLXAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPLNDFQ PNCDIRRLGL
51  TQSQHNELRK IRTAFKMAGD RARLKMVHSE HSRRRSVVEI ISSDVFNENE
101 ARDYVESRYL SGMDFAVDEL EIQHRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

1113

Homology with a predicted ORF from *N. meningitidis*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. meningitidis*:

m691/a691 97.2% identity in 144 aa overlap

	10	20	30	40	50	60
m691.pep	VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPND	FQPNCDIRRLGLTQSQHNELRK				
a691	VPLXAPCRFAKPAASFLSMALLSCQLSHAATAYIPLND	FQPNCDIRRLGLTQSQHNELRK				
	10	20	30	40	50	60
m691.pep	IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFN	RNEARDYVESRYLSGMDFAVDEL				
a691	IRAAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFN	RNEARDYVESRYLSGMDFAVDEL				
	70	80	90	100	110	120
m691.pep	IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFN	RNEARDYVESRYLSGMDFAVDEL				
a691	IRAAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFN	RNEARDYVESRYLSGMDFAVDEL				
	70	80	90	100	110	120
m691.pep	EIQHRFFHILTPQQQQMWLSSCLKX					
a691	EIQHRFFHILTPQQQQMWLSSCLKX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2309>

g692.seq

```

1  GTATCGCACA CACGCTGTCTG CTGTTCCGGAA TCGAtacGCC GGATTTGGCG
51  GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATGCGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGT ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTgacGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGCTCT TGGAAACAGG CTTCGGTCAG CTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTGCGCGGC
401 AGTTGTGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTTTCCGC
451 GATGTCGGCT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTTTACG ATCACCAGG CGCGTGCGAA GTTGGAcggG
551 TcgttGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATT
601 CAGTTTGCCC GGATACAGTC CCAAAGGCGC GGTGCGCACT TGGAAAGCCTT
651 CGGTGATGTC CAGGTTGTGT TCTTTTTTGA AATCGTCAAG ATAGGGTTTG
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCCGCCAATG CCAGATTCCG
751 CGGCACATAG TcggTAAATT cgaccaatTT gacgGTGTAg cCTTTTTTCT
801 CCAGCTCgGc tTGGATTGTG TCTTTGACCA TATcgccgaa gtcgcccacg
851 gTCGTGCCGA agacgaTTTC TTTTTTCGcC GcgCGTTAT CGGCAGAAGG
901 GCGGCGGgca gaggctgcGG GCGCGCTGTC TTTTtgaccG ccgCAGGCTG
951 CGAGGATGAG CGCGAGtgcg gcggcgga aa ggGTTTTGAA GAAGGTTTTc
1001 atATTTTCTc ctga

```

This corresponds to the amino acid sequence <SEQ ID 2310; ORF 692>:

g692.pep

```

1  VSHTRCRCSE SIRRIWRNGR EWRIKGQKCR LNTDAVQTAS FYTTALFGCA
51  FIPCGRVFVA LEAFVRVGF E RVGVI GLGYV FKPLAVFVGG FDGRPVDIGK
101 ARLLEQGFQ LHAAYGVVA VDDGKIHVGA AARQLCGFKL DDFDV FQVFR
151 DVGFQCGQRI DAVFEFDPTQ FVQHHQGACE VGRVVRGYG AAVDFDFQRF
201 QFARIQSQR GRHLEGFQDV QVFFFEIVK IGFVLEDVDV QLALRQCQIR
251 AHIVGKFQDF DGAFFFLQLG LDFFDHTIAE VAHGRAEDDF FFRAVIGRIR
301 GGRGCGGRAV FLTAAGCEDE RECGGKGFE EGFHIFS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2311>:

m692.seq

```

1  GTGTTGCACA CGCTTTGTCTG CTGTTCCGGAA TCGATACGCC GGATTCGGCG
51  GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACAGTTCA GCGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGAAACAGG CTTCGGTCAG CTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC

```

1114

```

401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTCCTCGG
451 GATGTCCGCT TTGGATGCGG TCAACGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTCGAGC ATCACCAGA CGCGGCGGAA GTTGACGGG
551 TCGTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATT
601 CAGCTTGCCC GGGTACAGTC CCAAAGGCGC GGTCCGCACT TGAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGGTTTG
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCCG
751 GCGTACATAG TCGGTAAACT CGACCAGTT GACGGTGTAG CCTTTTTTCT
801 CCAGCTCGGC TTGGATTGTG TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTC TTTTTCGCC GCGCCGTTGT CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGGCG CGCTGCTTT TTGACGCGC CAGGCGGCGA
951 GGATGAGCGC GAGTGCGGCG GCGGAAAGG TTTGAAGAA GGTTTTCATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2312; ORF 692>:

```

m692.pep
1  VLHTLCRCSE SIRRIRNRG EWRIKGQKCR LNTDTVQTAS FYTTALFGCA
51  FIPCGRGFVA LEAFVRVGF E RVGVIGLYV FKPLAVFVGG FDGRPVDIGK
101 ARFLEQGFQ LHAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVQVLG
151 DVRFGCGQRI DAVFEFDPQ FVEHHQDAGE VGRVVGGRYG AAVDFFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251 AYIVGKLDQF DGAFFLQLG LDFFDHIAE VADGRAEDDF FFRAVVG
301 RSGCGGRAV LTAAGGEDER ECGGKGFE FGHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 692 shows 91.1% identity over a 338 aa overlap with a predicted ORF (ORF 692) from *N. gonorrhoeae*:

m692/g692 91.1% identity in 338 aa overlap

	10	20	30	40	50	60
m692.pep	VLHTLCRCSESIRRIRNRGREWRIKGQKRLNTDTVQTASFYTTALFGCAFI PCGRGFVA					
g692	VSHTRCRCSESIRRIWRNGREWRIKGQKRLNTDAVQTASFYTTALFGCAFI PCGRVFVA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m692.pep	LEAFVRVGFERVGVIGLYVFKPLAVFVGGFDGRPVDIGKARFLEQGFQ LHAAYGVVA					
g692	LEAFVRVGFERVGVIGLYVFKPLAVFVGGFDGRPVDIGKARLEQGFQ LHAAYGVVA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m692.pep	VDDGKIHVGAATRQLRGFKLDDFDVQVLGDVRFVGGCGQRIDAVFEFDPQFVEHHQDAGE					
g692	VDDGKIHVGAARQLCGFKLDDFDVQVFRDVGFVGGCGQRIDAVFEFDPQFVQHHQDAGE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m692.pep	VGRVVGGRYGAAVDFDFQRFQLARVQSQRGRHLEDFGDVQIVFFFEVVKIGFVLEDVDV					
g692	VGRVVGGRYGAAVDFDFQRFQFARIQSQRGRHLEDFGDVQVVFVEIVKIGFVLEDVDV					
	190	200	210	220	230	240
	250	260	270	280	290	
m692.pep	QLALSQCQIRAYIVGKLDQFDGVAFFLQLGLDLFFDHIAEVADGRAEDDFFFRRAVVG--					
g692	QLALRQCQIRAHIVGKFDQFDGVAFFLQLGLDLFFDHIAEVAHGRAEDDFFFRRAVIGRR					
	250	260	270	280	290	300
	300	310	320	330		
m692.pep	GGRSGCGGRAVFLTAAGGEDERECCGGKGFEFGFHFISX					
g692	GGGRGCG-RAVFLTAAGCEDERECCGGKGFEFGFHFISX					
	310	320	330			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2313>

```

a692.seq
1  GTGTTGCACA CGCTTTGTCG CTGTTCCGAA TCGATACGCC GGATTTCGCG

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1115

```

51 GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGAACAGGG CTTGCGTCAG CTTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC
401 AGTTGCGCGG CTTCAAGCTC GACGATTTG ATGTTTTTCA GGTTTTCGGC
451 AATGTCCGCT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTCGAGC ATCACCAGA CGCGGCGCAA GTTGACGCGG
551 TCGTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATT
601 CAGCTTGCCC GGGTACAGTC CCAAAGGCGC GGTGCGCACT TGGGAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGGTTTG
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTTCG
751 GCGCACATAG TCGGTAAACT CGACCAGTTT GACGGTGTAG CCTTTTTTCT
801 CCAGCTCGGG TTGGATTGTG TCTTTGACCA TATCGCCGAA GTCGCGGACG
851 GTCGTGCCGA AGACGATTTC TTTTTCGCC GCGCGGTTGT CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGGCG CGCTATCTTT TTGACGCGC CAGGCGGCGA
951 GGATGAGCGC GAGTGCGGCG GCGGAAAGG TTTTGAAGAA GGTTTTCATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2314; ORF 692.a>:

**a692.pep**

```

1 VLHTLCRCSE SIRRIIRNGR EWRIKQKCR LNTDTVQTAS FYTTALFGCA
51 FIPCGRGFVA LEAFVRVGF E RVGVIGLVY FKPLAVFVGG FDGRFPVDIGK
101 ARFLEQGFQ LHAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVVFQVFG
151 NVRFGCGQRI DAVEFDPTQ FVEHHQDAGE VGRVVRGYYG AAVDFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251 AHIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRRAVVGGG
301 RSGCGGRAIF LTAAGGEDER ECGGKGFE E GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 692 shows 98.8% identity over a 336 aa overlap with a predicted ORF (ORF 692) from *N. meningitidis*:

**m692/a692** 98.8% identity in 336 aa overlap

	10	20	30	40	50	60
m692.pep	VLHTLCRCSE	SIRRIIRNGR	EWRIKQKCR	LNTDTVQTAS	FYTTALFGCA	FIPCGRGFVA
a692	VLHTLCRCSE	SIRRIIRNGR	EWRIKQKCR	LNTDTVQTAS	FYTTALFGCA	FIPCGRGFVA
	10	20	30	40	50	60
	70	80	90	100	110	120
m692.pep	LEAFVRVGF	ERVGVIGLV	YFKPLAVF	VGGFDGR	PVDIGKAR	FLEQGFQ
a692	LEAFVRVGF	ERVGVIGLV	YFKPLAVF	VGGFDGR	PVDIGKAR	FLEQGFQ
	70	80	90	100	110	120
	130	140	150	160	170	180
m692.pep	VDDGKIHV	GAATRQLR	GFKLDDF	VDVFGV	LDVRF	CGQRI
a692	VDDGKIHV	GAATRQLR	GFKLDDF	VDVFGV	LDVRF	CGQRI
	130	140	150	160	170	180
	190	200	210	220	230	240
m692.pep	VGRVVRG	YGA	AVDFD	FFQRF	QLARV	QSQR
a692	VGRVVRG	YGA	AVDFD	FFQRF	QLARV	QSQR
	190	200	210	220	230	240
	250	260	270	280	290	300
m692.pep	QLALSQC	QIRAYI	VGKLDQ	FDGVA	FFLQLG	LDLFF
a692	QLALSQC	QIRAYI	VGKLDQ	FDGVA	FFLQLG	LDLFF
	250	260	270	280	290	300
	310	320	330			
m692.pep	RSGCGGR	AVFLTA	AGGEDER	ECGGKG	FEEGF	HIFSX
a692	RSGCGGR	AVFLTA	AGGEDER	ECGGKG	FEEGF	HIFSX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2315>:

```

g694.seq
1   TCGGCATTTC TGTGCCCCAA ACATCCGATG CCTGCGTTAA CGCCTGCGTC
51  AACGTTTGCA CAAATCGGGT TTGGTTTCGC CCTCGCGGCG CAGCTCCTTG
101 GGCAGGACGA ACACGATGCT TTCTTCCGCG CCCCCCCTT CGCGCACGGT
151 TTCATGCCCC CATCCGCGTA TGGTTGCCAA TACTTCCCGC ACCAACACTT
201 CGGGCGCGGA CGGCGCTGCC GTTACGCCGA CTTTGCTTTT GCCTTCAAAC
251 CACGTGCGTT GcaggTAGGA CGCGTTGTCC ACCATATACG CATCGATTCC
301 GCGCGATGCC GCCACTTCGC GCAGGCGGTT GCTGTTGGAC GAATTGGGCG
351 AACCGACCAC AATCACGATG TCGCACTGTT CCGCCAGCTC TTTGACGGCG
401 GTTTGCCGGT TGGTCGTCGC ATAGCAGATG TCTTCTTGT GCGGATTGCG
451 GATATTGGGG AAACGCGCGT TCAGCGCGGC GATGATGTCT TTGGTTTCAT
501 CGACCGAGAG CGTGGTTTGG CTGACATAGG CGAGTTTGTG GGGGTTTCTG
551 ACTTCGAGTT TTGCCACATC TCCGACCGTT TCGACCAAAA GCATTTTGCC
601 CGGTGCAAGC TGCCCCATCG TGCTTCGAC CTCGGCGTGC CCCTTATGCC
651 CGATCATGAT GATTTCAAG TCTTGGGCAT CCAAGTCGGC GACTTCCTTA
701 TGCACTTTCC TCACAGCGG GCAAGTCGCA TCAAATACCC GGAACCGCG
751 CTCCGCCGCT TCTGCTGCA CCGCCTTCGA TACGCCGTGT GCCGAATAAA
801 CCAGTGTGCG GCCCGGCGGC ACTTCCGCCA AGTCTTCGAT AAACACCGCG
851 CCTTTTTCGC GCAGGTTGTC CACGACGAAT TTGTTGTGGA CGACTTCGTG
901 GCGCACATAA ACCGGCGCGC CGAATTCTTC CAAAGCACGT TCGACAATAC
951 TGATTGCCCG ATCCACACCG GCGCAGAAGC CGCGCGGATT GGCAAGGATG
1001 ATGGTTTTTC CGTTCATAAG TTTTGCATTC CGTGTTCAGA CGGCATTAC
1051 GTTTTTTTGC TNNATCTTG CGATGGACGA TATTGTCAAG CACCGCCAAC
1101 ACCGCACCGA CGCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2316; ORF 694 >:

```

g694.pep (partial)
1   SAFVLPKHPM PALTPASTFA QIGFGFALAA QLLGQDEHDA FFRAPPPFAHG
51  FMPPSAYGCO YFPHQHFGRG RACRYADFAF AFKPRALQVG RVVHHIRIDS
101 ARCRHFAQAV AVGRIGRTDH NHDVALFRQL FDGGLPVGRR IADVFLVRIA
151 DIGETRVQRG DDVFGFIDRE RGLADIGEFV GVSDFEFCHI SDRFDQKHFA
201 RCKLPHRAFED LGVPLMPDHD DFTVLGIQSG DFLMHFRHQR ASRIKYPETA
251 LRRFLLHRLR YAVCRINQCR ARRHFRQVED KHRAFFAQVV HDEFVVDDEV
301 AHNRRRAEFF QSTFDNTDCP IHTGAEEAARI GKDDGFSVHK FCIPCSDGIH
351 VFLLXLCDGR YCQAPPTPHR RR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2317>:

```

m694.seq
1   TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTCA
51  GACGGCATTG GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
151 CACAATGCTT TCTTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTGCCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCCTGCGG TTACGCCGAC TTTGTTTTTG CCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCACCTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCACGATGT CGCACTGTTC TGCCAACCTT TTGACGGCGG TTTGCCGGTT
451 GGTGCTGCGA TAGCAGATAT CTTCTTTGTG CGGATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTG GGGTTTCTGA CTTGAGATT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GCGCAAGCT
651 GCCCATCGT TCCTTCGACC TCGACGTGCC CTTATGCCC GATCATGATG
701 ATTTACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACGAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGGCGGGA CTCGCCCAA GTCTTCAATA AACACCGCAC CTTTTTCAG
901 CAGGTTGTCC ACGACGAAT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACCTCTCC AAAGCACGTT CGACAATACT GATT GCCCGA
1001 TCCACACCA GCGAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1051 GTTCATAAGC CCGGTATTTT GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGTCCAAC ACCGCCAACA CCGCACCGAC
1151 GCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2318; ORF 694>:

```

m694.pep
1   LVSASGTRQK CRLKPVQTAF VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDVALF CQLFDGGLPV

```

1117

```

151 GRRADIIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPKR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VENKHRTFFT
301 QVVHDEFVFN DVAHINRRA ELFQSTFDNT DCPHTSAEA ARIGKDDGFL
351 VHKGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 86.8% identity over a 372 aa overlap with a predicted ORF (ORF 694) from *N. gonorrhoeae*:

m694/g694 86.8% identity in 372 aa overlap

```

m694.pep      10      20      30      40      50
LVSASGTRQKRLKPVQTAFVLPKHS---TPASTFAQIGFGFALAAQLFGQDEHNAFFR
g694          10      20      30      40
SAFVLPKHMPALTPASTFAQIGFGFALAAQLFGQDEHDAFFR

m694.pep      60      70      80      90     100     110
TLFAYGFGVPPSAYGCQYFPHQHFGGRGRACRYADVFALKPCALQVACIIHHIRIDSARC
g694          50      60      70      80      90     100
APPFAGFMPPSAYGCQYFPHQHFGGRGRACRYADFAFAFKPRALQVGRVHHIRIDSARC

m694.pep     120     130     140     150     160     170
RHFAQAVAVGRIGRTDHNHDFALFCQLFDGGLPVGRRRIADIFLVRIADIGETRVQRGDDV
g694         110     120     130     140     150     160
RHFAQAVAVGRIGRTDHNHDFALFRQLFDGGLPVGRRRIADVFLVRIADIGETRVQRGDDV

m694.pep     180     190     200     210     220     230
FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPKRSFDLDVPLMPDHDDFT
g694         170     180     190     200     210     220
FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARCKLPKRAFDLGVPLMPDHDDFT

m694.pep     240     250     260     270     280     290
VLGIQSGDFLMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHR
g694         230     240     250     260     270     280
VLGIQSGDFLMHFRHQRASRIKYPETALRRFLHRLRYAVCRINQCRARRHFRQVFDKHR

m694.pep     300     310     320     330     340     350
TFFTQVVHDEFVFNDFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGI
g694         290     300     310     320     330     340
AFFAQVVHDEFVVDVVAHINRRAEFFQSTFDNTDCPIHTGAEAARIGKDDGFSVHKFCI

m694.pep     360     370     380
SFSDDGINIFLLGFYGGRCCTPPTPHRRRX
g694         350     360     370
PCSDGIHVFLXXLCDGRYCAFPPTPHRRRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2319>:

```

a694.seq
1   TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTCA
51  GACGGCATTG GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGCAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGGCG AACTCTTTGG GCAGGACGAA
151 CACAATGCTT TCTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTGGCCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCCTGCGG TTACGCGGAC TTTGTTTTTG CCCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCACTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCAGCATGT CGCACTGTTC TGCCAACCTT TTAGCGGCGG TTTGCCGGTT
451 GGTCGTGCGA TAGCAGATAT CTTCTTGTG CCGATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTG GGGTTTCTGA CTTGAGTTT
601 TGCCACATCT CCGACCGTT CGACCAAAAG CATTTGCCC GCGCAAGCT
651 GCCCCATCGT TCCTTCGACC TCGACGTGCC CTTATGCCC GATCATGATG

```



1118

```

701 ATTTACACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACCAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGC
851 CCCGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTTGTCC ACGACGAAT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACTCTTCC AAAGCACGTT CGACAATACT GATTGCCCGA
1001 TCCACACCAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1051 GTTCATAAGC CCGGTATTTC GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGTCACAC ACCGCCAACA CCGCACCGAC
1151 GCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2320; ORF 694.a>:

a694.pep

```

1  LVSASGTRQK CRLKPQTAF VLPKHSTPAS TFAQIGFGFA LAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDVALF CQLFDGGLPV
151 GRIADIIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPHR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRVAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVFN DFVAHINRRA ELFQSTFDNT DCPIHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 694 shows 100% identity over a 385 aa overlap with a predicted ORF (ORF 694) from *N. meningitidis*:

m694/a694 100.0% identity in 385 aa overlap

m694.pep	10	20	30	40	50	60
a694	10	20	30	40	50	60
m694.pep	70	80	90	100	110	120
a694	70	80	90	100	110	120
m694.pep	130	140	150	160	170	180
a694	130	140	150	160	170	180
m694.pep	190	200	210	220	230	240
a694	190	200	210	220	230	240
m694.pep	250	260	270	280	290	300
a694	250	260	270	280	290	300
m694.pep	310	320	330	340	350	360
a694	310	320	330	340	350	360
m694.pep	370	380				
a694	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2321>:

```
g695.seq
1   TTGCCTCAAA CTCGTCCGGC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTTGAACGG AAGGGTGATG CGCGAAGCGG CTTTGTATGC GCCGCCCAGT
101 GTCAAAATTC TCAAAGATTT CAATCAAAAC CTGCCGAACG ATACGCGGAT
151 TGTCCCCTATC ACCCTGCCCG TCGGCGACGG TTGACCCTG CTCTGAAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTAT CATTTGGCTG TCTGTGTCTG
251 CCTCCTGTGC TTCCGTTTCA CCGTTCGGG AGGCGAGCCG AACCGAAATG
301 CCGACACAGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCCACTCT
351 GCAAGACCGT TTGGACTATC TGGAAAGCAA AATCGTCCGG CTGTCGAACG
401 AAGTGGAAAT GTTAAACGGG AAAGTCAAAG CATTGGAGCA TACGAAAATA
451 CACCCTTCCG GCAGGACATA CGTCCAAAAA CTCGACGACC GCAAATTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACCGTCG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TCAAAACGGC
601 AGGTTTTCTG CCGCAGCCGC CTGTGTGAAG GGGCGGACG GCGGAGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGGAA CTGTGAATCT GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCGAA GTCATATCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTACGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2322; ORF 695>:

```
g695.pep
1   LPQTRPARRH HRHRQYFVER KGDARSGF*C AAQCQNSQRF QSKPAERYAD
51  CPHHPARRRR FDPASEKIMK TKLPLFIIWL SVSASCASVL PVEGSRTEM
101 PTQENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVEMLNG KVKALEHTKI
151 HPSGRYVQK LDDRKLKEHY LNTEGGSASA HTVETAQNLV NQALKHYQNG
201 RFSAAAALLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE VIFKIGECQY RLQQKDIARA TWRSLIQTYP GSPAACKRAAA
301 AVRKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2323>:

```
m695.seq
1   TTGCCTCAAA CTCGTCCGTC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGCTGAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
101 GTCGGCATCC TCAAAGATTT CAATCAAAAC CTGCCGAACG ACCCGCGCAT
151 CGTCCCCTATC ACCCTGCCCG TCGGCGACGG CTTGACCCTG CTCTGAAAA
201 AATAATGAAG ATCAAATTAC CGCTTTTAT CATTTGGCTG TCTGTGTCCG
251 CCTCCTGTGC TTCCGTTTCA CCGTTCGGG CAGGCAGCCA AACCGAAATG
301 TCGACACGGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCGACCTT
351 GCAAGACCGT TTGGACTATC TGGAAAGCAA AATCGTCCGG CTGTCGAACG
401 AAGTGGAAAC CTTAAACGGC AAAGTCAAAG CACTGGAACA CGCAAAAACA
451 CATTCTTCCG GCAGGGCATA CGTCCAAAAA CTCGACGACC GCAAGTTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACTGTCTG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TAAAAGCGGC
601 AAGTTTTCTG CCGCTGCCTC CTGTGTGAAA GCGCGGACG GAGGCGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGCAA CTGCGAATCC GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCTGAA GCCATGTTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTGCGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2324; ORF 695>:

```
m695.pep
1   LPQTRPSRRH HRHRQYFAER KGDARSGFRC AAQRRHPQRF QSKPAERPAH
51  RPHHPARRRR LDPASEKIMK IKLPLFIIWL SVSASCASVS PVPAGSQTEM
101 STRENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVETLNG KVKALEHAKT
151 HSSGRAYVQK LDDRKLKEHY LNTEGGSASA HTVETAQNLV NQALKHYKSG
201 KFSAAASLLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE AMFKIGECQY RLQQKDIARA TWRSLIQTYP GSPAACKRAAA
301 AVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 90.8% identity over a 305 aa overlap with a predicted ORF (ORF 695) from *N. gonorrhoeae*:

1120

m695/g695 90.8% identity in 305 aa overlap

	10	20	30	40	50	60
m695.pep	LPQTRPSRRHRRHQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAHRPHHPARRRR					
g695	LPQTRPARRRHRRHQYFVERKGDARSGFXCAAQCQNSQRFQSKPAERYADCPHHPARRRR					
	10	20	30	40	50	60
m695.pep	LDPASEKIMKIKLPLFIIWLSVSASCASVSPVPAGSQTEMSTRENASDGIPYPVPTLQDR					
g695	FDPASEKIMKTKLPLFIIWLSVSASCASVLPVPEGSRTemptQENASDGIPYPVPTLQDR					
	70	80	90	100	110	120
m695.pep	LDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLD DRKLKEHYLNTEGGSASA					
g695	LDYLEGKIVRLSNEVEMLNGKVKALEHTKIHPSGRITYVQKLD DRKLKEHYLNTEGGSASA					
	130	140	150	160	170	180
m695.pep	LDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLD DRKLKEHYLNTEGGSASA					
g695	LDYLEGKIVRLSNEVEMLNGKVKALEHTKIHPSGRITYVQKLD DRKLKEHYLNTEGGSASA					
	130	140	150	160	170	180
m695.pep	HTVETAQNLYNQALKHYKSGKFSAAASLLKGADGGDGGSI AQRSMYLLQLQSRARMGNCS					
g695	HTVETAQNLYNQALKHYQNGRFSAAALLKGADGGDGGSI AQRSMYLLQLQSRARMGNCS					
	190	200	210	220	230	240
m695.pep	HTVETAQNLYNQALKHYKSGKFSAAASLLKGADGGDGGSI AQRSMYLLQLQSRARMGNCS					
g695	HTVETAQNLYNQALKHYQNGRFSAAALLKGADGGDGGSI AQRSMYLLQLQSRARMGNCS					
	190	200	210	220	230	240
m695.pep	VIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRS LIQTYPGSPA AKRAAA					
g695	VIEIGGRYANRFKDSPTAPEVIFKIGECQYRLQKDIARATWRS LIQTYPGSPA AKRAAA					
	250	260	270	280	290	300
m695.pep	VIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRS LIQTYPGSPA AKRAAA					
g695	VIEIGGRYANRFKDSPTAPEVIFKIGECQYRLQKDIARATWRS LIQTYPGSPA AKRAAA					
	250	260	270	280	290	300
m695.pep	AVRKRKX					
g695	AVRKRKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2325>:

a695.seq

1	TTGCCTCAAG	CTTGTCGGCG	AAGGCGGCAT	CATTGCCATC	GACAATATT
51	TGTTGAACGG	AAGGGTGATG	CGCGAAGCGG	CTTCCGATGC	GCCGCCAGC
101	GTCGGCATCC	TCAAAGATTT	TAATCAAAC	CTGCCGAACG	ATACGCGGAT
151	TGTCCCCATC	ACCCTGCCCG	TCGGCGACGG	TTTGACCCTG	CTTCTGAAAA
201	AATAATGAAG	ACCAAATTAC	CGCTTTTAT	CATTGGCTG	TCCGTATCCG
251	CCGCCTGTT	TTCCCTGTT	TCCCGCAATA	TTGAGATAT	GCGGCTCGAA
301	CCGCAGGCAG	AGGCAGGTAG	TTCCGACGCT	ATTCCCTATC	CCGTTCAC
351	TCTGCAAGAC	CGTTTGATT	ATCTGGAAGG	CACACTCGTC	CGCTGTGCGA
401	ACGAAGTGA	AACCTTAAAC	GGCAAAGTCA	AAGCACTGGA	GCATGCGAAA
451	ACACACCCCT	CCAGCAGGCG	ATACGTCCAA	AAACTCGACG	ACCGCAAGTT
501	GAAAGAGCAT	TACCTCAATA	CCGAAGGCGG	CAGCGCATCC	GCACATACCG
551	TGGAAACCGC	ACAAAACCTC	TACAATCAGG	CACTCAAACA	CTATAAAGC
601	GGCAGGTTT	CTGCCGCTGC	CTCCCTGTTG	AAAGGCGCGG	ACGGAGGCGA
651	CGCGGCGCAG	ATCGCGCAAC	GCAGTATGTA	CCTGTTGCTG	CAAAGCAGGG
701	CGCGTATGGG	CAACTGCGAA	TCCGTCATCG	AAATCGGAGG	GCCTTACGCC
751	AACCGTTTCA	AAGACAGCCC	AACCGCGCCT	GAAGCCATGT	TCAAATCGG
801	CGAATGCCAA	TACAGGCTTC	AGCAAAAAGA	CATTGCAAGG	GCGACTTGCC
851	GCAGCCTGAT	ACAGACCTAT	CCGCGCAGCC	CGCGGCGAAA	ACGCGCCGCC
901	GCAGCCGTGC	GCAACGATA	G		

This corresponds to the amino acid sequence <SEQ ID 2326; ORF 695.a>:

a695.pep

1	LPQACPARRH	HCHRYFVER	KGDARSGFRC	AAQRRHPQRF	*SKPAERYAD
51	CPHHPARRRR	FDPASEKIMK	TKLPLFIIWL	SVSAACSSPV	SRNIQDMRLE
101	PQAEAGSSDA	IPYPVPTLQD	RLDYLEGLTV	RLSNEVETLN	GKVKALEHAK
151	THPSSRAYVQ	KLDDRKLKEH	YLNTEGGSAS	AHTVETAQNL	YNQALKHYKS
201	GRFSAAASLL	KGADGGDGGG	IAQRSMYLLL	QSRARMGNCE	SVIEIGGRYA
251	NRFKDSPTAP	EAMFKIGECQ	YRLQKQDIAR	ATWRS LIQTY	PGSPA AKRAA
301	AAVRKR*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 695 shows 88.3% identity over a 308 aa overlap with a predicted ORF (ORF 695) from *N. meningitidis*:

m695/a695 88.3% identity in 308 aa overlap

```

              10      20      30      40      50      60
m695.pep    LPQTRPSRRHRRHQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAHRPHHPARRRR
              |||: ||:|||| |||||:||||| ||||| ||||| ||||| |||||
a695        LPQACPARRHCHRRQYFVERKGDARSGFRCAAQRRHPQRFQSKPAERYADCPHHPARRRR
              10      20      30      40      50      60

              70      80      90      100     110
m695.pep    LDPASEKIMKIKLPLFIWLSVSASCASVSPVPAGSQT--EMSTRENASDGIPYPVPTL
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a695        FDPASEKIMKTKLPLFIWLSVSAACSS--PVSRNIQDMRLEPQAEAGSSDAIPYPVPTL
              70      80      90      100     110

              120     130     140     150     160     170
m695.pep    QDRLDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLLDRKLKEHYLNTEGGS
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a695        QDRLDYLEGLTVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLLDRKLKEHYLNTEGGS
              120     130     140     150     160     170

              180     190     200     210     220     230
m695.pep    ASAHTVETAQNLYNQALKHYKSGKFSAAASLLKGADGGDGGGIAQRSMYLLLQSRARMGN
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a695        ASAHTVETAQNLYNQALKHYKSGRFSAAASLLKGADGGDGGGIAQRSMYLLLQSRARMGN
              180     190     200     210     220     230

              240     250     260     270     280     290
m695.pep    CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAAGR
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a695        CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAAGR
              240     250     260     270     280     290

              300
m695.pep    AAAAVRKRKX
              |||||
a695        AAAAVRKRKX
              300

```

The following partial DNA sequence was identified in *N. gonorrhoeae*

g696.seq: not found

This corresponds to the amino acid sequence < ORF 696.ng>:

g696.pep: not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2327>:

```

m696.seq
1   TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTCATT TTGTCTGCCG CTCCTGAGT CGCGTCGGCA
101 GCTTTGTTCA AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTTGA
201 CTTGGTCTTT CGCTTCTTCG ACGGCAGAAG CGGCAGACTC GGCGGCAGAA
251 GCCGCAGTGT CTTTAACATC GGAATCAACG GCTTGAACCG CTCCTTAAC
301 CTCCTGTTTG GCTTCTTGCG AACAAGCTGC CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2328; ORF 696>:

```

m696.pep
1   LGCRQAASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRFNL
101 LLFGFLRTSC QGSRHHCNQ *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2329>:

a696.seq

1122

```

1  TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTCATT TTGTCTGCCG CTTCTAGAGT CGCGTCGGCA
101 GCTTTGTTCA AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTTGA
201 CTTGGTCTTT CGCTTCTTCG ACGGCAGAAG CGGCAGACTC GCGGCAGAA
251 GCCGCAAGTG CTTTAACATC GGAATCAACG GCTTGAACCG CTTCTTAAC
301 CTCCTGTTTG GCTTCTTTCG AACAAGCTGC CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2330; ORF 696.a>:

a696.pep

```

1  LGCRQAASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRVSFNI GLNGLNRFLN
101 LLFGFLRTSC QGSRHHCGNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 696 shows 100.0% identity over a 120 aa overlap with a predicted ORF (ORF 696.a) from *N. meningitidis*:

m696/a696 100.0% identity in 120 aa overlap

```

              10      20      30      40      50      60
m696.pep    LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFSYSFLGTCLC
              |||||
a696         LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFSYSFLGTCLC
              10      20      30      40      50      60

              70      80      90      100     110     120
m696.pep    ISRSIFDLVFRFFDGRSGRLGGRSRVSFNI GLNGLNRFLNLLFGFLRTSCQGSRHHCGNQ
              |||||
a696         ISRSIFDLVFRFFDGRSGRLGGRSRVSFNI GLNGLNRFLNLLFGFLRTSCQGSRHHCGNQ
              70      80      90      100     110     120

```

```

m696.pep    X
            |
a696         X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2331>:

g700.seq

```

1  ATGAGCAGCC TGATGACGTT GTTTTCGGTA TTGGTACCGA TGTTTGCCGG
51  ATTTTTTATC CGTGTTCCTCA AGCCTTACCT GCCCCTTCG GACAAGGTGC
101 TGTCGGTTTT GGTGTATGCC GTGCTGCTGC TGATCGGCGT ATCGTTGTCTG
151 CGCGTGGAGG ATTTGGGTTT GCGGTTGGGC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TAGGGGCGAA CCTGCTTGCC TTGGCAGTGT
251 TGGGAAAGTT GTCCCCGTGG CGGATAGGGG GAAAAGGGAA GGGCGTTTCG
301 GTCGGCGTGT CGGGCAGTGT GAGGCAGCTC GGATGCGTAC TGCTCGGTTT
351 TGTGTCCGGC AAATTGATGT GCGATATTTG GATGCCGTCT GAAAACGCGG
401 GTATGTACTG CCTGATGCTG CTGGTGTTCC TCATCGGCGT ACAGCTCAAA
451 AGTAGCGGCG TATCGTTGCG GCAGGTTTTG CTTAACCGGC GGGGCATCCG
501 GCTGTGCGTT TGGTTTATAT TGTCATCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGATGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC
601 GGCCTTCGGT GGTATTCCCT CTCGGGTTTG GTAATGACCG AGGCTTACGG
651 GCGGGTATGG GGCAGCATCA TGCTGCTGAA CGATTGGCA CGAGAGCTGT
701 TTGCACTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTCC GGATGCGGCG
751 GTGGGGTCTG GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTAATTCA
801 GGGTGCGGGC GGTTTGGAAG TCGTGCCGGT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCCCGG TTTCTGATGG TGGTGTTTTC CACGCTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2332; ORF 700>:

g700.pep

```

1  MSSLMTLFSV LVPMFAGFFI RVPKPYLPAS DKVLSVLVYA VLLLIGVSLS
51  RVEDLGSRLG DMALTVLWLF VCTVGANLLA LAVLGKLSPW RIGGKGKGV
101 VGVSGSVRQL GCVLLGFVSG KLMCDIWMP ENAGMYCLML LVFLIGVQLK
151 SSGVSLRQVL LNRRGIRLSV WFILSSLSGG LFAASADGV SWTKGLAMAS

```

m700.seq

m700.pap

m700/g700

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
g700	MSSLMTLFSVLVPMFAGFFIRVPKPYLPASDKVLSVLVYAVLLLIGVSLSRVEDLGSRLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLPFWRIKGGKGGVSVGVSQGLGCVLLGFAGF					
g700	DMALTVLWLFVCTVGANLLALAVLGKLSPWRIKGGKGGVSVGVSQGLGCVLLGFVSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGSVSLRQVLNRRGIRLSVWFMLSSLSGG					
g700	KLMCDIWMPSENAGMYCLMLLVFLIGVQLKSSGSVSLRQVLNRRGIRLSVWFILSSLSGG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYSLSGLVMTAYGAVWGSIMLLNDLARELFALAFIP					
g700	LLFAASADGVSWTKGLAMASGFGWYSLSGLVMTAYGAVWGSIMLLNDLARELFALAFIP					

		190	200	210	220	230	240		
		250	260	270	280	290	300		
m700.pep		LLMKRFPDA	AVGVGGAT	SMDFTLP	VIQGAGGLE	VVPVAVS	FGVVVNIA	AAPFLMV	VFSALG
g700		LLMKRFPDA	AVGVGGAT	SMDFTLP	VIQGAGGLE	VVPVAVS	FGVVVNIA	AAPFLMV	VFSTLG
		250	260	270	280	290	300		
m700.pep	X								
g700	X								

```
a700.seq
1 ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
51 ATTTTTTATC CGTGTCGCCA AGCCTTACCT GCCCGCTTTG GATAAGGTGC
101 TATCGGTCTT GTGGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTGTGTC
151 CGCGTGGAGG ATTTGGGTTT CCGGTTGGAC GATATGGCGT TCACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
251 TGGGAAAGTT ATTCCCGTGG CGGATAAAGG GGAAAGGGAA GGGCGTTTCG
301 GTCGGTGTGT CGGGCAGTGT GGGGCAGCTC GGATGCGTGT TGCTCGGATT
351 TGCATCCGGC AAACGTATGC GCGATATTTG GATGCCGTCT AAAAACCGCG
401 GTATGTATTG TCTGATGCTG CTGGTGCTCN TCATCGGCGT ACAGCTCAAA
451 AGCAGCGGCG TATCGTTGCG GCAGGTTTTG GTCAACCGCA GGGGTATTTCG
501 GTTGTGCGTC TGGTTTATGC TTTTCATCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCCGC AGACGGTGTG TCGTGGGTGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCTT CTCGGGTTTG GTGATGACCG AGGCTTACGG
651 CGCGGTATGG GCGAGTATCG CGCTTTTGAA CGATTTGGCA CGAGAGCTGT
701 TCGCGCTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTCC CGATGCGGCA
751 GTGGGGGTCT GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTGATTCTG
801 GGGTGCGGGC GGCTTGGAAG CCGTACCGGT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCTCCG TTTCTGATGG TGGTGTTTTT CGCTTTGGGC
901 TGA
```

a700.pep

1	MDSLMTLLSV	<u>LIPMFAGFFI</u>	RVPKPYLPAL	DKVLSVLVYA	VLLLIGVSL
51	RVEDLGSRLD	DMALTVLWLF	VTCTGANNLA	LAVLGKLPFW	RIKKGKGVGS
101	VGVSQSVGQL	CGVLLGFASG	KLMRDIWMP	ENAGMYCLML	LVLXIGVQLK
151	SSGVSLRQVL	VNRRGIRLSV	WFMLSSLSGG	LLFAASADGV	SWVKGLAMAS
201	GFGWYSLSGL	VMTEAYGAVW	GSIALLNDLA	RELFAFAFIP	LLMKRFPDAA
251	VGVGGSATSM	FTLPVIRGAG	GLEAVPVAVS	FGVVVNIAAP	FLMVVFSALG
301	*				

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMEAGFFIRVPKPYLPALDKVLSVLVYAVLLLLIGVSLSRVEDLGSRLD					
a700	MDSLMTLLSVLIPMEAGFFIRVPKPYLPALDKVLSVLVYAVLLLLIGVSLSRVEDLGSRLD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLF	PWRIKKGKGVSVGVSGSVGQLGCVLLGFAFG				
a700	DMALTVLWLFVCTVGANLLALAVLGKLF	PWRIKKGKGVSVGVSGSVGQLGCVLLGFAFG				
	70	80	90	100	110	120
	130	140	150	160	170	180
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGSVSLRQVLVNRRGIRLSVWFMLSSLSGG					
a700	KLMRDIWMPSENAGMYCLMLLVLXIGVQLKSSGSVSLRQVLVNRRGIRLSVWFMLSSLSGG					
	130	140	150	160	170	180

g701.seq

1	ATGTCCTTGGC	ACATATTCCA	AGTTGCAGGG	ATACCGACCG	CTTCGATGGC
51	ACAATCTACG	CCGCTCTTCG	CGACGATGGC	GAAAACTTGT	TTGGAGACGT
101	CGCCCGGAAG	GGGGCTCGAT	GTATGGGTGC	CGCCCAACTC	TTTCGCCGGT
151	TTCAAACGGT	TTTCGTCCAT	ATCGCACACG	ATAATTGCCG	CAGGGCTATA
201	CAGTTGGGCG	GTCAACAAGG	CGGACATACC	GACAGGGCCG	GCACCTGCGA
251	TGAATACGGT	ATCGCCGGGT	TTCACATCGC	CGTATTGCAC	GCCGATTTTCG
301	TGGGCGGTCG	GTAAAGCGTC	GCACAACAGC	AGGGCGGATT	CTTCGTTGAC
351	GTTGTCTGTC	GGCGGCACGA	GGCTGTTGTC	GGCATAA	

g701.pgp

1 MSWHIFQVAG IPTASMAQST PSSPTMAKTC LETSPEAGLM VVWAPNSFAG  
51 FKRFSISHT IMAAGLYSWA VNKADIPTGP APAMNTVSPG FTSPYCTPIS  
101 WAVGKASLNS RAISSLTLSG GGTRLLSA\*

**m701.seq**

1	ATGTCTTGGC	ACATATTCCA	TGTAGCAGGG	ATACCGACGG	CTTCGATGGC
51	GCAATCCACG	CCGTCTTCGC	CGACGATGCG	AAAGACTTGT	TTGGATACTT
101	CGCCGGGAAG	AGGGTTAATG	GTATGGGTGC	CACCCAATTG	TTTCGCCAGT
151	TTCAAACGGT	TTTCTGTCCAT	ATCGCAAACG	ATGATAGCGG	CGGGACTGTA
201	CAGTTGGGCG	GTCAACAGGG	CGGACATACC	GACAGGGCCT	GCCCCAGCGA
251	TGAATACGGT	GTCGCCGGGT	TTGACATACG	CGTATTGCAC	GCCGATTTCG
301	TGGGCGGTTCG	GCAAAGCGTC	GCTCAACAAC	AGGGCGATTT	CTTCGTTGAC
351	ATTATCGGGC	AGCGGAACGA	GGCTGTTGTC	GGCATAA	

m701.pgp

1 MSWHIFHVAG IPTASMAQST PSSPTMAKTC LDTSP EAGLM VVWAPNSFAS  
51 FKRFSISQT MMAAGLYSWA VNRAD IPTGP APAMNTVSPG LTSPYCTPIS  
101 WAVGKASLNN RAISSLT LSG SGTRLLSA\*

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

m701/g701

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASFKRFSISQT					
	:                             :         :         :					
q701	MSWHIFOVAGIPTASMAQSTPSSPTMAKTCLETSPEAGLMVWVAPNSFAGEKRFSSISHT					



1126

	10	20	30	40	50	60
	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISSLTLSG					
	:     :     :     :     :     :					
g701	IMAAGLYSWAVNKADIPTGPAPAMNTVSPGFTSPYCTPISWAVGKASLNSRAISSLTLSG					
	70	80	90	100	110	120

	129
m701.pep	SGTRLLSAX
	:
g701	GGTRLLSAX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2341>:

```
a701.seq
1  ATGTCTTGGC ACATATTCCA AGTTGCAGGG ATACCGACGG CTTCGATCGC
51  GCAGTCCACG CCGTCTTCGC CGACGATAGC GGCAACTTGC TTGCTTACAT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTTG CGCCCAACTC TTTCGCCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACA ATGATGGCGG CGGGGCTGTA
201 CAGTTGGGCG GTCGGCAAGG CGGACATACC GACAGGAGCG GCACCTGCGA
251 TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301 TGTGCGGTCG GCAAAGCGTC GCTCAACAAC AGGGCGACTT CTTCGTTGAC
351 GTTGTGCGGC AGCGGCACGA GGCTGTTGTC GGCATAA
```

This corresponds to the amino acid sequence <SEQ ID 2342; ORF 701.a>:

```
a701.pep
1  MSWHIFQVAG IPTASIAQST PSSPTIAATC LLTSPEAGLM VWVAPNSFAS
51  FKRESSISQT MMAAGLYSWA VGKADIPTGA APAMNTVSPG LTSPYCTPIS
101 CAVGKASLNN RATSSLTLSG SGTRLLSA*
```

m701/a701 92.2% identity in 128 aa overlap

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASFKRFSSISQT					
	:     :     :     :     :					
a701	MSWHIFQVAGIPTASIAQSTPSSPTIAATCLLTSPEAGLMVWVAPNSFASFKRFSSISQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISSLTLSG					
	:     :     :     :     :					
a701	MMAAGLYSWAVGKADIPTGAAPAMNTVSPGLTSPYCTPISCAVGKASLNNRATSSLTLSG					
	70	80	90	100	110	120

	129
m701.pep	SGTRLLSAX
a701	SGTRLLSAX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2343>:

```
g702.seq
1  ATGCCGTGTt ccaAAGCCAG TTGGACTTCG CCCGGAGtg cAACGCCGGG
51  AATCAGGGGA ATGCCGCTGT TGCGGCCGGC TCTGGCGAGG GATTCGTGCA
101 AACCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGAT TGGTTACCGT ACCTGCGCCG ATGATGGCGT TGGGCATTTC
201 TTTGGCAATC AGGCGGATGG CCTCGAGTCC GACGGGGGTG CGCAAGGTAA
251 TTTCGAGGGT GGGGATGCCG CCTTCGACAA GGGCGCGGGA CAAATCGACG
301 GCGGTGCTTA AGTCGTCAA t cGCCATCACA GGCACAAC TG CGCCGGCGGT
351 CAGGATTTCG cgggggggtca gttga
```

This corresponds to the amino acid sequence <SEQ ID 2344; ORF 702>:

g702.pep

```

1  MPCSKASWTS  PGVATPGIRG  MPLLRPALAR  DSCKPGLMAK  TAPASSTALS
51  CSQLVTVFAP  MMALGISLAI  RRMASPTGV  RKVISRVGMP  PSTRRADKST
101 AVLKSSIAIT  GTTAPAVRIS  RGVSV*

```

m702.seq

1	ATGCCCGTGT	CCAAAGCCAG	TTGGATTTCG	CCCGGGGTGG	CAACACCGGG
51	AATCAGGGGG	ATGCCGCTGT	TGTGGCCGGC	TTTGGCGAGG	GATTTCATGCA
101	GCCCCGGGT	GATGGCGAAA	ACCGCGCTCG	CGTCTTCGAC	GGCTTTGAGC
151	TGTTCCGGAT	TGGTTACCGT	ACCTGCGCCG	ACGATGGCGT	TGGGCACTTC
201	TTTGGCAATC	AGGCGGATGG	CATCGAGGCC	GACAGGGGTG	CGCAGGGTGA
251	TTTCGAGGGT	AGGGATGCCG	CCTTCGACAA	GGGCGTGGGA	CAAATCGATG
301	GCGGTGCTTA	AGTCGTCAAT	CGCCATTACC	GGCACAACTG	CGCCGGCGGT
351	CAAAATTTTC	CGGGGGGTCA	GTTTGACAT	TTTCGTTCTC	CGGGTGGAAAT
401	GGGGTATTTT	ATTAAGATGG	GACAGGTTGT	AG	

m702.pgp

1 MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS  
51 C~~SG~~LVTV~~PAP~~ TMALGTSLAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM  
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL\*

m702/g702

		10	20	30	40	50	60
m702.pep		MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTV	PAP				
g702		MPCSKASWTS	PGVATPGIRGMPLLR	PALARDSC	KPGLMAKTAPASSTALSCSGLVTV	PAP	
		10	20	30	40	50	60
		70	80	90	100	110	120
m702.pep		TMALGTSLAIRRMASRPTGVRRVISRVGMPPSTR	AWDKSMAVLKSSIAITGTTAPAVKIS				
g702		MMALGISLAIRRMAS	SPTGVRKVISR	VGMPSTR	ARDKSTAVLKSSIAITGTTAPAVRIS		
		70	80	90	100	110	120
		130	140				
m702.pep		RGVSLDISVLR	VEWGILLRWDR	LX			
g702		RGVSX					

a702.seq

1	ATGCCGTGTT	CCAAAGCCAG	TTGGATTTTCG	CCCGGGGTGG	CAACACCGGG
51	AATCAGGGGG	ATGCCGTGT	TGTGGCCGGC	TTTGGCGAGG	GATTCAATGCA
101	GCCCCGGGCT	GATGGCGAAA	ACCGCCGCTG	CGCTTTTCGAC	GGCTTTTGAGC
151	TGTTCCGGAT	TGTTTACCGT	ACCTGCGCCG	ACGATGGCGT	TGGCACTTTC
201	TTTGCAATC	AGGCGGATGG	CATCGAGGCC	GACAGGGGTG	CGCAGGGTGA
251	TTTCGAGGGT	AGGGATGCCG	CCTTCGACAA	GGGCGTGGGA	CAAATCGATG
301	GCGGTGCTTA	AGTCGTCAAT	CGCCATTACC	GGCAACAAGT	CGCCGGCGGT
351	CAAAATTTTCG	CGGGGGGTCA	GTTTGGACAT	TTTCGGTTCTC	CGGGTGGAAAT
401	GGGGTATTTT	ATTAAGATGG	GACAGGTTGT	AG	

a702.pcp

```

1      1  MPCSKASWIS  PGVATPGIRG  MPLLWPALAR  DSCSPGLMAK  TAPASSTALS
51     51  CSQLVTPAP  TMLGTS Lai  RRMSRPTGV  RRVISRVGMP  PSTRAWDKSM
101    101  AVLKSSIAIT  GTTAPAVKIS  RGVSLDISVL  RVEWGILLRW  DRL*

```

m702/a702 100.0% identity in 143 aa overlap

10                      20                      30                      40                      50                      60

1128

```

m702.pep      MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVPAP
a702          MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVPAP
              10      20      30      40      50      60

              70      80      90      100     110     120
m702.pep      TMALGTSLAIRRMASRPTGVRVRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
a702          TMALGTSLAIRRMASRPTGVRVRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
              70      80      90      100     110     120

              130     140
m702.pep      RGVSLDISVLRVEWGILLRWDR LX
a702          RGVSLDISVLRVEWGILLRWDR LX
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2349>:

g703.seq

```

1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCG CTGCTTGCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTTAA CCGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAGA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CACTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GTTTACGACA ATATCAGCGG TTTTATATAA
451 GGCACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCGAAAAAA GCGGTGCGCG ATTTGAAGGC GAAAAAAGGT TTTGATGCCG
551 TTTTGAAACA ATACTCGCTC AACGACCGCA CCAAACGGAC CGGCGCGCCG
601 GACGGATATG TGCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA
701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGcgaggTG
751 AAAGTGCCTT CTTTGTACGA AATGAAAGGA CAGATTGCCG GCAACCTTCA
801 GGCGGAACGG ATTGACCGTG CCGTctgTGc gcTGTgggt aaggCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2350; ORF 703>:

g703.pep

```

1  MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51  EDTPQLRQSL LENEVNTTV AQEVKRLKLD RSAEFKDALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA VYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTRKRTGAP
201 DGYVPLKDLE QGVPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNDREV
251 KVPSFDEMKG QIAGNLQAE IDRAVCALLG KANIKPAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2351>:

m703.seq

```

1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTCAA CCGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
201 TACCGTGGTC GCACAGGAAG TGAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CATTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTGCGCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAAACA ATATTCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
601 GTCGGATATG TGCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

```

1129

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA  
 751 AAAGTGCCCT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA  
 801 GCGGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA  
 851 TCAAACCTGC AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2352; ORF 703>:

m703.pep

1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA  
 51 EDTPQLRQSL LENEVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG  
 101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK  
 151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP  
 201 VGYVPLKDLE QGVPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSDREV  
 251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK\*

ORF 703 shows 98.3% identity over a 288 aa overlap with a predicted ORF (ORF703.ng) from *N. gonorrhoeae*:

m703/g703

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
g703						
	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
m703.pep	70	80	90	100	110	120
	LENEVNTVVVAQEVKRLKLDLSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
g703						
	70	80	90	100	110	120
	LENEVNTVVVAQEVKRLKLDLSAEFKDALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
m703.pep	130	140	150	160	170	180
	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
g703						
	130	140	150	160	170	180
	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPLYQAIKDLKKGEFTATPLKNGDFYG					
g703						
	190	200	210	220	230	240
	FDAVLKQYSLNDRTKRTGAPDGYVPLKDLEQGVPLYQAIKDLKKGEFTATPLKNGDFYG					
m703.pep	250	260	270	280	289	
	VYYVNSDREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
g703						
	250	260	270	280		
	VYYVNSDREVKVPSFDEMKGQIAGNLQAERIDRAVCALLGKANIKPAKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2353>:

a703.seq

1 ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG  
 51 CCTGTTTGCC CAAACGCTGG CAACCGTCAA CCGTCAGAAA ATCGACAGTT  
 101 CCGTCATTGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC  
 151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAAACG AAGTGGTCAA  
 201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CCGTCGGCAG  
 251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC  
 301 GACGACAAGA AACCGTCCCT CAAAACCGTT TGGCAGGCGG TAAAATATGG  
 351 CTGTAACGGC GAGGCATACG CGCTGCATAT CGCCAAAACC CAACCGGTTT  
 401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA  
 451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA  
 501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG  
 551 TCTTGAACA ATATTCCCTC AACGACCGTA CCAAACAGAC CCGTGCGCCG  
 601 GTCGGATATG TGCCGCTGAA AGATTGGGAA CAGGGTGTTC CGCCGCTTTA  
 651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

1130

```

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
751 AAAGTGCCTT CTTTTGATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
801 GCGGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
851 TCAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2354; ORF 703.a>:

```

a703.pep
  1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
 51 EDTPQLRQSL LENEVVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
201 VGYVPLKDL E QGVPPYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSDREV
251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

m703/a703 100.0% identity in 288 aa overlap

      10      20      30      40      50      60
m703.pep MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL
a703      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a703      MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL
      10      20      30      40      50      60

      70      80      90     100     110     120
m703.pep LENEVVNTVVVAQEVKRLKLD RSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG
a703      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a703      LENEVVNTVVVAQEVKRLKLD RSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG
      70      80      90     100     110     120

      130     140     150     160     170     180
m703.pep EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILT DKEENAKKAVADLKAKKG
a703      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a703      EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILT DKEENAKKAVADLKAKKG
      130     140     150     160     170     180

      190     200     210     220     230     240
m703.pep FDAVLKQYSLNDRTKQTGAPVGYVPLKDL EQGVPPYQAIKDLKKGEFTATPLKNGDFYG
a703      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a703      FDAVLKQYSLNDRTKQTGAPVGYVPLKDL EQGVPPYQAIKDLKKGEFTATPLKNGDFYG
      190     200     210     220     230     240

      250     260     270     280     289
m703.pep VYYVNSDREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX
a703      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a703      VYYVNSDREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX
      250     260     270     280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2355>:

```

a704.seq
  1 ATGAAAAAAA CCTGTTTCCA CTGCGGGCTG GACGTTCCCG AAAACCTGCA
 51 TCTGACCGTC CGTTACGAAA ACGAAGACCG CGAAACCTGC TGCGCCGGTT
101 GTCAGGCAGT CGCACAAAGC ATTATTGACG CGGGCTTGGG CAGTTATTAC
151 AAACAACGCA CCGCGACGCG GCAAAAAACC GAGCTGCCGC CCCAAGAAAT
201 CCTCGACCAA ATCCGCCTGT ACGACCTGCC CGAAGTCCAG TCCGACTTTG
251 TGGAACCCCA CGGCGGCACG CGCGAGGCGG TTTTAATGCT CGGCGGCATC
301 ACCTGCGCCG CCTGCGTCTG GCTGATCGAA CAGCAGCTTT TGCGTACAGA
351 CGGCATCGTC CGCATCGACC TCAATTACAG CACGCACCGC TGCCGCGTCG
401 TCTGGGACGA CGGCAAAATC CGCCTTTCCG ACATTCTGTT GAAAATCAGG
451 CAGATAGGCT ACACGCGCGC ACCCTATGAC GCGCAAAAAA TCGAAGCCGC
501 CAACCAAAAA GAACGCAAAC AATACATCGT CCGCCTCGCC GTTGCCGGGC
551 TGGGGATGAT GCAGACGATG ATGTTTCGCG TGCCGACCTA CCTTTACGGC
601 GCGGACATCG AACCCGATTT CCTGCAAATC CTCCATTGGG GCGGCTTTT
651 AATGGTGCTG CCCGTCGTAT TCTATTGCGC CGTCCCGTTT TATCAAGCG
701 CGCTGCGCGA CTTGAAAAAC CGCCGCGTCG GCATGGATAC GCCGATTACC
751 GTCGCCATCA TCATGACCTT TATCGCCGGC GTTTACAGCC TTGCGACAAA

```

```

801 TGC GGGG CAG GGGATGTATT TCGAATCCAT CGCGATGCTG CTGTTTTTCC
851 TGCTGGGCGG ACGCTTTATG GAACACATTG CCCGCCGTAA GGCAGGCGAT
901 GCGCGCGAGA GGCTGGTGAA GCTGATTCTT GCGTTTTGCC ATCATATGCC
951 CGATTACCCC GATACGCAGG AAACCTGCGA GGCAGCTGTC GTCAAATTGA
1001 AGGCGGGCGA TATCGTGCTG GTCAAACCGG GCGAAACCAT CCCCGTTGAC
1051 GGCACGGTGC TGGAAGGAAG CAGTGCCGTC AACGAATCTA TGCTGACCGG
1101 CGAGAGCCTG CCCGTCGCCA AAATGCCGTC TGAAAAAGTA ACCGCGGCA
1151 CACTCAACAC GCAAAGCCCC CTGATTATAC GCACCGACCG CACCGGCGGC
1201 GGCACGCGAC TGTCGCACAT CGTCCGCTG CTCGACCGCG CCTTAGCGCA
1251 AAAACCGCGC ACTGCCGAGT TGGCGGAACA ATACGCCCTG TCTTTTCATAT
1301 TCGGCGAACT CCTGCTTGCC GTCCCCGTCT TCATCGGCTG GACGCTGTAC
1351 GCCGACGCGC ACACCGCATT GTGGATTACC GTCGCCCTGC TGGTCAATTAC
1401 CTGCCCTGCG GCCTTATCGC TTGCCACGCC GACCGCGCTG GCAGCTTCTA
1451 CCGGTACGCT GGCGCGCGAA GGTATTTTAA TCGGCGGAAA GCAGGCAATC
1501 GAAACCTCG CCCAAACAC CGACATCATC TTCGACAAAA CCGGCACGCT
1551 GACCAAGGC AAACCGCGC TCCGCCGTAT CTCATTGTTG AGAGGCACAG
1601 ACGAAGCCTT TGTTCTCGCG GTGGCGCAGG CTTTAGAACA ACAGTCCGAA
1651 CATCCCTTG CCCGCGCCAT CCTCAACTGC CGCATTTTCA ACGGCAGCGT
1701 CCCGACATC GCTATTAAAC AACGCCTCAA CCGCATCGGC GAAGGCGTGG
1751 GCGCGCAACT GACCGTCAAC GGCGAAACAC AGGTTTGGGC ATTTGGGCGG
1801 GCATCCTATG TCGCCGAAAT TTCAGGTAAA GAACCGCAA CAGAAGGCGG
1851 CGGACGCGCG GTTTACCTCG GCAGTCAAAG CGGTTTCCAA GCCGTGTTCT
1901 ACCTGCAAGA CCCGCTCAA GACAGCGCGG CGGAGGCGGT GCGGCAGTTG
1951 GCAGGCAAAA ACCTGACGCT GCACATTCTC AGCGGCGACC GTGAAACCGC
2001 CGTTGCCGAA ACCGACGCG CCCTGGGTGT CGCGCACTAC CGCGCCCAAG
2051 CATTGCCGGA GGACAACTG GAATACGTC AAGCCTTGCA AAAAGAAGGG
2101 AAAAAAGTGC TGATGATAGG CGACGCGCAT AACGACGCG CCGTTTGGC
2151 GCAGGCAGAC GTATCCGCG CCAGCGCGG CGGGACGGAT ATTGCGAGGG
2201 ACGGCGCGGA CATTGTGTTA TTGAACGAAG ATTTGCGTAC CGTCGCCCAC
2251 CTGCTCGATC AGGCGCGGCG CACCCGCCAT ATTATCCGGC AAAACCTGAT
2301 ATGGGCGGGC GCGTACAATA TCATTGCCGT ACCGCTTGCC GTTTTGGGCT
2351 ATGTCCAACC GTGGATAGCC GCACTGGGTA TGAGCTTCAG TTCGCTGGCG
2401 GTTTTGGGCA ACGCCCTGCG CCTTCACAAA CGGGGGAAAA TGCAGTCTGA
2451 AAAAATGCCG TCCGAACAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2356; ORF 703>:

```

a704.pep
1 MKKTCFHCGL DVPENLHLTV RYENEDRET CAGCQAVAQS IIDAGLGSYY
51 KQRTADAQKT ELPPQEILDQ IRLYDLPEVQ SDFVETHGGT REAVLMLGGI
101 TCAACVWLIE QQLRRTDGIV RIDLNYSTHR CRVWDDGKI RLS DILKIR
151 QIGYTAAPYD AQKIEAANQK ERKQYIVRLA VAGLGMMQTM MFALPTYLYG
201 GDIEPDFLQI LHWGGFLMVL PVVFYCAVPF YQGA LRDLKN RRVGMDTPIT
251 VAIIMTFIAG VYSLATNAGQ GMYFESIAML LFFLLGGRFM EHIARRKAGD
301 AAERLVKLIP AFCHHMPDYP DTQETCEAAV VKLKAGDIVL VKPGETIPVD
351 GTVLEGSSAV NESMLTGESL PVAKMPSEKV TAGTLNTQSP LIIRTDRTGG
401 GTRLSHIVRL LDRALA QKPR TAE LAEQYAS SFIFGELL LLA VPVFIGWTLY
451 ADAHTALWIT VALLVITCPC ALSLATPTAL AASTGTLARE GILIGGKQAI
501 ETLAQTDDII FDKTGTLTQG KPAVRRISLL RGTDEAFVLA VAQALEQQSE
551 HPLARAILNC RISDGSVPDI AIKQRLNRIG EGVGAQLTVN GETQVWALGR
601 ASYVAEISGK EPQTEGGGSA VYLGSQSGFQ AVFYLDPLK DSAAEA VRQL
651 AGKNLTLHL SGRETAVAE TARALGVAHY RAQAMPEDKL EYVKALQKEG
701 KKVLMIGDGI NDAPVLAQAD VSAAGGTD IARDGADIVL LNEDLRTVAH
751 LLDQARRTRH IIRQNLIWAG AYNIIAVPLA VLGYPWPWIA ALGMSFSSLA
801 VLGNALRLHK RGKMQSEKMP SEQ*

```

m704/a704 99.8% identity in 823 aa overlap

```

          10      20      30      40      50      60
m704.pep MKKTCFHCGLDVPEHLHLTVRYENEDRETCCAGCQAVAQSIIDAGLGSYYKQRTADAQKT
          |||
a704      MKKTCFHCGLDVPEHLHLTVRYENEDRETCCAGCQAVAQSIIDAGLGSYYKQRTADAQKT
          10      20      30      40      50      60

          70      80      90     100     110     120
m704.pep ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLIEQQLRRTDGIV
          |||
a704      ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLIEQQLRRTDGIV

```

1132

	70	80	90	100	110	120
m704 . pep	130	140	150	160	170	180
a704	RIDLNSTHRCRVVWDDGKIRLS DILLKIRQIGYTAAPYDAQKIEAANQKERKQYIVRLA					
	130	140	150	160	170	180
m704 . pep	190	200	210	220	230	240
a704	VAGLGMMQTMFALPTYLYGGDIEPDLQILHWGGFLMVLPPVVFYCAVPFYQGALRDLKN					
	190	200	210	220	230	240
m704 . pep	250	260	270	280	290	300
a704	RRVGMDTPITVAIIMTFIAGVYSLATNAGQGMFESIAMLLFFLLGGRFMEHIARRKAGD					
	250	260	270	280	290	300
m704 . pep	310	320	330	340	350	360
a704	AAERLVKLI PAFCHHMPDYPDTQETCEAAVVKLKAGDIVLVKPGETIPVDGTVLEGSSAV					
	310	320	330	340	350	360
m704 . pep	370	380	390	400	410	420
a704	NESMLTGESLPVAKMPSEKVTAGTLNTQSPLIIRTDRTGGGTRL SHIVRLLDRLAQAQKPR					
	370	380	390	400	410	420
m704 . pep	430	440	450	460	470	480
a704	TAEAEQYASSFIFGELLAVPVFIGWTLYADAHTALWITVALLVITCPCALSLATPTAL					
	430	440	450	460	470	480
m704 . pep	490	500	510	520	530	540
a704	AASTGTLAREGILIGGKQAIETLAQTDDIIFDKTGTLTQGKPAVRRISLLRGTDEAFVLA					
	490	500	510	520	530	540
m704 . pep	550	560	570	580	590	600
a704	VAQALEQQSEHPLARAILNCRISDGSVPDIAIKQRLNRIGEGVGAQLTVNGETQVWALGR					
	550	560	570	580	590	600
m704 . pep	610	620	630	640	650	660
a704	ASYVAEISGKEPQTEGGGS AVYLGSSQSGFQAVFYLTDPDKDSAAEAVRQLAGKNLTLHIL					
	610	620	630	640	650	660
m704 . pep	670	680	690	700	710	720
a704	SGDRETAVAETARALGV AHYRAQAMPEDKLEYVKALQKEGKKVLMIGDGINDAPVLAQAD					
	670	680	690	700	710	720
m704 . pep	730	740	750	760	770	780
a704	VSAAAAGGTDIARDGADIVLLNEDLRTVAHLLDQARRTRHIIRONLIWAGAYNIIAVPLA					
	730	740	750	760	770	780
m704 . pep	790	800	810	820		
a704	VLGYVQPWIAALGMSFSSLAVLGNALRLHKGKMQSEKMPSEQX					
	790	800	810	820		

1133

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2357>:

```
g705.seq
  1 GTGTTCAATA ATTTCTtgC CTCTCTGCCG TTTATGACGG AAACACGCGC
  51 TGATATGCTC ATCAGCGCGT TTTGGCCCAT GGTTAAAGCC GGCTTTACAG
 101 TGTCTTtgC TTTGGCGATC GCTTCTTTCG TTATCGGCAT GATTATTGCC
 151 GTAGCCGTTG CTTTGGTAAG AATCATGCCT TCCGGCGGTA TTTCCAAAA
 201 ATGCTTGTTG AAGCTGGTGG AATTTTATAT TTCCGTCGTT CGCGGTACGC
 251 CGCTGTTGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC GTCCGTCGGC
 301 ATCTATATCA ATCCGATTCC CGCCGCCATC ATCGGCTTTT CGCTCAATGT
 351 CGGCGCATAC GCTTCCGAAA CCATACGCGC GGCGATTTTG TCCGTGCCGA
 401 AAGGGCAGTG GGAAGCAGGT TTCTCCATCG GTATGACCTA TATGCAGACG
 451 TTCCGCCGCA TCGTCGCACC GCAGGCATTC CGCGTCGCCG TTCCGCCGTT
 501 GAGCAACGAG TTTATCGGCT TGTTCAAAAA CACCTCGCTT GCCGCCGTGG
 551 TAACGGTAAC GGAGCTTTTC CGTGTGCAC AGGAAACGGC AAACCGCACT
 601 TATGACTTTT TGCCTGTCTA TATCGAAGCT GCATTGGTTT ATTGGTGGTT
 651 CTGTAAGATG CTGTTTTTGA TTCAGGCGCG TTTGAAAAA CGTTTCGACC
 701 GTTATGTCGC CAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2358; ORF 705>:

```
g705.pep
  1 VFNNFLASLP FMTETRADML ISAFWPMVKA GFTVSLPLAI ASFVIGMIIA
  51 VAVALVRIMP SGGIFQKLL KLVEFYISVV RGTPLLVLV IVFYGLPSVG
 101 IYINPIPAAI IGFSLVNGAY ASETIRAAIL SVPKGQWEAG FSIGMTYMQT
 151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTLEF RVAQETANRT
 201 YDFLPVYIEA ALVYWCFCKV LFLIQARLEK RFDRYVAK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2359>:

```
m705.seq
  1 GTGTTCAATA ATTTCTTGC TTCGCTGCCG TTTATGACGG AAACACGCGC
  51 CGATATGATT GTCAGCGCGT TTTGCGCTAT GGTCAAAGCC GGCTTCGCGG
 101 TCTCTCTGCC TTTGGCGGCA GCTTCTTTCG TTATCGGTAT GATGATTGCG
 151 GTAGCCGTGG CTTTGGTGCG GATTATGCCG GCCGGCGGCA TCGTGCCGAA
 201 AATCCTGCTG AAATTGGTGG AATTTTATAT TTCCGTCATT CGCGGTACGC
 251 CGCTGTTGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC TTCCGTCGGC
 301 ATCTATATCG ACCCGATTCC TGCCGCCATC ATCGGCTTTT CGCTCAATGT
 351 CGGCGCATAC GCTTCCGAAA CCATACGCGC GGCAATTTTG TCCGTACCTA
 401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
 451 TTCCGCCGCA TTGTCGCGCC GCAGGCATTC CGCGTTGCCG TGCCGCCCTT
 501 GAGCAACGAG TTTATCGGTT TGTTTAAAAA CACCTCGCTC GCGGCAGTCG
 551 TGACGGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGGC AAACCGCACT
 601 TATGACTTTT TGCCCGTCTA TATCGAAGCC GCTTTGGTTT ACTGGTGGTT
 651 TTGTAAGATG CTGTTCTCTA TTCAGGCGCG TTTGAAAAA CGTTTCGACC
 701 GCTACGTCGC CAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2360; ORF 705>:

```
m705.pep
  1 VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
  51 VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVLV IVFYGLPSVG
 101 IYIDPIPAAI IGFSLVNGAY ASETIRAAIL SVPKGQWEAG FSIGMTYMQT
 151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTLEF RVAQETANRT
 201 YDFLPVYIEA ALVYWCFCKV LFLIQARLEK RFDRYVAK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 705 shows 95.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. gonorrhoeae*:

```
m705/g705    95.0% identity in 238 aa overlap

          10      20      30      40      50      60
m705.pep    VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
g705         VFNNFLASLPFMTETRADMLISAFWPMVKAGFTVSLPLAIASFVIGMIIAVALVRIMP
          10      20      30      40      50      60

          70      80      90     100     110     120
m705.pep    AGGIVRKILLKLVEFYISVIRGTPLLVLVIVFYGLPSVGIYIDPIPAAIIGFSLVNGAY
          :|| :| |||||||||:|||||||||||||||:|||||||||||||||
```



1134

```

g705      SGGIFQKCLLKLVEFYISVVRGTPLLVQLVIVFYGLPSVGIYINPIPAAIIGFSLNVGAY
           70      80      90      100      110      120

           130      140      150      160      170      180
m705.pep  ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           |||
g705      ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130      140      150      160      170      180

           190      200      210      220      230      239
m705.pep  AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLFIQARLEKRFDRYVAKX
           |||
g705      AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLFIQARLEKRFDRYVAKX
           190      200      210      220      230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2361>:

```

a705.seq
1  GTGTCAATA ATTCCTTGC TTCGCTGCCG TTTATGACGG AAACACGCGC
51 CGATATGATT GTCAGCGCGT TTTTGCCTAT GGTCAAAGCC GGCTTCGCGG
101 TCTCTCTGCC TTTGGCGGCA GCTTCTTTCG TTATCGGTAT GATGATTGCG
151 GTAGCCGTGG CTTTGGTGCG GATTATGCCC GCCGGCGGCA TCGTGCGGAA
201 AATCCTGCTG AAATGGTGCG AATTTTATAT TTCCGTCATT CGCGGTACGC
251 CGCTGTGGTG TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC TTCCGTCGGC
301 ATCTATATCG ACCCGATTCC TGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGGCGCATAT GCTTCGAAA CCATACGCGC GGCAATTTTG TCCGTACCGA
401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451 TTCCGCCGCA TCGTCGCGCC GCAGGCATTG CGCGTGCCG TGCCGCCTTT
501 GAGCAACGAG TTTATCGGTT TGTTTAAAAA CACCTCGCTC GCGGCAGTCG
551 TGACGGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCCGTCTA TATCGAAGCC GCTTTGGTTT ACTGGTGTTT
651 TTGTAAAGTG CTGTTCTGA TTCAGGCGCG TTTGGAAAAA CGTTTCGACC
701 GCTACGTCGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2362; ORF 705.a>:

```

a705.pep
1  VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
51 VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVLVQ IVFYGLPSVG
101 IYIDFIPAAI IGFSNLVNGAY ASETIRAAIL SVPKGQWEAG FSIGMTYMQT
151 FRRIVAPQAF RAVVPPLSNE FIGLFKNTSL AAVVTVTLEF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVKV LFLFIQARLEK RFDYRVAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 705 shows 100.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. meningitidis*:

a705/m705 100.0% identity in 238 aa overlap

```

           10      20      30      40      50      60
a705.pep  VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
           |||
m705      VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
           10      20      30      40      50      60

           70      80      90      100     110     120
a705.pep  AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDFIPAAIIGFSLNVGAY
           |||
m705      AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDFIPAAIIGFSLNVGAY
           70      80      90      100     110     120

           130      140      150      160      170      180
a705.pep  ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           |||
m705      ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130      140      150      160      170      180

           190      200      210      220      230      239
a705.pep  AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLFIQARLEKRFDRYVAKX
           |||
m705      AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLFIQARLEKRFDRYVAKX
           190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2363>:

g706.seq

```

1   ATGAACTCCT CGCAACGCAA ACGCCTTTCC GgccGCTGGC TCAACTCCTA
51  CGAACGCTac cGCCaccGCC GCCTCATACA TGCCGTGCGG CTCGGCggaa
101 ccgtCCTGTT CGCCACCGCA CTCGCCGgGc tACTCCACCT CCAacacggc
151 gAATGGATAG GGAatgaCCGT CTTGTCGTC CTCGGCATGC TCCAGTTCCA
201 AGGcgcgatt tActccaacg cggtgGAacg taTgctcgtt acggtcatcg
251 ggctgGGCGC GGGTTTGGGc gTTTATGGC TGAACCAGCA TTAttttccac
301 ggcaacCTcc tcttctacct gaccatcggc acggcaagcg cactggccgg
351 ctGGGCGGGC GTCGGCAAAA acggctacgt ccctatgctg GCGGGGctgA
401 CGATGTGCAT gctcatcggc gACAACGGCA GCGAATGGCT CGACAGCGGC
451 CTGATGCGCG CGATGAACGT CCTCATCGGC GCCGCCATCG CCATTGCCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGACAACCT GGC CGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGCGGTATGA CGCGGAAACG TTTGGAGCAG AATATGGTCA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCGC CCACCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC TCCATGATGG AAGCCATGCA GCACGCCAC
751 CGCAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AAATCAACG GCAGCGAAAT CCGGCTGCTC GACCGCCACT
851 TCACACTGCT CCAAAACGAC CTGCAACAAA CCGCGCCCT CATCAACGGC
901 AGACACGCCG GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCGCGCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
1101 CTTGCTTGAA ACACGGGAAC ACGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2364; ORF 706.ng>:

g706.pep

```

1   MNSSQRKRLS GRWLSYERY RHRLIHAVR LGGTVLFATA LARLLHLQHG
51  EWIGMTVFVV LGMLQFQGA IYNAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPML AGLTMCMLIG DNGSEWLDSG
151 LMRAMNVLI GAAIAIAAKL LPLKSTLMWR FMLADNLADC SKMIAEISNG
201 RRMTRERLEE NMVKMRQINA RMVKSRSRLA ATSGESRISP SMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
351 TRRWLDAHE RQHLRQSLLE TREHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2365>:

m706.seq

```

1   ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA
51  CGAACGCTAC CGCTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG
101 CCGTCTGTT CGCCACCGCC TCCGCCCGGC TGCTCCACCT CCAACACGGC
151 GAGTGGATAG GGAAGACCGT CTTGTCGTC CTCGGCATGC TCCAGTTTCA
201 AGGGGCGATT TACTCCAAGG CCGTGGAACG TATGCTCGGC ACGGTCATCG
251 GCGTGGGCGC GGGTTTGGGc GTTTATGGC TGAACCAGCA TTATTTCCAC
301 GGCAACCTCC TCTTCTACCT CACCGTCGGC ACGCCAAGCG CACTGGCCGG
351 CTGGGCGGGC GTCGGCAAAA ACGGCTACGT CCTATGCTG GCAGGGCTGA
401 CGATGTGTAT GCTCATCGGC GACAACGGCA GCGAATGGCT CGACAGCGGA
451 CTCATGCGCG CCATGAACGT CCTCATCGGC GCCGCCATCG CCATCGCCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGCGCATGA CCCGCGAACG CCTCGAGGAG AACATGGCGA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCGC CCATCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCAC
751 CGTAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AAATCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT
851 TCACACTGCT CCAAAACGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC
901 AGACACGCCG GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCGCGCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
1101 CTTGCTTGAA ACACGGGAAC ACGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2366; ORF 706>:

m706.pep

```

1   MNTSQRNRLV SRWLSYERY RYRLIHAVR LGGAVLFATA SARLLHLQHG
51  EWIGMTVFVV LGMLQFQGA IYKAVRMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPML AGLTMCMLIG DNGSEWLDSG
151 LMRAMNVLI GAAIAIAAKL LPLKSTLMWR FMLADNLADC SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRSRLA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING

```

1136

301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR  
 351 TRRKWLDAHE RQHLRQSLLE TREHG\*

m706/g706 96.5% identity in 375 aa overlap

	10	20	30	40	50	60
m706.pep	MNTSQRNRLVSRWLSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
g706	MNSSQRKRLSGRWLSYERYRHRRLIHAVRLGGTVLFATALARLLHLQHGEWIGMTVFVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m706.pep	LGMLQFQGAIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTIVGTASALAGWAA					
g706	LGMLQFQGAIYSNAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTIGTASALAGWAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m706.pep	VGKNGYVPMLAGLTMCMILIGDNGSEWLD SGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
g706	VGKNGYVPMLAGLTMCMILIGDNGSEWLD SGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m706.pep	FMLADNLADCSKMAIEISNGRRMTREERLEENMAKMRQINARMVKSRSRLAATSGESRISP					
g706	FMLADNLADCSKMAIEISNGRRMTREERLEQNVMKMRQINARMVKSRSRLAATSGESRISP					
	190	200	210	220	230	240
	250	260	270	280	290	300
m706.pep	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTDLQQTVALING					
g706	SMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTDLQQTAALING					
	250	260	270	280	290	300
	310	320	330	340	350	360
m706.pep	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQRTTRRKWLDAHE					
g706	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQRTTRRKWLDAHE					
	310	320	330	340	350	360
	370					
m706.pep	RQHLRQSLLETREHGX					
g706	RQHLRQSLLETREHGX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2367>:

a706.seq

1	ATGAACACCT	CGCAACGCAA	CCGCCTCGTC	AGCCGCTGGC	TCAACTCCTA
51	CGAACGCTAC	CGCTACCGCC	GCCTCATCCA	CGCCGTCCGG	CTCGGCGGGG
101	CCGTCCTGTT	CGCCACCGCC	TCCGCCCGGC	TGCTCCACCT	CCAACACGGC
151	GAGTGGATAG	GGATGACCGT	CTTCGTCGTC	CTCGGCATGC	TCCAGTTTCA
201	AGGGGCGATT	TACTCCAAGG	CGGTGGAACG	TATGCTCGGC	ACGGTCATCG
251	GGCTGGGCGC	GGGTTTGGGC	GT TTTATGGC	TGAACCAGCA	TTATTTCCAC
301	GGCAACCTCC	TCTTCTACCT	CACCGTCGGC	ACGGCAAGCG	CAGTGGCCGG
351	CTGGGCGGCG	GTCGGCAAAA	ACGGCTACGT	CCCTATGCTG	GCGGGGCTGA
401	CGATGTGCAT	GTCATCGGC	GACAACGGCA	GCGAATGGTT	CGACAGCGGC
451	CTGATGCGCG	CGATGAACGT	CCTCATCGGC	GCGGCCATCG	CCATCGCCGC
501	CGCCAAACTG	CTGCCGCTGA	AATCCACACT	GATGTGGCGT	TTCATGCTTG
551	CCGACAACCT	GACCGACTGC	AGCAAAATGA	TTGCCGAAAT	CAGCAACGGC
601	AGGCGCATGA	CCCGCGAACG	CCTCGAAGAG	AACATGGCGA	AAATGCGCCA
651	AATCAACGCA	CGCATGGTCA	AAAGCCGCAG	CCACCTCGCC	GCCACATCGG
701	GCGAAAGCCG	CATCAGCCCC	GCCATGATGG	AAGCCATGCA	GCACGCCCCA
751	CGTAAAATTG	TCAACACCAC	CGAGCTGCTC	CTGACCACCG	CCGCCAAGCT
801	GCAATCTCCC	AAACTCAACG	GCAGCGAAAT	CCGGCTGCTT	GACCGCCACT
851	TCACACTGCT	CAAACCGAC	CTGCAACAAA	CCGTGCGCCT	TATCAACGGC

1137

```

901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACAGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2368; ORF 706.a>:

```

a706.pep
  1 MNTSQNRNLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
 51 EWIGMTVFVV LGMLQFQGA IYSKAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTVG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWFDSG
151 LMRAMNVLI GAAIAIAAAKL LPLKSTLMWR FMLADNLTDC SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRSHA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING
301 RHARRIRIDT AINPELEALA EHLHYQWGF LWLSTNMRQE ISALVILLQR
351 TRRKWLDAHE RQHLRQSLLE TREHS*

```

a706/m706 99.5% identity in 374 aa overlap

a706.pep	10	20	30	40	50	60
m706	10	20	30	40	50	60
a706.pep	70	80	90	100	110	120
m706	70	80	90	100	110	120
a706.pep	130	140	150	160	170	180
m706	130	140	150	160	170	180
a706.pep	190	200	210	220	230	240
m706	190	200	210	220	230	240
a706.pep	250	260	270	280	290	300
m706	250	260	270	280	290	300
a706.pep	310	320	330	340	350	360
m706	310	320	330	340	350	360
a706.pep	370					
m706	370					

g707.seq not found

g707.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2369>:

## m707.seq

```

1 ATGGAAATTA TTAACGATGC AGAACTTATC CGTTCCATGC AGCGTCAGCA
51 GCACATAGAT GCTGAATTGT TAACTGATGC AAATGTCCGT TTCGAGCAAC
101 CATTGGAGAA GAACAATTAT GTCCTGAGTG AAGATGAAAC ACCGTGTACT
151 CGGGTAAATT ACATTAGTTT AGATGATAAG ACGGTGCGCA AATTTCTTT
201 TCTTCCTTCT GTGCTCATGA AAGAAACAGC TTTTAAACT GGGATGTGTT
251 TAGGTTCCAA TAATTTGAGC AGGCTACAAA AAGCCGCGCA ACAGATACTG
301 ATCGTGCGTG GCTACCTCAC TTCCCAAGCT ATTATCCAAC CACAGAATAT
351 GGATTCGGGA ATTCTGAAAT TACGGGTATC AGCAGGCGAA ATAGGGGATA
401 TCCGCTATGA AGAAAAACGG GATGGGAAGT CTGCCGAGGG CAGTATTAGT
451 GCATTCAATA ACAAATTTCC CTTATATAGG AACAAAATTC TCAATCTTCG
501 CGATGTAGAG CAGGGCTTGG AAAACCTGCG TCGTTTGCCG AGTGTAAAA
551 CAGATATTCA GATTATACCG TCCGAAGAAG AAGGCAAAAG CGATTTACAG
601 ATCAAATGGC AGCAGAATAA ACCCATACGG TTCAGTATCG GTATAGATGA
651 TCGGGGCGGC AAAACGACCG GCAAATATCA AGGAAATGTC GCTTTATCGT
701 TCGATAACCC TTTGGGCTTA AGCGATTGT TTTATGTTTC ATATGGACGC
751 GGTTTGCGGC ACAAAACGGA CTGACTGAT GCCACCGTA CGGAAACGTA
801 AAGCGGATCC AGAAGTTACA GCGTGCATTA TTCGGTGCCC GTAAAAAAT
851 GGCTGTTTTC TTTAATCAC AATGGACATC GTTACCACGA AGCAACCGAA
901 GGCTATTCCG TCAATTACGA TTACAACGGC AAACAATATC AGAGCAGCCT
951 GGCCGCCGAG CGCATGCTTT GGCGTAACAG ACTTCATAAA ACTTCAGTCG
1001 GAATGAAATT ATGGACACGC CAAACCTATA AATACATCGA CGATGCCGAA
1051 ATCGAAGTAC AACGCCGCCG CTCTGCAGGC TGGGAAGCCG AATTGCGCCA
1101 CCGTGCTTAC CTCAACCGTT GGCAGCTTGA CGGCAAGTTG TCTTACAAAC
1151 GCGGGACCGC CATGCGCCAA AGTATGCCTG CACCGGAAGA AAACGGCGGC
1201 GATATTCTTC CAGGTACATC TCGTATGAAA ATCATTACTG CCAGTTTGGG
1251 CGCAGCCGCC CCATTTATTT TAGGCAACA GCAGTTTTTC TACGCAACCG
1301 CCATTCAAGC TCAATGGAAC AAAACGCCGT TGGTTGCCCA AGATAAATTG
1351 TCAATCGGCA GCCGCTACAC CGTTCGCGGA TTTGATGGGG AGCAGAGTCT
1401 TTTCCGAGAG CGAGGTTTCT ACTGGCAGAA TACTTTAACT TGGTATTTTC
1451 ATCCGAACCA TCAGTTCTAT CTCGGTGCGG ACTATGGCCG CGTATCTGGC
1501 GAAAGTGCAC AATATGTATC GGGCAAGCAG CTGATGGGTG CAGTGGTCGG
1551 CTTCAGAGGA GGGCATAAAG TAGGCGGTAT GTTTGCTTAT GATCTGTTTG
1601 CCGGCAAGCC GCTTCATAAA CCCAAAGGCT TTCAGACGAC CAACACCGTT
1651 TACGGCTTCA ACTTGAATTA CAGTTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2370; ORF 707>:

## m707.pep

```

1 MEIINDAELI RSMQROQHID AELLTDANVR FEQPLEKNNY VLSEDETPCT
51 RVNYISLDDK TVRKFSFLPS VLMKETAFKT GMCLGSNNLS RLQKAAQQIL
101 IVRGYLSQA IQPQNMDSG ILKLRSVAGE IGDIREYEEK DGKSAEGSIS
151 AFNNKFPLYR NKILNLRDVE QGLENLRRLP SVKTDIQIIP SEEEGKSDLQ
201 IKWQQNKPIR FSGIDDAGG KTTGKYQGNV ALSFDNPLGL SDFYVVSYGR
251 GLAHKTDLTD ATGTETESGS RSYSVHYSVP VKKWLFSFNH NGHRYHEATE
301 GYSVNYDYNG KQYQSSLAEE RMLWRNRLHK TSVGMKLWTR QTYKYIDDAE
351 IEVQRRRSAG WEAE LRHRAY LNRWQLDGKL SYKRGTGMRQ SMPAPEENG
401 DILPGTSRMK IITASLDAEA PFILGKQFF YATAIQAWN KPLVAQDKL
451 SIGSRYTVRG FDGEQSLFGE RGFYWQNTLT WYFHPNHQFY LGADYGRVSG
501 ESAQYVSGFK LMGAVVGFRG GHKVGGMFAY DLFAGKPLHK PKGFQTTNTV
551 YGFNLNYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2371>:

## a707.seq

```

1 NTGAAAGAAA CAGCTTTTAA AACTGGGATG TGTTTAGGTT CCAATAATTT
51 GAGCAGGCTA CAAAAAGCCG CGCAACAGAT ACTGATTGTG CGTGGCTACC
101 TCACTTCCCA AGCTATTATC CAACCACAGA ATATGGATTC GGGAATTCTG
151 AAATTACGGG TATCAGCAGG CGAAATAGGN GATATCCGCT ATGAAGAAAA
201 ACGGGATGNG AAGTCTGCCG AGGGCAGTAT TAGTGCATTC AATAACAAAN
251 TTCCCTTATA TAGGAACAAA ATTCTCAATC TTCGCGATGT AGAGCAGGGC
301 TTGGAAACC TGCGTCGTTT GCCGAGTGT AAAACAGATA TTCAGATTAT
351 ACCGTCCGAA GAAGAAGGCA AAAGCGATTT ACAGATCAAA TGGCAGCAGA
401 ATAAACCCAT ACGGTTCACT ATCGGTATAG ATGATGCGGG CGGCAAAACG
451 ACCGGCAAAT ATCAAGGAAA TGTCGCTTTA TCGTNCGATA ACCCTTTGGG
501 NTTAAGCGAT TNGTTTATG TTTTCATATG ACGCGGTTTG GTGCACAAAA
551 CGGACTTGAC TGNTGCCACC GGTACGGAAA CTGAAAGCGG ATCCAGAAGT
601 TACAGCGTGC ATTATTCGGT GNNCGTAAAA AAATGGCTGT TTTCTTTTAA
651 TCACAATGGA CATCGTTACC ACGAAGCAAC CGAAGGCTAT TCCGTCAATT
701 ACGATTACAA CGGCAACAAA TATCAGAGCA GCCTGGCCGC CGAGCGCATG

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1139

```

751 CTTTGGNNNN NNAGNTTTCN TNAAACTTCA GTCNGAATGA AATTATGGAC
801 ACGCCAAACC TATAAATACA TCGACGATGC CGAAATCGAA GTGCAACGCC
851 GCCGCTCTGC AGGCTGGGAA GCCGAATTGC GCCACCGTGC TTACCTCNAC
901 CGTTGGCAGC TTGACGGCAA GTTGTCTTAC AAACGCGGGA CCGGCATGCG
951 CCAAAGTATG CCCGCACCTG AAGAAAACGG CGGCGGTACT ATTCCAGNCA
1001 NATCCCGTAT GAAAATCATA ACCGCCGGAT TGGATGCAGC GGCCCCGTNT
1051 ATGTTGGGCA AACAGCAGTT TTTCTACGCA ACCGCCATTC AAGCTCAATG
1101 GAACAAAACG CCTTTGGTTG CCCAAGACAA GTTGTCTATC GGCAGCCGCT
1151 ACACCGTTCG CGGATTTGAT GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT
1201 TTCTACTGGC AGAATACTTT AACTTGGTAT TTTCATCCGA ACCATCAGTT
1251 CTATCTCGGT GCGGACTATG GCCGCGTATC TGGCGAAAGT GCACAATATG
1301 TATCGGGCAA GCAGCTGATG GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT
1351 AAAGTAGGCG GTATGTTTGC TTATGATCTG TTTGCCGGCA AGCCGCTTCA
1401 TAAACCAAAA GGCTTTCAGA CGACCAACAC CGTTTACGGC TTCAACTTGA
1451 ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2372; ORF 707.a>:

```

a707.pep
  1 XKETAFTKGM CLGSNNLSRL QKAAQQILIV RGYLTSQAI QPQNMDSGIL
  51 KLRVSAGEIG DIRYEKRDY KSAEGSISAF NNKXPLYRNL ILNLRDVEQG
 101 LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQONKPIRFS IGIDDAGGKT
 151 TGKYQGNVAL SXDNPLGLSD XFYVSYGRGL VHKTDLTXAT GTETESGSR
 201 YSVHYSVXVK KWLFSFNHNG HRYHEATEGY SVNYDYNKQ YQSSLAERM
 251 LWXXXFXXTS VXMKLWTRQT YKYIDDAEIE VQRRRSAGWE AELRHRAYLX
 301 RWQLDGKLSY KRGTMGRQSM PAPEENGGGT IPXXSRMKII TAGLDAAAPX
 351 MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD GEQSLFGERG
 401 FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM GAVVGFRGGH
 451 KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

a707/m707 95.3% identity in 486 aa overlap

```

a707.pep                                10      20      30
                                         XKETAFTKGMCLGSNNLSRLQKAAQQILIVR
                                         |||
m707      EDETPCTRVNYISLDDKTVRKFSFLPSVLMKETAFTKGMCLGSNNLSRLQKAAQQILIVR
              50      60      70      80      90      100

a707.pep      40      50      60      70      80      90
GYLTSQAI IQPQNMDSGILKLRVSAGEIGDIRYEKRDYKSAEGSISAFNNKXPLYRNLKI
|||
m707      GYLTSQAI IQPQNMDSGILKLRVSAGEIGDIRYEKRDGKSAEGSISAFNNKXPLYRNLKI
              110      120      130      140      150      160

a707.pep      100      110      120      130      140      150
LNLRDVEQGLENLRLPSVKTDIQUIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
|||
m707      LNLRDVEQGLENLRLPSVKTDIQUIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
              170      180      190      200      210      220

a707.pep      160      170      180      190      200      210
GKYQGNVALSXDNPLGLSDXFXFYVSYGRGLVHKTDLTXATGTETESGSRYSVHYSVXVKK
|||
m707      GK YQGNVALSFDNPLGLSDLFYVSYGRGLAHKTDLTDATGTETESGSRYSVHYSVPVKK
              230      240      250      260      270      280

a707.pep      220      230      240      250      260      270
WLFSFNHNGHRYHEATEGYSVNYDYNKQYQSSLAERMLWXXXFXXTSVXMKLWTRQTY
|||
m707      WLFSFNHNGHRYHEATEGYSVNYDYNKQYQSSLAERMLWRNRLHKT SVGMKLWTRQTY
              290      300      310      320      330      340

a707.pep      280      290      300      310      320      330
KYIDDAEIEVQRRRSAGWEAELRHRAYLXRWQLDGKLSYKRGTMGRQSM PAPEENGGGTI
|||
m707      KYIDDAEIEVQRRRSAGWEAELRHRAYLNRWQLDGKLSYKRGTMGRQSM PAPEENGGDIL
              350      360      370      380      390      400

```

1140

	340	350	360	370	380	390
a707.pep	PXXSRMKIIITAGLDAAAPXMLGKQQFFYATAIQAWNKTPLVAQDKLSIGSRYTVRGFDG					
m707	PGTSRMKIIITASLDAAAPFILGKQQFFYATAIQAWNKTPLVAQDKLSIGSRYTVRGFDG					
	410	420	430	440	450	460
	400	410	420	430	440	450
a707.pep	EQSLFGERGFYWNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRGGHK					
m707	EQSLFGERGFYWNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRGGHK					
	470	480	490	500	510	520
	460	470	480			
a707.pep	VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX					
m707	VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX					
	530	540	550	560		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2373>:

g708.seq

```

1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TTCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCGA TGGAAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCAACGGC AAGTATTGAA GATGCCTTGA AATCGAACCC
201 TAAAAACGAA CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACCTAC GGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTGACAAA GCCCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGTATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGTGCA GCGGCATAC GAATATGAAG
701 CACAATTGCA GGCAAATTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ACCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2374; ORF 708.ng>:

g708.pep

```

1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQATASIE DALKSNPKNE LAWLVRAEIY QYLVNDKAQ ESFRQALSIK
101 PDSAEINNNY GWFLCGRLLR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQQQFGLA EAYLKRSLAA QPQFPFAFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLLLGWKIA KALGNVQAAY EYEAQLQANF PYSEELQTVL
251 TGQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2375>:

m708.seq

```

1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTCG TTCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCGACGGC AAGTATTGAA GACGCCCTGA AATCGGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACCTAC GGTTGGTTCC TATGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTGACAAA GCTCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GCGGCATAC GAATATGAAG
701 CACAATTGCA GGCGAATTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ACCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2376; ORF 708>:

m708.pep

1141

```

1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51 DYRQATASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAQ ESFRQALSIK
101 PDSAEINNNY GWFLCGRLLR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSLLA QPQFPAPFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLLLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 TGQ*

```

m708/g708 99.2% identity in 253 aa overlap

```

              10      20      30      40      50      60
m708.pep      MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
              |||||
g708           MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
              10      20      30      40      50      60

              70      80      90      100     110     120
m708.pep      DALKSDPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSDAEINNNYGWFLCGRLLR
              |||||:|||||
g708           DALKSNPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSDAEINNNYGWFLCGRLLR
              70      80      90      100     110     120

              130     140     150     160     170     180
m708.pep      PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSLLAQPQFPAPFKE
              |||||
g708           PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSLLAQPQFPAPFKE
              130     140     150     160     170     180

              190     200     210     220     230     240
m708.pep      LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF
              |||||:|||||
g708           LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNVQAAYEYEAQLQANF
              190     200     210     220     230     240

              250
m708.pep      PYSEELQTVLTGQX
              |||||
g708           PYSEELQTVLTGQX
              250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2377>:

```

a708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TCCTTGCCTT
51 GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGNGACGGC AAGTATTGAA GACGCCTTGA AATCAGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGNCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACACTAC NGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCCCTGGCCG
401 ACCCCACNTA CCCGANCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCGAATTTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ATCGGTCAAT AA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2378; ORF 708.a&gt;:

```

a708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51 DYRQXTASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAQ ESFRQXLSIK
101 PDSAEINNNY XWFLCGRLLR PAESMAYFDK ALADPTYXPX YIANLNKGIC
151 SAKQGQFGLA EAYLKRSLLA QPQFPAPFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLLLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 IGQ*

```

a708/m708 98.0% identity in 253 aa overlap



1142

	10	20	30	40	50	60
a708.pep	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQXTASIE					
m708	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a708.pep	DALKSDPKNELAWLVRAEIYQYLKVNDKAQESFRQXLSIKPDSAEINNXYWFLCGRNLNR					
m708	DALKSDPKNELAWLVRAEIYQYLKVNDKAQESFRQALSIPKPSAEINNXYWFLCGRNLNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a708.pep	PAESMAYFDKALADPTYXPYPIANLNKGICSAKQGQFGLAEAYLKRSALAAQPQFPFAFKE					
m708	PAESMAYFDKALADPTYPTPIYPIANLNKGICSAKQGQFGLAEAYLKRSALAAQPQFPFAFKE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a708.pep	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLWKIAKALGNAQAAYEYEAQLQANF					
m708	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLWKIAKALGNAQAAYEYEAQLQANF					
	190	200	210	220	230	240
	250					
a708.pep	PYSEELQTVLIGQX					
m708	PYSEELQTVLTGQX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2379>:

g709.seq

1	ATGTTTGCTT	TCAAATCCTT	ACTCGATATG	CCGCGCGGTG	AGGCACTTGC
51	CGTCGTCGTC	GCTCTGATTG	CCGCAATGGG	CTATACCATC	ATTTCATTGG
101	AGTGGCTGCC	GCATATGTCC	ATTATTGCCG	CCATCGTCGT	GCTGATTTTG
151	TACGGCTTGG	CGCGCGGTTT	GAAATACAAC	GATATGCAGC	CAGGGATGAT
201	AGGCGCGTTG	AATCAGGGTA	TGGGCGCGGT	TTACCTGTTT	TTCTTCATCG
251	GGCTGATGGT	CAGCGCGCTG	ATGATGAGCG	GCGCGATTCC	GACGCTGATG
301	TATTACGGTT	TCGGGCTGAT	TTCCCCGACT	TATTTTATT	TTTCCGCCTT
351	CGCGCTGTGT	TCCGTCATCG	GCGTGTCAT	CGGCAGCAGC	CTGACCGCCT
401	GCGCCACTGT	CGCGCTTGCC	TTTATGGGGA	TGGCGGCGGC	GTTTCAGGCC
451	GATATGGCGA	TGACGgcggg	cgcgattgTT	tccggtGTGT	TTTTCGGCGA
501	TAAAATGTCC	CCGCTTTCCG	ACACCAACGG	CATTTCGCG	TCCATCGTCG
551	GTATCGACCT	GTTTGAACAC	ATCAAAAACA	TGATGTACAC	CACCATCCCT
601	CGCTGGCTTA	TCAGCGCGGC	ACTGATGCTT	TGGCTTCTTC	CCAGCGTCGC
651	CGGCGAGGAT	TTGAACAGCG	TCGAATCCTT	CCGCAGCCAG	CTTGAAGCCA
701	CGGGATTGGT	GCACGGCTAT	TCGCTGATTC	CGTTTGCAT	GTTGGTCGTT
751	TTGGCATTGA	TGCGCGTCAA	TGCCGTGGTC	GCCATGCTCT	TTACCGTCAT
801	TGCCGCCGTT	GCCGTAACGT	ATCTGCACAG	CACGCCCGAT	CTGCGTCAGC
851	TCGGCGCGTG	GTTTATGGC	GGCTACAAAC	TCGAAGGCCA	AGCGTTTAAA
901	GACATTGCCA	AACTGATTTT	GCGCGGCGGC	TTGGAGAGTA	TGTCTTTTAC
951	GCAGACCATC	GTTATCCTCG	GTATGAGTTT	GGGCGGGGTG	CTGTTTGCGC
1001	TCGGTGTGAT	TCCTTCCTTG	CTGGAGGCCG	TCCGTACCTT	CTTGACGAAT
1051	GCCGGACGCG	CGACGTTTCA	CGTTGCCATG	ACTTCGGTCG	GGGTCAATTT
1101	CCTGATTGGA	GAGCAATATT	TGAGCATCCT	GCTTCGGGGA	GAAACGTTCA
1151	AACCCGTTTA	CGACAACTC	GGCCTGCATT	CGTGCAACCT	GTCGCGGACT
1201	CTGGAAGATG	CGGGGACGGT	GATTAACCCG	CTCGTGCCGT	GGAGCGTGTG
1251	CGGCGTATTT	ATCAGCCACG	CCCTTGGCGT	ACCCGTTTGG	GAATATCTGC
1301	CTTATGCCTT	TTTCTGCTAT	TTGAGTTTGG	CTTTAACCCCT	GTTATTTCGGC
1351	TGACGCGGGC	TGACTTTGAG	CAAAAAATAA		

This corresponds to the amino acid sequence <SEQ ID 2380; ORF 709.ng>:

g709.pep

1	MF	AFKSL	LD	PR	GEAL	AVV	AL	IA	AMGY	TI	IS	LE	WL	PH	MS	II	AA	IV	VL	LIL
51	Y	G	L	A	R	G	L	K	Y	N	D	M	Q	A	G	M	I	G	A	L
101	Y	F	Y	F	S	A	F	A	L	C	S	V	I	G	V	S	I	G	S	S
151	D	M	A	M	T	A	G	A	I	V	S	G	V	F	F	G	D	K	M	S
201	A	W	L	I	S	A	A	L	M	L	W	L	P	S	V	A	A	Q	D	
251	L	A	L	M	R	V	N	A	V	V	A	M	L	F	T	V	I	A	A	V
301	D	I	A	R	L	I	S	R	G	G	L	E	S	M	F	F	T	Q	T	I

351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSCNLSRT  
 401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLLFG  
 451 WTGLTLSKK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2381>:

m709.seq  
 1 ATGTTTCGCTT TCAAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC  
 51 CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTCAATTGG  
 101 AGTGGTTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG  
 151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT  
 201 AGGCGCGTTG AATCAGGGTA TGGGCGCGAT TTACCTGTTT TTCTTCATCG  
 251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG  
 301 TATTACGGTT TCGGACTGAT TTCCCGGACT TATTTTATT TTTCTCCTT  
 351 CCGCGCTGTG TCCGTCATCG GCGTGTCCAT CCGCAGCAGC CTGACCACCT  
 401 GCGCCACTGT CCGCGTTGCC TTTATGGGGA TGGCGGCGGC GTTTCAGGCC  
 451 GATATGGCGA TGACGGCGGG CCGGATTGTT TCGGGCGCAT TTTTGGCGA  
 501 CAAAATGTCC CCGCTTTCGG ATACGACGGG TATTTCCGCG TCCATCGTCG  
 551 GCATCGACTT GTTTGAGCAC ATCAAAAATA TGATGTACAC CACCATCCCC  
 601 GCGTGGCTCA TTAGTGCGGC ACTGATGCTT TGGCTTTTGC CGAATGTGCG  
 651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA  
 701 CGGGATTTGG GCACGGCTAT TCGCTGATTC CGTTTGCCTT GTTGGTCATT  
 751 TTGGCATTGA TCGCATCAA CGCCGTCGTC GCCATGCTCT TTACCGTCAT  
 801 GGTGTCCGTT GCTGTAACGT ATCTGCACAG CACGCCGAT CTGCGTCAGC  
 851 TCGGTGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCGA AGCGTTTAA  
 901 GATGTTGTCA AACTGATTTC GCGCGGCGGT TTGGAAAGTA TGTTTTTCA  
 951 GCAAACCATC GTGATTCTCG GGATGAGTTT GGGCGGACTG TTGTTTGGCG  
 1001 TCGGTGTGAT TCCTTCCCTG TTGGAGGCCA TCCGTACCTT CTTGACGAAT  
 1051 GCCGGACGCG CGACGTTTCA GCTTGCCATG ACTTCGGTCG GGGTTAATTT  
 1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTCGGGT GAAACGTTC  
 1151 AACCCGTTTA CGATAAGCTC GGCTGCAATT CCGCAATCT CTCGCGGACG  
 1201 CTGGAAGATG CGGGGACGGT GATTAACCCG CTCGTACCGT GGAGCGTATG  
 1251 CCGCGTGTTC ATCAGCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC  
 1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT  
 1351 TGGACGGGGC TGACTTTGAG CAAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 2382; ORF 709>:

m709.pep  
 1 MFAFKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL  
 51 YGLARGLKYN DMQQGMIGAL NQMGAIYLF FFIGLMVSAL MMSGAIPTLM  
 101 YYGFLISPT YFYSSFALC SVIGVSIGSS LTTCATVGVA FMGMAAFQA  
 151 DMAMTAGAIV SGAFFGDKMS PLSDTTGISA SIVGIDLFH IKNMMYTTIP  
 201 AWLISAALML WLLPNVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVI  
 251 LALMRINAVV AMLFTVMVAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK  
 301 DVVKLISRGG LESMFFTQTI VILGMSLGLL LFALGVIPSL LEAIRTFTLN  
 351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLSRT  
 401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLLFG  
 451 WTGLTLSKK\*

m709/g709 96.9% identity in 459 aa overlap

	10	20	30	40	50	60
m709.pep	MFAFKSLDDMPRGEALAVVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
g709	MFAFKSLDDMPRGEALAVVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
	10	20	30	40	50	60
m709.pep	DMQQGMIGALNQMGAIYLFFFIGLMVSALMMSGAIPTLMYYGFLISPTYFYFSSFALC					
g709	DMQAGMIGALNQMGAVYLFFFIGLMVSALMMSGAIPTLMYYGFLISPTYFYFSAFALC					
	70	80	90	100	110	120
m709.pep	DMQQGMIGALNQMGAIYLFFFIGLMVSALMMSGAIPTLMYYGFLISPTYFYFSSFALC					
g709	DMQAGMIGALNQMGAVYLFFFIGLMVSALMMSGAIPTLMYYGFLISPTYFYFSAFALC					
	70	80	90	100	110	120
m709.pep	SVIGVSIGSSLTTCATVGVAFMGMAAFQADMAMTAGAIVSGAFFGDKMSPLSDTTGISA					
g709	SVIGVSIGSLTACATVGVAFMGMAAFQADMAMTAGAIVSGVFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
m709.pep	SVIGVSIGSSLTTCATVGVAFMGMAAFQADMAMTAGAIVSGAFFGDKMSPLSDTTGISA					
g709	SVIGVSIGSLTACATVGVAFMGMAAFQADMAMTAGAIVSGVFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
m709.pep	SIVGIDLFHEIKNMMYTTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFHEIKNMMYTTIPAWLISAALMLWLLPSVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240
m709.pep	SIVGIDLFHEIKNMMYTTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFHEIKNMMYTTIPAWLISAALMLWLLPSVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240

1144

	250	260	270	280	290	300
m709.pep	SLIPFALLVILALMRINAVVAMLFTVMVAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK					
g709	SLIPFALLVVLALMRVNAVVMVAMLFTVIAAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK					
	250	260	270	280	290	300
	310	320	330	340	350	360
m709.pep	DVVKLISRGGLESMTFTQIVILGMSLGGLLFALGVIPSLLEAIRFTLTNAGRATFSVAM					
g709	DIAKLISRGGLESMTFTQIVILGMSLGGLLFALGVIPSLLEAVRTLTNAGRATFSVAM					
	310	320	330	340	350	360
	370	380	390	400	410	420
m709.pep	TSVGVNFLIGEQLSILLSGETFKPVYDKLGLHSRNLSTRTLEDAGTVINPLVPWSVCGVF					
g709	TSVGVNFLIGEQLSILLSGETFKPVYDKLGLHSCNLSRTLEDAGTVINPLVPWSVCGVF					
	370	380	390	400	410	420
	430	440	450	460		
m709.pep	ISHALGVVPWEYLPYAFFCYLSLALTLLFGWTGLTSLKXX					
g709	ISHALGVVPWEYLPYAFFCYLSLALTLLFGWTGLTSLKXX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2383>:

```

a709.seq
1  ATGTTTCGCTT TCNAATCCTT ACTCGATATG CCGCGCGGTG AGGCNCTTGC
51  CGTCGCTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTNNTTGG
101 AGTGGCTGCC GCATATGTCC ATTATTGCCG CCATCGTNGT GCTGATTTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGGCGCGTTG AATCAGGGTA TGGGCGCGAT TTACCTNNTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCCGACT TATTTTTATT TTTCCGCCTT
351 CGCGCTGTGT TCCGTCATCG GCGTGTCAT CCGCAGCAGC CTGACCACCT
401 GCGCCACTGT CCGCGTTGCC TTNATGGGTA TNNNGNCGGC GTTTCNNGCC
451 NANATGGNGN NGNNGNNGN CNNGATTGTN NNGGNCGCAT TTTTNGGCGN
501 CAAAATGTCN CCGCTTTCCG ATACGNCGGG CATNTCCGCG TCCATTGTCT
551 GTATCGACCT GTTTGAACAC ATCAAAAATA TGATGTACAC NACCATTCCC
601 GCGTGGCTCA TCACTGNNNC ACTGATGCTG TNGCTTCTTC CCAGCGTCGC
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CCGGATTGGT GCACTGCTAT TCGCTGATTC CGTTTGGCGT GTTGGTCGTT
751 TTGGCATTGA TGCGCGTCAA TGCCGTGGTC GCTATGCTCT TTACCGTCAT
801 TGCCGCGGTT GCCGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC
851 TCGGCGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCCA AGCGTNTANA
901 GACATTGCCA AACTCATTTT TCGCGGCGGT TTGGAAAGTA TGTTTTTCAC
951 GCAGACCATC GTGATTCTTG GGATGAGCCT TGCGGGGCTG CTGTTTGCAC
1001 TGGGCGCGAT TCCTTCCCTG CTGGATGCCG TCCGCAGCTT TTTGACGAAT
1051 GCCGGGCGTN CCACATTCAG CGTTGCCATG ACTTCGGTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTCTGGT GAAACGTTCA
1151 AACCTGTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG
1201 CTGGAAGATG CGGGGACGGT CATCAACCCG CTCGTACCGT GGAGCGTATG
1251 CGGCGTGTTT ATCANCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC
1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT
1351 TGGACGGGGC TGACTTTGAG CAAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2384; ORF 709.a>:

```

a709.pep
1  MFAFXSLDM PRGEALAVVV ALIAAMGYTI IXLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMQQGMIGAL NQGMGAIYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFLISPT YFYFSAFALC SVIGVSIGSS LTTCATVGVA XMGXXXAFXA
151 XMXXXXXXIV XXAXXGXKMS PLSDTXGXA SIVGIDLFH IKNNMYTTIP
201 AWLISXXLML XLLPSVAAQD LNSVESFRSQ LEATGLVHCY SLIPFALLVV
251 LALMRVNAV AVMLFTVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAXX
301 DIAKLISRGG LESMTFTQTI VILGMSLGG L FALGAIPSL L DAVRSFLT N
351 AGRXTFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLST

```

1145

401 LEDAGTVINP LVPWSVCGVF IXHALGVPVW EYLPYAFFCY LSLALTLLFG  
 451 WTGLTLSKK\*

a709/m709 91.1% identity in 459 aa overlap

	10	20	30	40	50	60
a709.pep	MFAFXSLDMPRGEALAVVVALIAAMGYTII	XLEWLPHMSIIAAIVVLILYGLARGLKYN				
m709	MFAFKSLDMPRGEALAVVVALIAAMGYTII	SLEWLPHMSIIAAIVVLILYGLARGLKYN				
	10	20	30	40	50	60
	70	80	90	100	110	120
a709.pep	DMQQGMIGALNQGMGAIYLFFFI	GLMVSALMMSGAIPTLMYYGFLISPT	YFYFSAFALC			
m709	DMQQGMIGALNQGMGAIYLFFFI	GLMVSALMMSGAIPTLMYYGFLISPT	YFYFSSFALC			
	70	80	90	100	110	120
	130	140	150	160	170	180
a709.pep	SVIGVSIGSSLTTCATVG	VAXMGXXXAF	XAXMXXXXXIVXXAXXG	XKMSPLSDTXG	XS	
m709	SVIGVSIGSSLTTCATVG	VAFMGMAAFQAD	MAMTAGAIVSGAFFGDKMSPLSDTTG	IS		
	130	140	150	160	170	180
	190	200	210	220	230	240
a709.pep	SIVGIDLFEHIKNM	MYTTIPAWLISXXLM	XLPSVAAQDLNSVESFRSQLEATGLV	H		
m709	SIVGIDLFEHIKNM	MYTTIPAWLISAA	LMWLPLNVAAQDLNSVESFRSQLEATGLV	H		
	190	200	210	220	230	240
	250	260	270	280	290	300
a709.pep	SLIPFALLVVLALMR	VNAVVLFTVIAAV	AVTYLHSTPDLRQLGAWFYGGYKLEGE	AXX		
m709	SLIPFALLVILALMR	INAVVLFTVMVAV	AVTYLHSTPDLRQLGAWFYGGYKLEGE	AFK		
	250	260	270	280	290	300
	310	320	330	340	350	360
a709.pep	DIAKLISRGGLESM	FFTQTIVILGMSL	GGLLFALGAIPSL	LDVRSFLT	NAGRXTFS	VAM
m709	DVVKLISRGGLESM	FFTQTIVILGMSL	GGLLFALGVIPSL	LEAIRFTLT	NAGRATFS	VAM
	310	320	330	340	350	360
	370	380	390	400	410	420
a709.pep	TSVGVNFLIGE	QYLSILLSGETFK	PVYDKLGLHSRNL	SRTLEDAGTVIN	PLVPWSVCGVF	
m709	TSVGVNFLIGE	QYLSILLSGETFK	PVYDKLGLHSRNL	SRTLEDAGTVIN	PLVPWSVCGVF	
	370	380	390	400	410	420
	430	440	450	460		
a709.pep	IXHALGVPVWEYLPYA	FFCYLSLALTLLFG	WTGLTLSKKX			
m709	ISHALGVPVWEYLPYA	FFCYLSLALTLLFG	WTGLTLSKKX			
	430	440	450	460		

g710.seq not found

g710.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2385>:

m710.seq  
 1 ATGGAACCC ACGAAAAAT CCGCCTGATG CGCGAATTGA ATAAATGGTC  
 51 CCAGGAGGAT ATGGCGGAAA AGCTGGCGAT GTCGGCAGGC GGGTATGCCA  
 101 AAATCGAACG GGGCGAAACG CAGTTAAATA TCCCGCGTTT GGAGCAGTTG  
 151 GCTCAGATTT TCAAAATCGA TATGTGGGAC TTGCTCAAAT CGGGCGGTGG  
 201 TGGGATGGTG TTTCAGATTA ATGAAGGTGA TAGTGGTGGC GATATTGCGT  
 251 TGTATGCGTC GGGTGATGTT TCGATGAAAA TAGAATTTTT AAAAATGGAG

301 TTGAAACACT GCAAAGAAAT GTTGGAAACAA AAAGACAAAG AAATCGAGCT  
351 GCTCCGCAAG CTGACCGAAA CCGTTTAA

```
m710.pep
  1  METHEKIRLM RELNKSQED MAEKLAMSAG GYAKIERGET QLNIPRLQL
 51  AQIFKIDMWD LLKSGGGGMV FQINEGDSGG DIALYASGDV SMKIEFLKME
101  LKHCKEMLEQ KDKEIELLRK LTETV*
```

```
a710.seq
1  ATGGAAACCC  ACGAAAAAAT  CCGCCTGATG  CGCGAATTGA  ATAAATGGTC
51  CCAGGAGGAT  ATGGCGGAAA  AGCTGGCGAT  GTCGCGAGGC  GGGTATGGTA
101 AAATCGAACG  AGTCGAAACG  CAGTTGAAT  TCCCGCGTTT  GGAGCAGCTT
151 GCGCAGATTT  TCAAATTGA  TATGTGGGAC  TTGCTCAAAT  CGGGCGGCGG
201 CGGGATGGTG  TTGCAGATTA  ACGATGTGGA  TACCAACAGC  GGGGAATTTG
251 CAATCTATAC  CGCTCAGGAT  GCATCNGGTA  AAGCTGGATT  TGTTAAATAT
301 GAATTAATAA  ACTGTAAGAT  ATAGTTGGAA  CACAAAGACA  AAGAAATCGA
351 GCTGCTCCGC  AAGCTGACCG  AAACCGTTTA  A
```

a710.pep

1	METHEKIRLM	RELNKWSQED	MAEKLAMSAG	GYAKIERGET	QLNIPRLEQL
51	AQIFKIDMWD	LLKSGGGGMV	LQINDVDTNS	GEFAIYTAQD	ASGKAGFVKM
101	ELKHCKEMLE	HKDKIEILLR	KLTETV*		

```

      10      20      30      40      50      60
a710.pep  METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLEQLAQIFKIDMWD
          |||||||||||||||||||||||||||||||||||||||||||||||
m710      METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLEQLAQIFKIDMWD
          10      20      30      40      50      60

      70      80      90      100     110     120
a710.pep  LLKSGGGGMVLQINDVDTNSGEFAIYTAQDASGKAGFVKMELKHCKEMLEHKDKETIELLR
          |||||||::||: |:|::|::|:| |:| |::| |||||::| |||||
m710      LLKSGGGGMVFAQINEGDSG-GDIALYASGDVSMKIEFLKMELEHKCKEMLEQKDKETIELLR
          70      80      90      100     110

a710.pep  KLTETVX
          |||||
m710      KLTETVX
          120

```

1147

g711.seq not found

g711.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2389>:

```
m711.seq
1  ATGCCCCGCGC CTGATTGTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAGTA AAAAGGTTAC GGCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAACTTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GGCGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTTCCGCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAT ATGCAAAC TGCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAAC TGCC
551 GCTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTTGGGC AAAGCACGGC GGACAATCTG GTCGAGACCC ATAAATCTA
651 CAACAAAAAA GGCGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAACACAGC TTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AGGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG
```

This corresponds to the amino acid sequence <SEQ ID 2390; ORF 711>:

```
m711.pep
1  MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTASEIA KVYTIARMTD
51  LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTRPAHSAI DGLVRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTADNL VETHKIYNKK GDTYLTLAYK APDGSlyTTD RGFdynAGRM
251 NYRPDLDKYD RALAHQFAKA EMGGADFKTS FKQLEKEFYE VKQRLDIDGK
301 PDKEQKIKIR NALSRQLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYYAFLPDM LQNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2391>:

```
a711.seq
1  ATGCCCCGCGC CTGATTGTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAGTA AAAAGGTTAC GGCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAACTTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GGCGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTTCCGCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAC ATGCAAAC TGCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAAC TGCC
551 GTTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTTGGGC AAAGCACGTC GGACAATCTT GTTGAGACCC ATAAATCTA
651 CAACAAAAAA GGCGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAACACAGC TTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
```

1148

```

901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTGCT GCGGGTGAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AAGGGCAGAA TTTTCGATGAC TCCTACTATG CTTTTTTTGGC
1101 GGATATGCTG CAAAACCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2392; ORF 711.a>:

```

a711.pep
1  MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTAASEIA KVYTIARMTD
51  LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTTPAHSAL DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTSDNL VETHKIYNKK GDTYLTLAYK APDGSlyTD RGFdynAGRM
251 NYRPDLDKYD RALAHQFAKA EMGGADFKTS FKQLEKEFYE VKQRLDIDGK
301 PDKEQKIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*

```

a711/m711 99.8% identity in 431 aa overlap

	10	20	30	40	50	60
a711.pep	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTAASEIAKVYTIARMTDLDMLNDIKTS					
m711	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTAASEIAKVYTIARMTDLDMLNDIKTS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a711.pep	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
m711	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
	70	80	90	100	110	120
	130	140	150	160	170	180
a711.pep	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTTPAHSALDGLVYRYDDPFWATFYPPNG					
m711	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTTPAHSALDGLVYRYDDPFWATFYPPNG					
	130	140	150	160	170	180
	190	200	210	220	230	240
a711.pep	YNCRCSVIALSERDVERQGRIVGQSTSDNLVETHKIYNKKGDTYLTLAYKAPDGSlyTDD					
m711	YNCRCSVIALSERDVERQGRIVGQSTADNLVETHKIYNKKGDTYLTLAYKAPDGSlyTDD					
	190	200	210	220	230	240
	250	260	270	280	290	300
a711.pep	RGFDYNAGRMNYRPDLDKYDRALAHQFAKAEMGGADFKTSFKQLEKEFYEYVKQRLDIDGK					
m711	RGFDYNAGRMNYRPDLDKYDRALAHQFAKAEMGGADFKTSFKQLEKEFYEYVKQRLDIDGK					
	250	260	270	280	290	300
	310	320	330	340	350	360
a711.pep	PDKEQKIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
m711	PDKEQKIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
	310	320	330	340	350	360
	370	380	390	400	410	420
a711.pep	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
m711	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
	370	380	390	400	410	420

1149

a711.pep	AKFMAKKKVLKX
m711	AKFMAKKKVLKX
	430



1150

g712.seq not found yet

g712.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2393>:

```

m712.seq
1   ATGATGCCCC ATATTGATTT TGACACGATT CCGGGCAGCA TCCGCGTGCC
51  CGGGCAGTAT ATTGAATTTA ACACCCGCAA TGCCGTACAA GGTTTGCCGC
101 AAAATCCGCA AAAGGTATTG ATGGTTGCAC CCATGCTGAC CGCGGGCATA
151 CAGCCCGCCT TAGAGCCGGT GCAACTATTT AGCGATGCCG AGGCGGCCGA
201 TTTGTTCGGA CAAGGCTCGC TGGCGCATTT GATGGTGCGC CAAGCATTTG
251 CCAACAACCC TTATTTGGAT TTGACCGTTA TCGGTATTGC CGACCACAGC
301 GCAGGCGTGC AGGCAACCGC AACCGTTACC CTTTCCGGCA CGGCCACCGC
351 GCCGGGCGTG GTGGAATCA CGATTGGCGG CAAGCAGGTA AGCACGGCCG
401 TTAACACCGG CGAGACCGCC GCCACAGTGG CAGACCGTCT GAAAACCGCC
451 ATCACTGCCG CCGATGTAAC CGTTACCGCA TCCGGCAGCG GCGCAGCCGT
501 TACGCTGACG GCCAAACACA AAGGCGAGAT CGGCAACGAG AGCGGCTTAA
551 CCGTGAGCAC CGGCAATACC GGCCTAACCT ATCAAGCCAA TGCCTTTACC
601 GGCGGTGCCA AAAATGCGGA CATTGCCACG GCCTTGTTCA AAGTGGCGGG
651 CAAGCATTAT CACATTATTT GCAGCCCGTT TAGCGATGAC GCCAACGCCA
701 AAGCCTTGAG CAACCATATT ACCAACGTAT CCAACGCCAT CGAGCAGCGC
751 GGCTGTATCG GCGTATTGGG TATGAGTGCG GCCTTGAGCA CGGCCACCAC
801 CGCTACCGGC GAAATCAACG ACGGCCGCAT GACCTGTGCT TGGTACAAAG
851 GTGCGGTAGA GCCAAACGGC ATCATCGCCG CAGGTTATGC GCGCGTGTG
901 GCCTTTGAAG AAGACCCTGC CAAGCCGCTG AACACGCTGG AAATCAAAGG
951 GCTGGCCGTT ACACCTGATG CGCAATGGCC GCTGTTTGCA GAATGCAACA
1001 ATGCGCTGTA CAACGGCTTG ACCCCGCTCA CAGTGGTCAA CAACCGCGTG
1051 CAGATTATGC GTGCCGTATC CACCTATACC AAGTCGGCCA ACAACACCGA
1101 CGACCCGGCA CTACTCGACA TTACCACCAT CCGCACGCTG GATTATGTGC
1151 GCCGCAGCGT TAAAGAGCGC ATTGCCCTGC GTTTTCCGCG CGACAAATTG
1201 AGCGACCGCC TGCTGCCCAA GGTTAAGAGC GAGATTTTGG ACGTGCTGAT
1251 TAAGCTCGAC CAAGCCGAAA TCATCGAAAA CGCCGAGGCC AACAAAGGCA
1301 AGCTGGTGGT GGCGCGTGCG CAAAACGACC CCAACCGTGT TAATGCCATT
1351 ATCCCCGCGG ATGTGGTCAA CGGCCTGCAC GTCTTTGCCG GGCGCATTGA
1401 TTTGATTTTG TAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2394; ORF 712&gt;:

```

m712.pep
1   MMPHIDFDTI PGSIRVPGQY IEFNTRNAVQ GLPQNPKVL MVAPMLTAGI
51  QPALEPVQLF SDAEAADLFG QGSLAHL MVR QAFANNPYLD LTVIGIADHS
101 AGVQATATVT LSGTATAPGV VEITIGKQV STAVNTGETA ATVADRLKTA
151 ITAADVTVTA SGSGAAVTLT AKHKGEIGNE SGLTVSTGNT GLTYQANAFT
201 GGAKNADIAT ALSKVAGKHY HIICSPFSDD ANAKALSNHI TNVSNAIEQR
251 GCIGVLGMSA ALSTATTATG EINDGRMTCA WYKGAVEPNG IIAAGYAAVL
301 AFEEDPAKPL NTLEIKGLAV TPDAQWPLFA ECNNALYNGL TPLTVVNNRV
351 QIMRAVSTYT KSANNDDPA LLDITTIRTL DYVRRSVKER IALRFPRDKL
401 SDRLLPKVKS EILDVLKLD QAEIENAEA NKGKLVVARA QNDPNRVNAI
451 IPADVNVNGLH VFAGRIDLIL *

```

a712.seq not found yet

a712.pep not found yet

1151

g713.seq not found yet

g713.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2395>:

m713.seq

```

1   ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTTCGATTTT GTCATCGGCA GGTGTTGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCA
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 CCGAAAACAA CCCCCTTTG GGCAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGCGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CTGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCCTTTT CCGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGAGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGCC GCATTGCAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAAACCCGC GACGGCGTAT TGTGGCAACC TGGCCTGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CCCGCATGGA TGGTACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
1101 CAAAAGGC GGCAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2396; ORF 713&gt;:

m713.pep

```

1   MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51  IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGSRELSLS GRDLAGFLVD
101 CSAPQLNVKG MVLDAKKL AAPWPQIKAV VLKAENNPAL GKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLVVGGAD YSSPPVATLC WSRTDSRCNI
201 ERMIDIEWTD NRFSEVTFLA QSHGRSGDSA KHDLLKVVYKD PTMTLHRPKT
251 VVVSADANLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVLWQPLR
301 VHVIDDEHGI DAVFFLMGRR FMLSRMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGRK KGVSHKGKKG GKKQAEAVF E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2397>:

a713.seq

```

1   ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTTCGATTTT GTCATCGGCA GGTGTTGGGCC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCG
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 TCGAAAACAA CCCCCTTTG GACAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGTGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CCGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCCTTTT CTGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGAGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGCC GCATTGCAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAAACCCGC GACGGCGTAT TGTGGCAACC TGGCCAGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CTCGCATGGA TGGCAGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG

```

1152

1101 CAAAAAAGGC GGCAAAAAC AAGCAGAAAC GCGGGTGT TT GAATGA

This corresponds to the amino acid sequence &lt;SEQ ID 2398; ORF 713.a&gt;:

## a713.pep

```
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSDFD VIGRLGPEAA
51  IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGGRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTVLDAAKKL AAPWPQIKAV VLKVENNPAL DKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLLVGGVD YSSPPVATLC WSRTDSRRNI
201 ERMDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDLLKVVYKD PTMTLHRPKT
251 VVVSDADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVWLQPGQR
301 VHVIDDEHGI DAVFFLMGRR FMLSMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGRK KGVSHKGGKG GKKQAETAVF E*
```

## a713/m713 98.4% identity in 381 aa overlap

	10	20	30	40	50	60
a713.pep	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSDFDVIGRLGPEAAIPDLSGESCE					
m713	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSDFDVIGRLGPEAAIPDLSGESCE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a713.pep	VVIDGQIVMTGIIGSQRHGKSKGGRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAAKKL					
m713	VVIDGQIVMTGIIGSQRHGKSKGSRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAAKKL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a713.pep	AAPWPQIKAVVLKVENNPALDKIDIEPGETVWQALTHIANSVGLHPWLEPDGTLLVGGVD					
m713	AAPWPQIKAVVLKAENNPALGKIDIEPGETVWQALTHIANSVGLHPWLEPDGTLLVGGAD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a713.pep	YSSPPVATLCWSRTDSRRNIERMDIEWDTDNRFSEVTFLAQSHGRSGDSAKHDLKVVYKD					
m713	YSSPPVATLCWSRTDSRCNIERMDIEWDTDNRFSEVTFLAQSHGRSGDSAKHDLKVVYKD					
	190	200	210	220	230	240
	250	260	270	280	290	300
a713.pep	PTMTLHRPKTVVVSADNLAALQKQAKKQLADWRLEGFTLTITVGGHKTRDGVWLQPGQR					
m713	PTMTLHRPKTVVVSADNLAALQKQAKKQLADWRLEGFTLTITVGGHKTRDGVWLQPGRLR					
	250	260	270	280	290	300
	310	320	330	340	350	360
a713.pep	VHVIDDEHGIDAVFFLMGRRFMLSMDGTQTELRLKEDGIWTPDAYPKKAEAAARKRKGR					
m713	VHVIDDEHGIDAVFFLMGRRFMLSMDGTQTELRLKEDGIWTPDAYPKKAEAAARKRKGR					
	310	320	330	340	350	360
	370	380				
a713.pep	KGVSHKGGKGGKKQAETAVFEX					
m713	KGVSHKGGKGGKKQAETAVFEX					
	370	380				

1153

g714.seq not found yet

g714.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2399>:

```
m714.seq
1   ATGAGCTATC AAGACATCTT GCGGGGCTGT TTGCCCCCGG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GGCGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 CGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGG
201 CGGTACGGGC AAAAACC GCCGCGTGT GTTGGCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAAACCGC GCCGGCGACC GTCTTGC GCCAGGAAATC ATGTGGGTGT
401 GGCACGTTAA CGTGC GCGGC GGCAACAACC GCATTACCCG ATCCGCGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGCTA A
```

This corresponds to the amino acid sequence <SEQ ID 2400; ORF 714>:

```
m714.pep
1   MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
51  RSAGQMLADW ERLGLDGTG KNRQHRVLAV MAKNETGGL SIPYFVRLAE
101 AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVVRG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2401>:

```
a714.seq
1   ATGAGCTATC AAGACATCTT GCGGGGCTGT TTGCCCCCGG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GGCGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 AGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGG
201 CGGTACGGGC AAAAACC GCCGCGTGT GTTGGCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAAACCGC GCCGGCGACC GTCTTGC GCCAGGAAATC ATGTGGGTGT
401 GGCACGTTAA CGTGC GCGGC GGCAACAACC GCATTACCCG ATCCGCGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGATA A
```

This corresponds to the amino acid sequence <SEQ ID 2402; ORF 714.a>:

```
a714.pep
1   MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
51  SSAGQMLADW ERLGLDGTG KNRQRRVLAV MAKNETGGL SIPYFVRLAE
101 AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVVRG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

**a714/m714 98.9% identity in 186 aa overlap**

	10	20	30	40	50	60
a714.pep	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPSSAGQMLADW					
m714	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPSSAGQMLADW					
	10	20	30	40	50	60
	70	80	90	100	110	120
a714.pep	ERVLGLDGTGKNRQRRVLAVMAKNETGGLSIPYFVRLAEAAAGYQIQIDE PQPFRAGVNR					
	:					
m714	ERVLGLDGTGKNRQHRVLAVMAKNETGGLSIPYFVRLAEAAAGYQIQIDE PQPFRAGVNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a714.pep	AGDRLAPQEI MWVWHVNVVRG GNNRITRFRA GISAAGDRLT DYSDAVIESL FNRLKPAHTA					

1154

m714 AGDRLAPQEIMWVHVNVVRGGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA  
 130 140 150 160 170 180

a714.pep IRFTYRX  
 |||||  
 m714 IRFTYRX

g715.seq not found yet

g715.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2403>:

m715.seq  
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA  
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT  
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT  
 151 CCGAAATGGG TTGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTTC  
 201 GGGTCGTCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC  
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCTT CGGCGGTATG  
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT  
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT  
 401 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2404; ORF 715>:

m715.pep  
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR  
 51 PKWVGLKYRD GKPLSDSRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM  
 101 AGRNRKVRIP QREFLTLD DD KQALMDDVQ DYFSGSLIP\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2405>:

a715.seq  
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA  
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT  
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT  
 151 CCGAAATGGT TGGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTTC  
 201 GGGTCGTCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC  
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCTT CGGCGGTATG  
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT  
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT  
 451 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2406; ORF 715.a>

a715.pep  
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR  
 51 PKWLGLKYRD GKPLSDSRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM  
 101 AGRNRKVRIP QREFLTLD DD KQALMDDVQ DYFSGSLIP\*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2407>:

g716.seq  
 1 ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT  
 51 GGCCGCCGCG GCCGTGCGG CCCACAAACC GGCAAGCAAC GCAACAGGCG  
 101 TTCAAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT  
 151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC  
 201 TAAAGCAGGC GAAGGCAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA  
 251 AAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC  
 301 GAAGGCAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2408; ORF 716.ng>:

g716.pep  
 1 MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG  
 51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA

m716.seq

1	ATGAACAAAA	ACATTGCTGC	CGCTCTCGCC	GGTGCTTTAT	CCCTGTCTTT
51	GGCCGCCGGT	GCAGTTGTCT	CCAACAAACC	GGAAGCAAC	GCAACAGGCG
101	TTCTATAATT	CGCCCATGGC	TCTTGGCGGC	CGTCCAAAT	TGCCCAAGGT
151	TCGTGCGCGC	CGGCTGGTTC	TAAAGCAGGC	GAAGGCAAT	CGCGCGAGGG
201	CAAATGCGGT	GCGACCGTAA	AAAAAACCCA	CAACACACC	AAAGCATCTA
251	AAGCCAAGGC	CAAATCTGCC	GAAGGCAAT	GCGCGAAGG	CAAATGCGGT
301	TCTAAATAA				

m716.pgp

1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG  
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG  
101 SK\*

m716/g716 86.6% identity in 112 aa overlap

```

      10      20      30      40      50
m716.pep  MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKS AHGSCGASKSAEGSCGA-----
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g716      MNKNIAAALAGALSLSLAAGAVA AHKPPASNATGVQKSAQGSCGASKSAEGSCGASKSAEG
          10      20      30      40      50      60

      60      70      80      90      100
m716.pep  ----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
          :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g716      SCGAAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX
          70      80      90      100      110

```

a716.seq

1	ATGAACAAAA	ACATTGCTGC	CGCACTCGCC	GGTGCTTTAT	CCCTGTCTTT
51	GGCCGCGCGT	GCAGTTGCTG	CCAAACAAAC	GGCAAGCAAC	GCACACGGCG
101	TTCATAAAATC	CGCCCATGGC	TCTTGGCGCG	CGTCCAAATC	TGCCGAAGGT
151	TCGTGCGGCG	CGGCTGGTTC	TAAAGCAGGC	GAAGGCAAAAT	GC GCGAGGG
201	CAAATGCGGT	GCGACCGTAA	AAAAAACCCA	CAACACACC	AAAGCATCTA
251	AAGCCAAGGC	CAAATCTGCC	GAAGGCAAAAT	GCGGCGAAGG	CAAATGCGGT
301	TCTAAATAA				

a716.pgp

1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG  
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG  
101 SK\*

```

              10          20          30          40          50          60
a716.pep  MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKS AHGSCGASKSAEGSCGAAGSKAG
          |||||
m716      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKS AHGSCGASKSAEGSCGAAGSKAG
              10          20          30          40          50          60

              70          80          90          100
a716.pep  EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
          |||||
m716      EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
              70          80          90          100

```

g717.seq

1 ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC

1156

```

51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCcccgCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  ACTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CGCCGCCGAC  AAAGACACTT  TGTTCAAAAC  CCTGTTCTGT  CCGCCGCTGC
251  TGTTTTCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCGCT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  GCGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAA
451  CTCGCCATCC  TGCTGCTGTT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  GCGGAACACC  TCCGTCCTGA  CCGCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCT  TTTGCTGTTT  CAAAACCGAT  GCCGTCTGAA  GGCCGTCCGG
601  CGCGCGCCGT  TTTCCGCCGC  CGTCCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGCTCGCA  CTGAGCAGCC  TTGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTTCT  GAAAAAATAT  GCGGGCCTGG  AACAGCTCGG  CGTTTATTTC
751  ATGGGTATTT  CGTTCGGCGG  GCGGCATTAT  TTGCTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTTCCGTGC  AATCGAAGAA  AACGCCACGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAATCCG  CCGCCGCCCT  GCTTGCCTCC
901  GCCCTCTGCC  TGACCGGAAT  TTTCTCGCCC  CTCGCCTCCC  TCCTGTGCTC
951  GGAAAACACT  GCCGCCGTCC  GGTTTACCGT  CGTATCGTGT  ATGCTGCCGC
1001  cgtGTTTTTA  CACGCTGACC  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GTCGATCGCG  GCTTGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CTGCTGCTG  CTGGGGCTTG  CCGTACCGTC  CGGCGGCACG  CGCGGCGCGG
1151  CGGTTGCCCT  TGCCGCCTCA  TTCTGGTTGT  TTTTGTGTTT  CAAGACAGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAAA  CGCTGCGCGC  TTTATATGCA
1251  CACATTGTTT  TGCTTgCCCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACAC
1301  CGGCAAACTA  CCCctgttt  gccggcgat  GGGCGGCATA  TCTGGCAGGC
1351  TGATCCTGCT  GCCACCGGAA  AAATTGACAC  AAAGTGTTC  ATTATTTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2414; ORF 717.ng>:

g717.pep

```

1  MDTKEILGYA  AGSIGSAVLA  VIILPLLSWY  FPADDIGRIV  LMQTAAGLTV
51  SVLCLGLDQA  YVREYYAAAD  KDTLFKTLFL  PPLLFSAIA  ALLLSRPSLP
101  SELFLSLDDA  AAGIGLVLE  LSFLPIRFL  LVLRMGRAL  AFSSAQLVPK
151  LAIIIIIIPLT  VGLLHFPANT  SVLTAVYALA  NLAAAFLLF  QNRCRLKAVR
201  RAFPSPAVLH  RGLRYGIPLA  LSSLAYWGLA  SADRLFLKKY  AGLEQLGVYS
251  MGISFGGAAL  LLOSFSTVW  TPYIFRAIEE  NATPARLSAT  AESAAALLAS
301  ALCITGIFSP  LASLLLPENY  AAVRFTVVS  MLPLFYTLT  EISGIGLNVV
351  RKTRPIALAT  LGALANLLL  LGLAVPSGGT  RGAAVACAAS  FWLFVFKTE
401  SSCRLWQPLK  RPLMYHTLF  CLASSAAYTC  FGTPTYPLF  AGVWAAYLAG
451  CILRHRKNLH  KLFHYLKKQG  FPL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2415>:

m717.seq

```

1  ATGGACACAA  AAGAAATCCT  CGGCTACGCG  GCAGGCTCGA  TCGGCAGCGC
51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCCCGCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  GCTGACGGTG
151  TCGGTGTTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CACCGCCGAC  AAAGACACCT  TGTTCAAAAC  CCTGTTCTGT  CCGCCGCTGC
251  TGTCTGCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCACT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  ACGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAG
451  CTCGCCATCC  TGCTGCTGCT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  AGCGAACACC  GCCGTCCTGA  CCGCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCT  TTTGCTGTTT  CAAAACCGAT  GCCGTCTGAA  GGCCGTCCGG
601  CACGCACCGT  TTTCCGCCGC  CGTCCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGATCGCA  CTGAGCAGCA  TCGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTTCT  GAAAAAATAT  GCCGGCCTGG  AACAGCTCGG  CGTTTATTTC
751  ATGGGTATTT  CGTTCGGCGG  GCGGCATTAT  TTGTTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTTCCGCGC  AATCGAAGAA  AACGCCCCGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAATCCG  CCGCCGCCCT  GCTTGCCTCC
901  GCCCTCTGCC  TGACCGGCAT  TTTCTCGCCC  CTTGCCTCCC  TCCTGTGCTC
951  GGAAAACACT  GCCGCCGTCC  GGTTTATCGT  CGTATCGTGT  ATGCTGCCGC
1001  CGCTGTTTTG  CACGCTGGCG  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GTCGATCGCG  GCTCGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCTGCTGCTG  CTGGGGCTTG  CCGTGCCGTC  CGGCGGCGCG  CGCGGCGCGG
1151  CGGTTGCCCT  TGCCGCCTCA  TTCTGGCTGT  TTTTGTGCTT  CAAGACCGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAAA  CGCCTGCCGC  TTTATCTGCA
1251  CACATTGTTT  TGCTTgACCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACAC
1301  TCGCAAACTA  TCCCTGTGTT  GCCGCGTAT  GGGCGGCATA  TCTGGCAGGC
1351  TGATCCTGCT  GCCACCGGAA  AGATTGACAC  AAAGTGTTC  ATTATTTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2416; ORF 717>:

## m717.pep

```

1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCLGLDQA YVREYYATAD KDTLFKTLFL PPLLSAAAIA ALLSRPSLP
101 SEILFSLDDA AAGIGLVLEF LSFLPIRFLF LVLRMGRAL AFSSAQLVPK
151 LAIIIIIIPLT VGLLHFPANT AVLTAVYALA NLAAAAFLLF QNRCRLKAVR
201 HAPFSPAVLH RGLRYGIPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFQSIFFSTVW TPYIFRAIEE NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLLPENY AAVRFIVVSC MLPPLFCTLA EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFAFKTE
401 SSCRLWQPLK RLPLYLHTLF CLTSSAAYTC FGTANYPLF AGVWAAYLAG
451 CILRHRKDLH KLFHYLKKQG FPL*

```

m717/g717 96.4% identity in 473 aa overlap

m717.pep	10	20	30	40	50	60
	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
g717	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
m717.pep	70	80	90	100	110	120
	YVREYYATADKDTLFKTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLEF					
g717	YVREYYAAADKDTLFKTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLEF					
m717.pep	130	140	150	160	170	180
	LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAIIIIIIPLTVGLLHFPANTAVLTAVYALA					
g717	LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAIIIIIIPLTVGLLHFPANTSVLTAVYALA					
m717.pep	190	200	210	220	230	240
	NLAAAAFLLFQNRCLKAVRHAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY					
g717	NLAAAAFLLFQNRCLKAVRRAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY					
m717.pep	250	260	270	280	290	300
	AGLEQLGVYSMGISFGGAALLFQSIFFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS					
g717	AGLEQLGVYSMGISFGGAALLFQSIFFSTVWTPYIFRAIEENATPARLSATAESAAALLAS					
m717.pep	310	320	330	340	350	360
	ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLAIEISGIGLNVVRKTRPIALAT					
g717	ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFYTLTEISGIGLNVVRKTRPIALAT					
m717.pep	370	380	390	400	410	420
	LGALANLLLGLAVPSGGARGAACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF					
g717	LGALANLLLGLAVPSGGTRGAACAASFWLFFVFKTESSCRLWQPLKRLPLYMHTLF					
m717.pep	430	440	450	460	470	
	CLTSSAAYTCFGTPANYPLFAGVWAAYLAGCILRHRKDLHKLHLYLKKQGFPLX					
g717	CLASSAAYTCFGTPANYPLFAGVWAAYLAGCILRHRKDLHKLHLYLKKQGFPLX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2417>:

## a717.seq

```

1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
51  GGTTTTAGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCCCTGCCG
101 ACGACATCGG ACGCATCGTG CTGATGCAGA CGGCGGCGGG GCTGACGGTG
151 TCGGTGTTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC
201 CGCCGCCGAC AAAGACACTT TGTTCAAAAC CCTGTTCTCT CCGCCGCTGC

```



1158

```

251 TGTCTGCCGC CGCGATAGCC GCCCTGCTGC TTTCCCGCCC ATCCCTGCCG
301 TCTGAAATCC TGTTTTCGCT CGACGATGCC GCCGCCGGCA TCGGGCTGGT
351 GCTGTTTGAA CTGAGCTTCC TGCCCATCCG CTTTCTCTTA CTGGTTTTGC
401 GTATGGAAGG ACGCGCCCTT GCCTTTTCGT CCGCGCAACT CGTGTCCAAG
451 CTCGCCATCC TGCTGCTGCT GCCGCTGACG GTCGGGCTGC TGCACTTTCC
501 GGCGAACACC GCCGTCCTGA CCGCCGTTTA CGCGCTGGCA AACCTTGCCG
551 CCGCCGCCTT TTTGCTGTTT CAAAACCGAT GCCGCTGAA GGCCGTCGGG
601 CGCGCACCGT TTTCATCCGC CGTCCTGCAT CGCGGCCTGC GCTACGGCAT
651 ACCGATCGCA CTAAGCAGCA TCGCCTATTG GGGGCTGGCA TCCGCCGACC
701 GTTTGTTTCT GAAAAAATAT GCCGGCCTAG AACAGCTCGG CGTTTATTCTG
751 ATGGGTATTT CGTTCGGCGG AGCGGCATTA TTGTTCCAAA GCATCTTTTC
801 AACGGTCTGG ACACCGTATA TTTTCCGCGC AATCGAAGCA AACGCCCCCG
851 CCGCCCGCCT CTCGGCAACG GCAGAAATCCG CCGCCGCCCT GCTTGCCCTCC
901 GCCCTCTGCC TGACCGGCAT TTTCTGCCCC CTCGCCTCCC TCCTGCTGCC
951 GGAAACTAC GCCGCCGTCC GGTTTATCGT CGTATCGTGT ATGCTGCCTC
1001 CGCTGTTTTG CACGCTGGTA GAAATCAGCG GCATCGGTTT GAACGTCGTC
1051 CGAAAAACAC GCCCGATCGC GCTCGCCACC TTGGGCGCGC TGGCGGCCAA
1101 CCTGCTGCTG CTGGGGCTTG CCGTACCGTC CGGCGGCGCG CGCGGCGCGG
1151 CGGTTGCCTG TGCCGCCTCA TTTTGGCTGT TTTTGTGTTT CAAGACCGAA
1201 AGCTCCTGCC GCCTGTGGCA GCCGCTCAAA CGCCTGCCGC TTTATATGCA
1251 CACATTGTTT TGCTGGCCTT CCTCGGCGGC CTACACCTGC TTCGGCACTC
1301 CGGCAAACTA CCCCTGTTT GCCGCGGTAT GGGCGGTATA TCTGGCAGGC
1351 TGCATCCTGC GCCACCGGAA AGATTGTCAC AAAGTGTTC ATTATTTGAA
1401 AAAACAAGGT TTCCATTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2418; ORF 717.a>:

```

a717.pep
  1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
 51  SVLCLGLDQA YVREYYAAAD KDTLFKTLFL PPLLSAAAIA ALLLSRPSLP
101  SEILFSLDDA AAGIGLVLFE LSFLPIRFL LVLMEGRAL AFSSAQLVSK
151  LAILLLLPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201  RAPFSSAVLH RGLRYGIPIA LSSIAYWGLA SADRLFLKKY AGLEQLGVYS
251  MGISFGGAAL LFQSFSTVW TPYIFRAIEA NAPPARLSAT AESAAALLAS
301  ALCLTGIFSP LASLLLPENY AAVRFIVVSC MLPPLFCTLV EISGIGLNVV
351  RKTRPIALAT LGALAAANLLL LGLAVPSGGA RGAAVACAAS FWLFFVFKTE
401  SSCRLWQPLK RPLYMHTLF CLASSAAYTC FGTPANYPLF AGVWAVYLAG
451  CILRHRKDLH KLFHYLKKQG FPL*

```

a717/m717 97.9% identity in 473 aa overlap

```

              10      20      30      40      50      60
a717.pep      MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
              |||
m717           MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
              10      20      30      40      50      60

              70      80      90      100     110     120
a717.pep      YVREYYAAADKDTLFKTLFLPPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLFE
              |||
m717           YVREYYATADKDTLFKTLFLPPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLFE
              70      80      90      100     110     120

              130     140     150     160     170     180
a717.pep      LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLLLPLTVGLLHFPANTAVLTAVYALA
              |||
m717           LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLLLPLTVGLLHFPANTAVLTAVYALA
              130     140     150     160     170     180

              190     200     210     220     230     240
a717.pep      NLAAAFLLFQNRCLKAVRRAPFSSAVLHRLRYGIPIALSSIAYWGLASADRLFLKKY
              |||
m717           NLAAAFLLFQNRCLKAVRHAPFSPAVLHRLRYGIPIALSSIAYWGLASADRLFLKKY
              190     200     210     220     230     240

              250     260     270     280     290     300
a717.pep      AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEANAPPARLSATAESAAALLAS

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1159

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|||||
m717      AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS
           250      260      270      280      290      300

           310      320      330      340      350      360
a717.pep  ALCLTGIFSPASLLLPENYA AVR FIVVSCMLPPLFCTLVEISGIGLN VVRKTRPIALAT
           310      320      330      340      350      360
m717      ALCLTGIFSPASLLLPENYA AVR FIVVSCMLPPLFCTLA EISGIGLN VVRKTRPIALAT
           310      320      330      340      350      360

           370      380      390      400      410      420
a717.pep  LGALAANLLLLGLAVPSGGARGAAVACAASFVWFFVFKTESSCRLWQPLKRLPLYMHTLF
           370      380      390      400      410      420
m717      LGALAANLLLLGLAVPSGGARGAAVACAASFVWFFAFKTESSCRLWQPLKRLPLYLHTLF
           370      380      390      400      410      420

           430      440      450      460      470
a717.pep  CLASSAAYTCFGTPANYPLFAGVWAVYLAGCILRHRKDLHKL FHYLKKQGFPLX
           430      440      450      460      470
m717      CLTSSAAYTCFGTPANYPLFAGVWAA YLAGCILRHRKDLHKL FHYLKKQGFPLX
           430      440      450      460      470

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g718.seq not found yet

g718.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2419>:

```

m718.seq
1   TCAGACGGCC TTTACGTACC CCGAAACTTT ATCCACCGCC CGCAAAGCTG
51  GTTCAAATGG GACAAAGACA ACGGGCTGCT GCTGCGTACC CGCGAAAATC
101 CGGAAGGCGA AGCGTTGTGG CCGCTGGGCT GGGTCGTTCA TACCCAAAAA
151 TCGCGCAGCG TCCAGCAGGC GCGCAACGGG CTTTTCGCA CGCTTTCCTG
201 GCTGTATATG TTCAAACACT ACGCCGTCCA CGATTTTGCC GAGTTTTTGG
251 AGCTGTACGG CATGCCCATC CGTATCGGCA AATACGGCGC GGGCGCAACC
301 AAAGAGGAAA AAAACACCCT GCTTCGAGCG GTGGCGGAAA TCGGTCACAA
351 CGCGGCAGGC ATCATGCCAG AAGGTATGGA AATAGAGTC CACAACGCGG
401 CAAACGGTAC GACGGCAACC AGCAATCCGT TTTTGCAGAT GGCCGACTGG
451 TGCGAAAAAT CGGCGGCGCG GCTGATTTTG GGGCAAACGC TGACCAGCGG
501 TGCGGACGGA AAATCCAGCA CCAACGCGCT GGGCAATATC CACAACGAGG
551 TACGCCGCGA TTTGCTGGTG TCGGACGCAA AACAGGTGGC GCAAACCATC
601 ACAAGCCAAA TCATCGGACC GTTCCTGCAA ATCAACTATC CCCATGCCGA
651 CCCAAACCGC GTGCCGAAAT TTGAATTTGA CACGCGCGAG CCGAAAGACA
701 TCGCGGTCTT TGCCGACGCT ATCCCGAAAC TGGTGGATGT CGGCGTACAA
751 ATCCCCGAAA GCTGGGTGCG CGACAACTG GTCATTCCAG ATGTGCAGGA
801 GGGTGAGGCT GTGTTGGTGC GGCAGGTACC GGACAATCCG GTAAACAGAA
851 CTGCATTGGC GGCTTTATCC GCCCACACCG TACCATCTAA GGCTACGGGC
901 AGGCATCAGG AAATATTGGA CGGCGCGTTG GATGACGCGC TGGTTGAGCC
951 CGATTTCAAT TCTCAGCTCA ACCCGATGGT GCGTCAGGCG GTTGCCGCAC
1001 TTAATGCTTG CAACAGCTAC GAGGAGGCAG ATGCCGCACT GAATGCGCTT
1051 TATCCGAATT TGGACAACGC GAAACTGCGT ACCTATATGC AGCAGGCCTT
1101 GTTATCAGC GATATTTTGG GACAAGACCA TGCCCGCGCC TGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2420; ORF 718&gt;:

```

m718.pep
1   SDGLYVPRNF IHRPQSWFKW DKDNGLLLRT RENPEGEALW PLGWVVHTQK
51  SRSVQQARNG LFRTLRWLYM FKHYAVHDFE EFLELYGMPD RIGKYGAGAT
101 KEEKNTLLRA VAEIGHNAAG IMPEGMEIEL HNAANGTTAT SNPFQMDADW
151 CEKSAARLIL GQTLTSGADG KSSTNALGNI HNEVRRDLLV SDAKQVAQTI
201 TSQIIGPFLQ INYPHADPNR VPKFEFDTRE PKDIAVFADA IPKLVDVGVQ
251 IPESWVRDKL VIPDVQEGEA VLVVRQVPDNP VNRTALAALS AHTVPSKATG
301 RHQEILDGAL DDALVEPDFN SQLNPMVRQA VAALNACNSY EEADAALNAL
351 YPNLDNAKLR TYMQQALFIS DILGQDHARA *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2421>:

1160

**a718.seq**

```

1   ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACGCCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TGCCTACCCG CGAAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCTTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GGCGGAAATC GGTCACAACG CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCCGG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACCGGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCT GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACCTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2422; ORF 718.a>:

**a718.pep**

```

1   MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHELFADI EERDS DIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEEKLSL QAYEMMDSLP TLEDLIMDLM DAVGHGFSAL EVEWVFS DGL
151 YLPRNFIHRP QSWFKWDKDN GLLRLTREN PEGEALWPLGW VVHTQKSR SV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRLRAVAEI GHNAAGIMPE GMEIELHNA NGMTSAGNPF LQMA DWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGFPLQINYP HADPNRVPKF EFDTRPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAAVAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

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**a718/m718** 98.4% identity in 380 aa overlap

	120	130	140	150	160	170
a718.pep	DSLPTLEDLIMDLMDAVGHGFSALEVEWVFS					
m718	SDGLYVPRNFIHRPQSWFKWDKDNGLLLRT					
				10	20	30
	180	190	200	210	220	230
a718.pep	RENPEGEALWPLGWVVHTQKSRVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI					
m718	RENPEGEALWPLGWVVHTQKSRVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI					
	40	50	60	70	80	90
	240	250	260	270	280	290
a718.pep	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLQMA DW					
m718	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQMA DW					

1161

	100	110	120	130	140	150
a718.pep	300	310	320	330	340	350
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLQ					
m718	160	170	180	190	200	210
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKQVAQTITSQIIGPFLQ					
a718.pep	360	370	380	390	400	410
	INYPHADPNRVPKFEFDTREPKDIAVFADAIPKLVDPVGVQIPESWVRDKLVIPDVQEGEA					
m718	220	230	240	250	260	270
	INYPHADPNRVPKFEFDTREPKDIAVFADAIPKLVDPVGVQIPESWVRDKLVIPDVQEGEA					
a718.pep	420	430	440	450	460	470
	VLVRQVPDPNPNVRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
m718	280	290	300	310	320	330
	VLVRQVPDPNPNVRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
a718.pep	480	490	500	510	520	
	VAAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDCHARAX					
m718	340	350	360	370	380	
	VAAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDCHARAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2423>:

m718-1.seq

```

1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACGGCG ACCGGTCGGG
101 TTATCGCCGA GCATCCGTCC AATTTTATTA CGCCGCAAAA GATGCGGGCC
151 CTCTTCGAGG ACGCAGAAAG CGGCGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TGCCTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTCATA CCCAAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCCTGGC TGTATATGTT
651 CAAACACTAC GCGTCCACG ATTTGGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GCGGAAATC GGTCAACAAG CCGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TAGAGCTCCA CAACGCGGCA AACGGTACGA
851 CGGCAACCAG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTG ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACCGCTGG GCAATATCCA CAACGAGGTA CGCCGCGATT
1001 TGTGTTGTCT GAGCGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCCG CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2424; ORF 718-1>:

m718-1.pep.

```

1  MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHELFADI EERDS DIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEEKLSQ QAYEMMDSLP TLEDLIMDLM DAVGHGFSAL EVEWVFSDDL
151 YLPRNFIHRP QSWFKWDKDN GLLLRTRNP EGEALWPLGW VVHTOKSRSV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRLAVAEI GHNAAGIMPE GMEIELHNAA NGTTATSNPF LQADWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEV RRDLLVSDAK QVAQTITSQI

```

1162

351 IGPFLQINYP HADPNRVPKF EFDTPREPKDI AVFADAIPKL VDVGVQIPES  
 401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE  
 451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAL NACNSYEEAD AALNALYPNL  
 501 DNAKLRTYMQ QALFISDILG QDHARA\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2425>:

a718.seq  
 1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC  
 51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG  
 101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC  
 151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT  
 201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC  
 251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT  
 301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA  
 351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGGTAG  
 401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT  
 451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA  
 501 CAAAGACAAC GGGCTGCTGC TGCCTACCCG CGAAAATCCG GAAGGCGAAG  
 551 CGTTGTGGCG GCTGGGCTGG GTCGTTCTAT CCCAAAAATC GCGCAGCGTC  
 601 CAGACGGCGC GCAACGGGCT TTTCCGCACG CTTTCTGTCG TGTATATGTT  
 651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA  
 701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA  
 751 AACACCCTGC TTGAGCGCGT GGCGGAAATC GGTCACAACG CGGCAGGCAT  
 801 CATGCCAGAA GGTATGGAAA TCGAGCTGCA CAACGCGGCA AACGGCATGA  
 851 CTTCCGCGCG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG  
 901 GCGGCGCGCG TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA  
 951 ATCCAGCACC AACCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT  
 1001 TGGTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC  
 1051 ATCGGACCGT TCCTGCAAA CAACTATCCC CATGCCGACC CAAACCGCGT  
 1101 CCGGAAATTT GAATTTGACA CGCGCGAGCG GAAAGACATC GCGGTCTTTG  
 1151 CCACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC  
 1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT  
 1251 GTTGGTGCCG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG  
 1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCGG GCATCAGGAA  
 1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC  
 1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA  
 1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTG  
 1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA  
 1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

This corresponds to the amino acid sequence <SEQ ID 2426; ORF 718-1.a>:

a718.pep  
 1 MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA  
 51 LFEDAESGDI RAQHELFDI EERDSIAAN MGTRKRALLT LNWRVAPPRN  
 101 ATPEEEKLSL QAYEMMDSL TLEDLIMDL DAVGHGFSAL EVEWVFSGL  
 151 YLPRNFIHRP QSWFKWDKN GLLLRTRNP EGEALWPLGW VVHTQKRSV  
 201 QQRNGLFRT LSWLYMFKHY AVHDFAEFL LYGMPIRIGK YGAGATKEEK  
 251 NTLRLRAVEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQMDWCEKS  
 301 AARLILGQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI  
 351 IGPFLQINYP HADPNRVPKF EFDTPREPKDI AVFADAIPKL VDVGVQIPES  
 401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE  
 451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAL NACNSYEEAD AALNALYPNL  
 501 DNAKLRTYMQ QALFISDILG QDHARA\*

a718/m718-1 99.0% identity in 526 aa overlap

	10	20	30	40	50	60
a718.pep	MEPIMAKKNNKTKIQKPEAALQTDVAQITATGRVIAEHPSNFITPQKMRALFEDAESGDI					
m718-1	MEPIMAKKNNKTKIQKPEAALQTDVAQITATGRVIAEHPSNFITPQKMRALFEDAESGDI					
	10	20	30	40	50	60
a718.pep	RAQHELFDIEERDSIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSLQAYEMMDSL					
m718-1	RAQHELFDIEERDSIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSLQAYEMMDSL					
	70	80	90	100	110	120
a718.pep	TLEDLIMDLMDAVGHGFSALEVEWVFSGLYLPRNFIHRPQSWFKWDKNGLLLRTRNP					
m718-1	TLEDLIMDLMDAVGHGFSALEVEWVFSGLYLPRNFIHRPQSWFKWDKNGLLLRTRNP					
	130	140	150	160	170	180
a718.pep	TLEDLIMDLMDAVGHGFSALEVEWVFSGLYLPRNFIHRPQSWFKWDKNGLLLRTRNP					
m718-1	TLEDLIMDLMDAVGHGFSALEVEWVFSGLYLPRNFIHRPQSWFKWDKNGLLLRTRNP					

1163

	190	200	210	220	230	240
a718.pep	EGEALWPLGWVVHTQKSRSVQQARNGLFRTL	SWLYMFKHYAVHDFAEFLELYGMP	IRIGK			
m718-1	EGEALWPLGWVVHTQKSRSVQQARNGLFRTL	SWLYMFKHYAVHDFAEFLELYGMP	IRIGK			
	190	200	210	220	230	240
	250	260	270	280	290	300
a718.pep	YGAGATKEEKNTLLRAVAEIGHNAA	GIMPEGMEIELHNAANGMTSAGNPFLQ	MADWCEKS			
m718-1	YGAGATKEEKNTLLRAVAEIGHNAA	GIMPEGMEIELHNAANGTTATSNPFLQ	MADWCEKS			
	250	260	270	280	290	300
	310	320	330	340	350	360
a718.pep	AARLILGQTLTSGADGKSSTNALGNIHNEIRRD	LLVSDAKOVAQTITSQIIGPFLQINYP				
m718-1	AARLILGQTLTSGADGKSSTNALGNIHNEVRRD	LLVSDAKOVAQTITSQIIGPFLQINYP				
	310	320	330	340	350	360
	370	380	390	400	410	420
a718.pep	HADPNRVPKFEEDTREPKDIAVFADAIPKLVDVG	VQIPESWVRDKLVIPDVQEGEAVLVR				
m718-1	HADPNRVPKFEEDTREPKDIAVFADAIPKLVDVG	VQIPESWVRDKLVIPDVQEGEAVLVR				
	370	380	390	400	410	420
	430	440	450	460	470	480
a718.pep	QVPDNPVNRTALAALSAHTVPSKATGRHQEILD	GALDDALVEPDFNSQLNPMVRQAAAL				
m718-1	QVPDNPVNRTALAALSAHTVPSKATGRHQEILD	GALDDALVEPDFNSQLNPMVRQAAAL				
	430	440	450	460	470	480
	490	500	510	520		
a718.pep	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFIS	DILGQDHARAX				
m718-1	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFIS	DILGQDHARAX				
	490	500	510	520		

g719.seq not found yet

g719.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2427>:

m719.seq

```

1   ATGGCAAACG GGAACATGAA ACTGTCGTTG GTGTTAACCG CCCGAGATGA
51  CGGAGCGAGA CGGCTACTGG CTGATACTCA ACGACAATTA GATCGTACCG
101 CGAAATCGCG GCGCAACTT GAACGGCAA GCCATACTTA TCGGTTGACC
151 GGCATCCGCT CAGAAAAACA GATTCAACGC GAAATCATGC TGACACAGGC
201 TCGGTTTAAC CGTTTGGCGC GCAGCGGCAA GGCATCACAA AATGATTGCG
251 CACGGCGGCG GGTGCTACG CGTAACCGAA TTCGCGAGCT GAACGCGGAA
301 CTGAAACAGG GCACGGGATT TCGGACAAG ATGGGAAAAA TCGGAAGATT
351 CGGTGCAGCT GCGGTGGCTG GTGGCGCGGC AGCGTATACG GTGCTTAAGC
401 CTGCTATGGA CAACAGAAAG CAGCTTGATG AGAACATCAA CCGCGTGTCC
451 AGACAGGCAT TTATTGAGGA TAACAGTAAA TCGGCAGCGT GGATTGCAAC
501 TGAAGGTGCG CAACAGATCA AGGATTGGC ACTTGAACCT GTCGAGAAAA
551 ATGGCGGGAC CCACGATAAG GCTTTGGATT TAATCAGCGG CATGATGACC
601 ACCGCTCTGA ATTTTGCCCA AACCAAGAAT GAAGCGCAGG CGGCATATGC
651 TTTTGCACTT GCCTCAGAAG GCAGTGGCGA GGATACGGCA AAACCTGATTA
701 AAACCTGAA AGATGGCGGC ATGAGCGGTA AAGACCTGCA ACTCGGGCTT
751 GAGCACGTCT TGCAATCGGG TTTAGACGGC ACTTTCGAGG TGCGGGATAT
801 GGTTGCGGAG CTGCCGAGCC TGCTCTCTGC CGCGCAACAG GCAGGGATGA
851 ATGGTGTGCG CGGTTTGGAC TACCTGCTCT CACTCTTACA ATCTGCGGCG
901 AATAAATCGG GCAGTCCTGC CGAAGCGGCG ACTAATGTGC AAAATCTTTT
951 GAGTAAAACT CTGTCGCCTG ACACGATAGG TCGTCTGAAG AAGATGGCAA
1001 ATCCGAATGA CCCGAAGAAA GGTGTCGATT GGATAGGCTC GGTGTGCAA
1051 GGCAAGCAAA ACGGCGAAAA CGCAGTGCAG GTGTTGTCCC GTCTTGCCGA
1101 TGCCATGCTA GTAAAGGATA AGCAATACCA AGATTATAAG AAACGCGCGG
1151 CTGACGGCGA TAAGACGGCG GCGGAGCAGG CAAATATGCT TAAGGGCGCG
1201 CTTTGGCGC AACTGCTGCC TGATTGCGAG GCAAAACAA GTTTGCTGGC
1251 TGCAACGGAT ATGACGCAAA TCCGTGAATA TATGGCTTCG TTGGCTGGCG

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1164

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1301 TAACGTTGGA TAACGGAAAA ATTGCTAAGA ACAACGAGGC GCGAATGTTG
1351 TCGGCAGCGG CGCAACAAGA GCAACAGGAA TCGCTGGCAA TGTTGCGGGA
1401 AAGTCTGACG GGAACATTGG TGGATATGGA AACCTCGTTT AAAAAGCTGG
1451 CAGCGGAATA CCCTAATGCC ACTCTAGCCC TGCAAGCATT GACGACGGCG
1501 GCAACAGCGG CGTCTGCCGC AATGTTATTA ACCGCCGGTG GCGGTAAAGG
1551 TGCAGGCTTT CTGAAAGATG TAGGTAGTAA AGCGTTGGGA TGGGGTAAGG
1601 CTTCCGCAGG CGGCGTGGCA GCAGGTGCCA CAGCGGCAGG CGGTAAGTTG
1651 CTGTCATGGG GAAATCTGC CGGTAGCGGG CTCATGAATA ATCCAGCGTT
1701 AGTTAAACGG GCGGGTTTGT TAGGTATGTT GCTGTATTCC GAGTCTTTGG
1751 GTGACGGCAC ATTGCCAAAG GGTTTGCGTG GTACCAAGAC AACTCCTGAA
1801 ATGATTAATC GTCTGAAAA CAACGGTATC CGATTTGAAC CTGCGCCGAA
1851 GCGGGAACAG GCGCGGGGTG GTGTCCCTCA GTATTTGGCT GCTCCGTCAG
1901 CGCAGCCTAC CGATAAGATG TTGTCTCCGT TGTTTTCAAC TCAGACGGCG
1951 GCGTATCAGG CAGCCATTCA GCAGCAGACG GCGGCGTATC AGGCAGCATT
2001 GCGCAGGAT ACGGCTGCAG TTACAACAGG TTTGGCACAA GTGCAAAGTG
2051 CGATGGCGTC GGCAAGTCAG ACCATCAATA CCAATGTGAG CCTGAATATC
2101 GACGGACGTG TTATCGCGAA TGAGGTATCG CGGTATCAAG TGGCCATGTT
2151 CGGCCGTGGA GCGGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2428; ORF 719>:

**m719.pep**

```

1 MANGNMKLSL VLTARDDGAR RLLADTQRQL DRTAKSRAQL ERQSHTYALT
51 GIRSEKQIQR EIMLTQAAFN RLARSGKASQ NDLARAAVAT RNRIRELNAE
101 LKQGTGFADK MGKIGRFGAA AVAGGAAAYT VLKPAMDNRK QLDENINRVS
151 RQAFIEDNSK SAAWIATEGA QQIKDLALEL VEKNGGTHDK ALDLISGMMT
201 TGLNFAQTKN EAQAAAFAL ASEGSGEDTA KLIKTLKDDG MSGKDLQLGL
251 EHVLSQGLDG TFEVRDMVRE LPSLLSAAQQ AGMNGVGGLD YLLSLLQSAA
301 NKSQSPAEAA TNVQNLLSKT LSPDTIGRLK KMANPNDPKK GVDWIGSVVQ
351 GKQNGENAVQ VLSRLADAML VKDKQYQDYK KRAAAGDKTA AEQANMLKGA
401 LLAQLLPDLQ AKQGLLAATD MTQIREYMAS LAGVTLDNKG IAKNNEARML
451 SAAAQQEQQE SLAMLRESLT GTLVDMETSF KKLAAEYPNA TLALQALTTA
501 ATAASAAMLL TAGGGKGAGF LKDVGSKALG WGKASAGGVA AGATAAGGKL
551 LSWGKSAGSG LMNNPALVKR AGLLGMLLYS ESLGDGTLPK GLRGTKTTPE
601 MINRLKNNGI RFEPAPKREQ ARGGVPPQYLA APSAQPTDKM LSPLFSTQTA
651 AYQAAIQQQT AAYQAALAQD TAAVTTGLAQ VQSAMASASQ TINTNVSLNI
701 DGRVIANEVs RYQVAMFGRG AGQ*

```

a719.seq not found yet

a719.pep not found yet

g720.seq not found yet

g720.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2429>:

**m720.seq**

```

1 ATGAGCGGAT GGCATACCTT ATTGCAGGAC GCATCTTACA AGGGCGTCGG
51 CTTTGATATT GAGGTGGTGG ACGAGAGCAA CGGCAAGGCA TTGGCCGAGC
101 ATGCGCGGCC GTTTGTGCAG GGTATCGACC TTGAAGACAT GGGCATGACC
151 GGGCGGCAGG TGCAGATTAA TGCGGTGTTT TGGGGCAAGG GCTATGCAGG
201 CCGTCTGAAA AAGCTGCTGG ATGCGCTGGA GCAGCCGGGC GCGGCGGTGC
251 TGGTGACCCC TGTTTGGGGG CGGATGCACA ACATGATTGC GGCATCATGG
301 AGTTACCGAC ATGAGGCCGA TTATGTGGAT TATGCGGGCA TCGATATTAC
351 TTTCCGCGAG GCGGCCGAAG CGCAGGAAAT CTTTGTTTTT GAAAACGCCT
401 TTTTGGTCTG GCTTGAGGCG TTGATTGCTA ATATCGACAC CTACCGCGAG
451 GCGGCTATCG GCTTTGTTGA TGCGGTGTTG GCGGTGGATG CCGGCGTATC
501 AGCTTTATGG GGCAGCGCGC TGGGCATTG GAGTGCGGCA TCGGGTACGT
551 TTGGCGCGGT GCGCCGTTTG TTTGATTTGG ACAAATTCG CTTTCCCGAT
601 CCGGCGGAT ACAGTGCAGC GGCGTTTAAA AACGGCTCGG CCAAGCTGTT
651 TGCGGATATA TCGGTCATGG TAGATACTGG CATACGCCGT GAGGCGGGTT
701 TGGCCGATAA TGCCATGCAC CATGCCGTT GGTGCGCGCG ACAGCGGTTT
751 GACGGGGCTG CGGCTGTTGC CGACCGCGCC GCCGCTATCC CTGATAATTT
801 GCTGACCGGC CGCTTTTCAG ACGGCCTGCA AAACCGCCTG AACCGGTTAA

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1165

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851 CCGCCAAACA GGTGCAGCCG GTAGCGCAGG CCGTGCGCCT GTTATCCACG
901 TCATCGCTGT TGTGCGTGGC AACGGCATTG ATCGAGGCGC ATGGCGAAGA
951 GATGACCGCG CCCGATTTGA TTGAGGTTAA CCGCGCCATG CGCCGCCGTA
1001 TGCAGGCCGA GATTGCCGCC TTGCGGGCGG TGCAGACGGC TGCTGCCGAG
1051 TCTGGTGGGC TGACGGCCAA CGCCGTGTAT ACCGAGGCTT ACCAAACGGC
1101 AGAATCCCTG CGCGCGGCGG CAGGCCGTCT GAATGCGTTG GTTGCGGCGG
1151 TCATCAACCA AAAGCCGCCG CTGATTGTGC GCCAAGCCCC AATCGACGGT
1201 ACGATACACC AAATCGCCCC CGAGTTTTAC GGCGATATAG CCCGCGCAGC
1251 AGAGCTGGTG CGGCTCAATC CCCATATCCA CCACCCCGCG TTTATCAAGC
1301 GCGGCACTTT GGTCAACAGC TATGCAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2430; ORF 720>:

```

m720.pep
  1 MSGWHTLLQD ASYKGVGFDI EVVDESNGKA LAEHARPFVQ GIDLEDMGMT
 51 GRQVQINAVF WGKGYAGRLK KLLDALEQPG GGVLVHPVWG RMHNMIAASW
101 SYRHEADYVD YAGIDITFRE AAEAEIIFVF ENAFLVELEA LIANIDTYRE
151 AAIGFVDAVL AVDAGVSALW GSALGIWSAA SGTFGAVRRL FDLDKIAFPD
201 RGGYSAAAFK NGSAKLFADI SVMVDTGIRR EAGLADNAMH HAGWSPRQRF
251 DGAAAVADRA AAIPDNLLTG RFSDGLQNRL NRLTAKQVQP VAQAVRLLST
301 SSLLSVATAL IEAHGEEMTA PDLIEVNRAM RRRMQAEIAA LRAVQTAAAE
351 SGGLTANAVY TEAYQTAESE RAAAGRLNAL VAAVINQKPP LIVRQAPIDG
401 TIHQIAHEFY GDIARAAELV RLNPHIHHPA FIKRGTLVNS YAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2431>:

```

a720.seq (partial)
  1 GGCCTGCAAA ACCGCCTGAA CCGGTTAACC GCCAACAGG TGCAGCCGGT
 51 AGCGCAGGCG GTGCGCCTGT TATCCACGTC ATCGCTGTTG TCGGTGGCAA
101 CGGCATTAAT CGAGGCGCAT GGCGAAGAGA TGACCGCGCC CGATTTGATT
151 GAGGTTAACC GCGCCATGCG CCGCCGTATG CAGGCCGAGA TTGCCGCCTT
201 ACGGCGGGTG CAGACGGCTG CTGCCGAGTC TGGTGGGCTG ACGGCCAACG
251 CCGTGATATAC CGAGGCTTAC CAAACGGCAG AATCCCTGCG CGCGGCGGCA
301 GGCCGTCTGA ATGCGTTGGT TGCGGCGGTC ATCAACCAA AGCCGCGGCT
351 GATTGTGCGC CAAGCCCCAA TCGACGGTAC GATACACCAA ATCGCCCACG
401 AGTTTTACGG CGATATAGCC CGCGCAGCAG AGCTGGTGCG GCTCAATCCC
451 CATATCCACC ACCCGCGGTT TATCAAGCGC GGCACTTTGG TCAACAGCTA
501 TGCAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2432; ORF 720.a>:

```

a720.pep (partial)
  1 GLQNRLNRLT AKQVQVQA VRLSTSSLL SVATALIEAH GEEMTAPDLI
 51 EVNRAMRRRM QAEIAALRAV QTAAAESGGL TANAVYTEAY QTAESLRAAA
101 GRNLALVA AV INQKPLIVR QAPIDGTI HQ IAHEFYGDIA RAAELVRLNP
151 HHHHPAFIKR GTLVNSYAK*

```

m720 / a720 100.0% identity in 169 aa overlap

```

      250      260      270      280      290      300
m720.pep  SPRQRFDGAAAVADRAAAIPDNLLTGRFSDGLQNRLNRLTAKQVQVQAQAVRLLSTSSLL
a720      |||||
      10      20      30
      310      320      330      340      350      360
m720.pep  SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAAESGGLTANAVYTEAY
a720      |||||
      40      50      60      70      80      90
      370      380      390      400      410      420
m720.pep  QTAESLRAAAGRLNALVAAVINQKPLIVRQAPIDGTI HQIAHEFYGDIARAAELVRLNP
a720      |||||
      100      110      120      130      140      150
      430      440
m720.pep  HHHHPAFIKRGTLVNSYAKX

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1166

a720                    |||||  
                       HIHHPAFIKRGTLVNSYAKX  
                           160            170

g721.seq not found

g721.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2433>:

m721.seq  
 1 ATGTCCAAAA ATGCACAAAA AACCCCTACTT GCCGTGTGCA GTTTCGAGGT  
 51 GCAGCCAAAA GACGGGCGAA TCCAACCTGCT GCCATATGGC GAATTTTCGCG  
 101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA  
 151 AACGGTCATG ATGTCGCGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT  
 201 TGTCGATTAT GAACACCAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG  
 251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG  
 301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAA  
 351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG  
 401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCGCG GTTGGACGGT  
 451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC  
 501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GACCTGCCTG  
 551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCCGCGCT CGTGGAAGCC  
 601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTTCGCG AGCTGGCGGA  
 651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT  
 701 TGAATAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC  
 751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC  
 801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAA  
 851 AAGGCGTATT GAAACAGCCG GCGGCGTTGG CATTTTGTAC CGGCTTTATT  
 901 GAAAACGCCC AGCCGGTTCG TGCCTGGCA GGCTCGCAA CGGGCGGCAA  
 951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGCG  
 1001 CAAAAATGCT GGGCATGTCC GGCGAAGAAT TTGTAAAAAT CAAAGAAAGC  
 1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence &lt;SEQ ID 2434; ORF 721&gt;:

m721.pep  
 1 MSKNAQKTL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAYWLTEE  
 51 NGHDVALLAN SSRNQLVVDY EHQTLYKEKN GQFAPAAGWM RWLEFTPKGM  
 101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG  
 151 MDEVLAASA QILKPETEON PMKELLQQLF DLPDAGEEEL KAALSALVEA  
 201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTXYAPI SVVQELQSKV  
 251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAKGVLPQ GGLAFLTGFI  
 301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES  
 351 EKG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2435>:

a721.seq  
 1 ATGTCCAAAA ATGCACAAAA AACCCCTACTT GCCGTGTGCA GTTTCGAGGT  
 51 GCAGCCAAAA GACGGGCGAA TCCAACCTGCT GCCATATGGC GAATTTTCGCG  
 101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA  
 151 AACGGTCATG ATGTCGCGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT  
 201 TGTCGATTAT GAACACTAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG  
 251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG  
 301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAA  
 351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG  
 401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCGCG GTTGGACGGT  
 451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC  
 501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GGTCTGCCTG  
 551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCCGCGCT CGTGGAAGCC  
 601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTTCGCG AGCTGGCGGA  
 651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT  
 701 TGAATAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC  
 751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC  
 801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCG  
 851 AAGGCGTATT GAAACAGCCG GCGGCGTTGG CATTTTGTAC CGGCTTTATT  
 901 GAAAACGCCC AGCCGGTTCG TGCCTGGCA GGCTCGCAA CGGGCGGTAA  
 951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGCG  
 1001 CAAAAATGCT GGGCATGTCC GGCGAAGAAT TTGTAAAAAT CAAAGAAAGC

1167

1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence &lt;SEQ ID 2436; ORF 721.a&gt;:

```

a721.pep
  1 MSKNAQKTLL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
 51 NGHDVALLAN SSRNQLVVDY EH*TLYKEKN GQPAPAAGWM RWLEFTPKGM
101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEQN PMKELLQQLF GLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTKYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAEGVLKQP GGLAFLTGFI
301 ENAQPVAAALA GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*

```

a721/m721 99.2% identity in 353 aa overlap

a721.pep	10	20	30	40	50	60
	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN					
m721	10	20	30	40	50	60
	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN					
a721.pep	70	80	90	100	110	120
	SSRNQLVVDYEHXTLYKEKNQGPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
m721	70	80	90	100	110	120
	SSRNQLVVDYEHQTLYKEKNQGPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
a721.pep	130	140	150	160	170	180
	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEQNPMKELLQQLF					
m721	130	140	150	160	170	180
	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEQNPMKELLQQLF					
a721.pep	190	200	210	220	230	240
	GLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
m721	190	200	210	220	230	240
	DLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
a721.pep	250	260	270	280	290	300
	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGLVKQPGGLAFLTGFI					
m721	250	260	270	280	290	300
	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGLVKQPGGLAFLTGFI					
a721.pep	310	320	330	340	350	
	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAKMLGMSGEEFVKIKES					
m721	310	320	330	340	350	
	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAKMLGMSGEEFVKIKES					

g722.seq not found yet

g722.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2437>:

```

m722.seq
  1 GTGTTTGAAG CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
 51 TACCAAAGAG CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TGCGCGGCTT GAGCCGCCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGACCTGC AAGTGCGTAT CGGCCAGCGT TTTTACCGCA CTACCGCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG

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1168

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401 AGCCGGGGCGC GGCCGCCAAT GTGGGCGACG GCGAGGCGCA ACTGATGGCC
451 GCGCCCGCCG GTGTGGCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCCGACCGCC CGCAGGCGGC AACC GTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG TCGTCGGAAG
701 AAAGTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GTATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTTCGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCTGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCGCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2438; ORF 722>:

**m722.pep**

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLSRR NPTTASGTLT VSGIAQSMLS
101 DDLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VGDGEAQLMA
151 APAGVATECR LTVQGGTDRE SDASLLARLL EIIRRPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV SSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPDGG
301 LTVSQIEAAI SNVDGVIDRR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2439>:

**a722.seq**

```

1 GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
51 TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TGC GCGGCTT GCGCCGCCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGGCCTGC AAGTGCGTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCGAGCGCG GCACGGCGGA AATACCGGCA ATCGCGCAGC
401 AGCCGGGGCG GGCCGCCAAT GTGCGCGACG GCGAGGCGCA ACTGATGGCC
451 GCGCCCGCCG GTGTGTCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCCGACCGCC CGCAGGCGGC AACC GTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG CCATCGGAAG
701 AAAGTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GCATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTTCGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCGGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCTCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2440; ORF 722.a>:

**a722.pep**

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLRRR NPTTASGTLT VSGIAQSMLS
101 DGLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VRDGEAQLMA
151 APAGVSTECR LTVQGGTDRE SDASLLARLL EIIRRPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV PSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPDGG
301 LTVSQIEAAI SNVDGVIDLR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

**g723.seq not found yet**

1169

g723.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2441>:

m723.seq

```

1   ATGCGACCCA AGCCCCGTTT CAGACGGTCT GTTATCGCTT GCTCAATATC
51  AGTGATCACG CCCGAACACC TTATTTTAC CGTTTACAAA CACAATACCG
101 TCTTCGCCCC CGGCCACTTC TTCGCCGCTA TCATCCACGC CCAGCTGCAC
151 TTCGCCTTTG GCCATAGCAC GCAGCAGGTC GAGCACGTCG ATTTTGTAGC
201 GGTTCGCGAT TTCGTCGGTA ATCAACACGC CCTGAGCCGC CGTCAGACGG
251 TAGCGGGCAA TGTCGCAGCA AAGGCGCACC AAGATGGGCG GCAGATCCTC
301 AAAAGGTTCG CTGAACCGCC CCAGATACGC GTCGATTTTC GCAGTGGCGT
351 CCACCAGCGC GGTTCGTGCG ACCTCGCGGT CAATCAGCCC CTCGTTGTTG
401 CGGTCGGTGA GCTGCAAGAC TTCCAGCTCA CCGAAACGCG CAACCATATC
451 CTAACCGTC GCGTATGCCA TTACTCGACC GCCTGCGTTC GCAGCATAGG
501 CTCGGCGCAG ATTGCCTTCC ACACCGCTTC GCCGACTTCG GCGCGCTTCA
551 CTTCGCGCCA GCCGCCGTC AAGAGCAGGC CGCCGCGCCA AAATCTCTTG
601 CCGTCTGCGC CGGTACTGAC GAGCATCACA TCGCGGCTGT CCGCCAAAGC
651 GTCGGCGGCA CGTTCGCTAT GCTGCACTTT GAGTTCGGCA AGTTCGCGCG
701 ACAGTGCCTT TTTGTCGTCT TCGGCTTTTT CCAAGGCTGT GGTCAGCATT
751 TCGACATCGT TTCGGGCGGC GGCAAGCTCT GCCTGCACGG CGTCCAATTC
801 GGCTTTGATG TCTTCAAACG ACGGGGCGGC GGTTTCGGCG GTTTCGGTT
851 TGTGTTGGT TTTTGCCATG ATGACTCCTT GTTTCAGACG GCGGCGGATT
901 CGCATTTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2442; ORF 723&gt;:

m723.pep

```

1   MRPKPRFRRS VIACISVIT PEHLIFTVYK HNTVFARGHF FAAIHAQLH
51  FAFGHSTQQV EHVDFVAVAD FVGNQHALSR RQTVAGNVAA KAHQDGRQIL
101 KRSSEPPQIR VDFGSGVHQR GLCDLAVNQP LVVAVGELQD FQLTETRNHI
151 LNRRVCHYST ALRCSIGSAQ IAFHTASPTS ARFTSRQPPS NSRPPRQNSL
201 PSAPVLTSIT SRLSAKASAA RVCCTLSSA SSADSAFLSS SAFSKAVVSI
251 STSFRAAASS ACTASNSALM SSNDGA AVSA VSGLLLVFAM MTPCFRRRRI
301 RI*

```

a723.seq not found yet

a723.pep not found yet

g724.seq not found yet

g724.pep not found yet

The following partial DNA sequence, shown with its encoded amino acid sequence, was identified in *N. meningitidis* <SEQ ID 2443>:

m724.map

```

1   ATGAGTTTGAGTAAATTGGCGAAAAAACGGCACAACTGCTAAAAATATCGGCGAAACC
-----+-----+-----+-----+-----+-----+-----+ 60
a   TACTCAAACATTTAACCGCTTTTGTCCGTGTTGACGATTTTATAGCCGCTTTGG
    M S L S K L A K K T A Q T A K N I G E T -

61  CTGCGCGCGCCTTTCGGGGAAAAATCACGCTGGTGGTGTCTCCGAGCCGATAACAGCGC
-----+-----+-----+-----+-----+-----+ 120
a   GACGCGCGCCGAAAGCCCTTTTAGTGCGACCACACAGCAGGCTCGGCTATGTCGCG
    L R A A F R G K I T L V V S S E P I Q R -

121 GTGCAGTTGAGCGGCTTGCCGACGAAACCCTGCAAGACCTTGAACATTTGCAGGAATAC
-----+-----+-----+-----+-----+-----+ 180
a   CACGTCAACTCGCCGAACCGGCTGCTTTGGGACGTTCTGGAAGTTGTAACGTCCTTATG
    V Q L S G L A D E T L Q D L E H L Q E Y -

181 GGCTTTGCCAGCCATCCGCCGACGGCAGCGAAGCGGTAGTGATACCGCTGGGCGGCAAT
-----+-----+-----+-----+-----+-----+ 240
a   CCGAAACGGTCGGTAGGCGGGCTGCCGTGCTTCGCCATCACTATGGCGACCCGCCGTTA
    G F A S H P P D G S E A V V I P L G G N -

```

1170

```

      ACTTCGCACGGTGTGATTGTGTGCAGCCAGCACGGCAGCTACCGCATCAAAAACCTTAAG
241 -----+-----+-----+-----+-----+-----+-----+-----+ 300
      TGAAGCGTGCCACACTAACACACGTCGGTCGTGCCGTCGATGGCGTAGTTTTTGGAAATTC
a      T S H G V I V C S Q H G S Y R I K N L K -

      CCCGGCGAGACGGCGATTTTAAATCATGAGGGTGCAAAAATCGTGATTAAGCAAGGCAAA
301 -----+-----+-----+-----+-----+-----+-----+-----+ 360
      GGGCCGCTCTGCCGCTAAAAATTAGTACTCCACGTTTTTAGCTAATTTCGTTCCGTTT
a      P G E T A I F N H E G A K I V I K Q G K -

      ATCATTGAGGCCGATTGCGACGTGTACCGGGTTAACTGCAACAATACGAGGTTAATGCG
361 -----+-----+-----+-----+-----+-----+-----+-----+ 420
      TAGTAACTCCGGCTAACGCTGCACATGGCCCAATTGACGTTTGTATGCTCCAATTACGC
a      I I E A D C D V Y R V N C K Q Y E V N A -

      GCCACGGATGCCAAATTTAACGCTCCGTTGGTGGAGACCAGTGCAAGTGTGACGGCGCAA
421 -----+-----+-----+-----+-----+-----+-----+-----+ 480
      CGGTGCCTACGGTTTAAATTGCGAGGCAACCACCTCTGGTCACGTCACAACCTGCCGCGTT
a      A T D A K F N A P L V E T S A V L T A Q -

      GGCCAAATCAACGGCAACGGCGGCATGCCGCTCGAGGGCGGCGACGGAGCCACCTTTAGC
481 -----+-----+-----+-----+-----+-----+-----+-----+ 540
      CCGGTTTAGTTGCCGTTGCCGCGTACCGGCAGCTCCCGCCGCTGCCTCGGTGGAAATCG
a      G Q I N G N G G M A V E G G D G A T F S -

      GGCGATGTTAACCAAACGGGCGGCAGCTTTAACACCGACGGCGACGTGGTGGCCGGCAAT
541 -----+-----+-----+-----+-----+-----+-----+-----+ 600
      CCGCTACAATTGGTTTGGCCGCCGTCGAAATTGTGGCTGCCGCTGCACCACCGGCCGTTA
a      G D V N Q T G G S F N T D G D V V A G N -

      ATATCGTTGCGCCAGCACCCGCATACCGACAGCATCGGCGGCAAAACCTTACCGGCGGAA
601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
      TATAGCAACGCGGTCGTGGGCGTATGGCTGTCGTAGCCGCGTTTTGGAATGGCCGCTT
a      I S L R Q H P H T D S I G G K T L P A E -

      CCGGCATAG
661 ----- 669
      GGCCGTATC
a      P A * -

```

Enzymes that do cut: NONE

Enzymes that do not cut: BamHI BglIII EcoRI HindIII KpnI NdeI NheI PstI SacI  
Sali SmaI SphI XbaI XhoI

This corresponds to the amino acid sequence &lt;SEQ ID 2444; ORF 724&gt;:

m724 . pep

```

1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK
101 PGETAIFNHE GAKIVIKQ GK IIEADC DVYR VNCKQYEVNA ATDAKFNA PL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTGDGDVVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2445>:

a724 . seq

```

1  ATGAGTTTGA GTAAATTGGC GAAAAAACG GCACAACTG CTAAAAATAT
51  CGGCGAAACC CTGCGCGCGG CCTTTCGGGG AAAAATCAG CTGGTGGTGT
101 CGTCCGAGCC GATACAGCGC GTGCAGTTGA GCGGCTTGGC CGACGAAACC
151 CTGCAAGACC TTGAACATTT GCAGGAATAC GGCTTTGCCA GCCATCCGCC
201 CGACGGCAGC GAAGCGGTAG TGATACCGCT GGGCGGCAAT ACTTCGCACG
251 GTGTGATTGT GTGCAGCCAG CACGGCAGCT ACCGCATCAA AAACCTTAAG
301 CCCGGCGAGA CGGCGATTTT TAATCATGAG GGTGCAAAAA TCGTGATTAA
351 GCAAGGCAAA ATCATTGAGG CCGATTGCGA CGTGTACCGG GTTAACTGCA
401 AACAATACGA GGTTAATGCG GCCACGGATG CCAAATTTAA CGCTCCGTTG
451 GTGGAGACCA GTGCAGTGTT GACGGCGCAA GGCCAAATCA ACGGCAACGG

```

1171

```

501 CGGCATGGCC GTCGAGGGCG GCGACGGAGC CACCTTTAGC GGCGATGTTA
551 ACCAAACGGG CGGCAGCTTT AACACCGACG GCGACGTGGT GGCCGGCAAT
601 ATATCGTTGC GCCAGCACCC GCATACCGAC AGCATCGGCG GCAAAACCTT
651 ACCGGCGGAA CCGGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 2446; ORF 724.a>:

**a724.pep**

```

1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK
101 PGETAIFNHE GAKIVIKQKG IIEADCDVYR VNCKQYEVNA ATDAKFNAFL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

**a724/m724** 100.0% identity in 222 aa overlap

	10	20	30	40	50	60
a724.pep	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY					
m724	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a724.pep	GFASHPPDGS EAVVIPLGGN TSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQKG					
m724	GFASHPPDGS EAVVIPLGGN TSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQKG					
	70	80	90	100	110	120
	130	140	150	160	170	180
a724.pep	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGGQINGNGGMAVEGGDGATFS					
m724	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGGQINGNGGMAVEGGDGATFS					
	130	140	150	160	170	180
	190	200	210	220		
a724.pep	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
m724	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
	190	200	210	220		

**g725.seq** not found yet

**g725.pep** not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2447>:

**m725.seq**

```

1  ATGGTGCGCA CGGTTAAAAG CTACAACGGC GAGGCCGACG ATTTGGCGGG
51  GCAAATCCAT ACGCTGCCTG CCGTTTGGGT AACGTATGGC GGCAGCAAAG
101 TTGAGCCTGC CAGCACCGGC GGCGTATGCG GACGTTATCA GGATACCGCC
151 GAATTTGTGG TGATGGTGGC GGCCCGCAAT CTGCGCAACG AGCAGGCGCA
201 GCGGCAAGGC GGCATCGACA GCCGCGAAAT CGGCAGCAAC GATTTAATCC
251 GCGCTGTTTC CCGCTGCTT GACGCCAGC GGCTCGGTTT TGCCGATAGC
301 CGCGGCTTGG TGCCCAAAGC GGTGCGCGCG ATTGCCAATC ATGTGCTGGT
351 GCAAACGCC GCAGTAAGCA TATATGCGGT TGAGTATGCC ATCCGCTTTA
401 ACACCTGCGG GTTGGAATAA GACCGCTACC CCGAACGCAC CGACAATCCC
451 GACGACCCCA ACCATATCTT TACCAAGTAT CAGGGTACAT TGAGCGAGCC
501 GTGGCCTGAT TTCGAGGGGT TGGACGGCAA AATTACGAC CCGCAATCCG
551 CCGATGAAAT ACCTGTAAAC CTAACCCTTA AGGATAAGCA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 2448; ORF 725>:

**m725.pep**

```

1  MVRTVKSUNG EADDLAQIHL TLPVWVVTYG GSKVEPASTG GVCGRYQDTA
51  EFVVMVAARN LRNEQAQRQG GIDSREIGSN DLIRAVRRLD DGQRLGFADS
101 RGLVPKAVRA IANHVLVQNA AVSIYAVEYA IRFNTCGLEN DRYPERTDNP
151 DDPNHIFTKY QGTLSEFPWD FEGLDGKIYD PQSADEIPVN LTLKDKQ*

```

a725.seq not found yet

a725.pep not found yet

g726.seq not found yet

g726.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2449>:

```
m726.seq
1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACAT TGGGCGGCAT
51  CCCC GAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101 CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151 GTTTTAACCC CGCCGCGCCC GTCCGATTAC CACGAATGGG ACGGCAAAAA
201 ATGGAAAATC AGCAAAGCCG CCGCCGCCGC CCGTTTCGCC AAACAAAAAA
251 CCGCCTTGGC ATTCCGCCTC GCGGAAAAGG CGGACGAACT CAAAAACAGC
301 CTCTTGCGCG GCTATCCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351 AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401 TGGCGCAAAT CGCCGCCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
451 AAAGTTATCG AAAAATCCGC CCGCCTGGCT GTTGCCGCCG GCGCGATTAT
501 CGGAAAGCGT CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551 CCGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601 GGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2450; ORF 726>:

```
m726.pep
1  MTIYFKNGFY DDTLGGIPEG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
51  VLTPPRPSDY HEWDGKKWKI SKAAAAARFA KQKTALAFRL AEKADELKNS
101 LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVIE
151 KVIEKSARLA VAAGAIIGKR QQLEDKINTI ETAPGLDALE KEIEEWTLNI
201 G*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2451>:

```
a726.seq
1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACCT TGGGCAGCAT
51  CCCC GAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101 CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151 GTTTTAACCC CGCCGCGCCC GTCCGAATAC CACGAATGGG ACGGCAAGAA
201 ATGGGAAATC GGCGAAGCCG CTGCCGCCGC CCGTTTCGCC GAACAAAAAA
251 CCGCCACGGC ATTCCGCCTC GCGGCAAAGG CGGACGAACT CAAAAACAGC
301 CTCTTGCGCG GCTATCCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351 AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401 TGGCGCAAAT CGCCGCCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
451 AAAGTTGTCG AAAAATCCGC CCGCCTGGCC GTTGCCGCCG GCGCGATTAT
501 CGGAAAGCGG CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551 CAGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601 GGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2452; ORF 726.a>:

```
a726.pep
1  MTIYFKNGFY DDTLGSIPEG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
51  VLTPPRPSEY HEWDGKKWEI GEAAAAARFA EQKTATAFRL AAKADELKNS
101 LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVIE
151 KVVEKSARLA VAAGAIIGKR QQLEDKINTI ETAPGLDALE KEIEEWTLNI
201 G*
```

a726/m726 95.5% identity in 201 aa overlap

```

          10      20      30      40      50      60
a726.pep  MTIYFKNGFYDDTLGSIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTPPRPSEY
          |||
m726      MTIYFKNGFYDDTLGSIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTPPRPSDY
          10      20      30      40      50      60
```

1173

```

              70      80      90      100      110      120
a726.pep      HEWDGKKWEIGEAAAAARFAEQKTATAFRLAAKADELKNSLLAGYPQVEIDSFYRQEKEA
              |||||:|:|||||:||||| ||||| ||||| ||||| ||||| ||||| |||||
m726          HEWDGKKWKISKAAAAARFAKQKTALAFRLAEKADELKNSLLAGYPQVEIDSFYRQEKEA
              70      80      90      100      110      120

              130      140      150      160      170      180
a726.pep      LARQADNNAPTMLAQIAAARGVELDVLEIKVVEKSARLAVAAGAIIGKRQQLEDKLNITI
              |||||:|:|||||:||||| ||||| ||||| ||||| ||||| ||||| |||||
m726          LARQADNNAPTMLAQIAAARGVELDVLEIKVIEKSARLAVAAGAIIGKRQQLEDKLNITI
              130      140      150      160      170      180

              190      200
a726.pep      ETAPGLDALEKEIEEWTLNIGX
              |||||:|:|||||:||||| ||||| ||||| ||||| ||||| ||||| |||||
m726          ETAPGLDALEKEIEEWTLNIGX
              190      200

g727.seq      not found yet
g727.pep      not found yet

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2453>:

```

m727.seq
1   ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATTAT
51  CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTTGC GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAAC
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAGA
301 GACCTTTGCA AAATTCCTTT CCCTCCCGAC AGCCGAAACC CAAACACAGG
351 TTTTCGGCTG TTTTCGCCCC AAATACCGCC TAATTTTACC CAAATACCCC
401 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2454; ORF 727>:

```

m727.pep
1   MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51  AQALLLSAQN YARELELARA EAKKYEKKAH AVGMALAKKQ AEVSRLKTER
101 DLCKIPFPDP SRNPNTGFRL FSPQIPNFT QIPP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2455>:

```

a727.seq
1   ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
51  CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GGCAGCGTGC GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCTGAA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAT
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCTCGGCTA CGGAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2456; ORF 727.a>:

```

a727.pep
1   MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51  AQALLLSAQN YARELEQARA EAKKYEKKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DGFGHHGLQL YKRALGYGN*

```

a727/m727 83.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
a727.pep      MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN
              |||||:|:|||||:||||| ||||| ||||| ||||| ||||| ||||| |||||

```



1174

```

m727      MNLVKLLANNWQPIAIIALVGTGLAVSHHQYKSAFAKQQAVIDKMERDKAQALLLSAQN
              10      20      30      40      50      60

              70      80      90      100     110     119
a727.pep   YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENV-LTQDRKNAGGGC
              |||||  |||||||  |||||||  |||||||  |||  ::  ::  :  |  :  |
m727      YARELELARAFAAKKYEVKAHAVGMALAKKQAEVSRLKTE--RDLCKIPFPDSDRNPTGF
              70      80      90      100     110

              120     130     140
a727.pep   IDGFGHHGLQLYKRALGYGNX

m727      RLFSPQIPPNTQIPPX
              120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2457>:

**g728.seq**

```

1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGGAATAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAAATCCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG GGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACC CCAGAGTTTC GAATATTATT TGA AAAACCG AAATCTTTT
901 ATTGCACAAT CTTGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATCGAGACC TATCATGCGC AACAGACGTG GTATTTGATG GCGGGGCGGA
1001 TTATCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATTT TCCTTTGAAC
1051 TTGGAAGATT TGGAAAAAGA GGTGAGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG GCCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2458; ORF 728>:

**g728.pep**

```

1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNAFV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFAVNAEYL
151 YRNDRPFSVN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGICYM AQVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGMK ANSLVVGYDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
301 IAQSSTVALK ADGVTADMQT YHAQQTWYLD GGRIIREEKQ GDRLPDFPLN
351 LEDLEKEVSR YAEAAAARRSG GRRGLSH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2459>:

**m728.seq**

```

1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAAATCT TGCCGGAACT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA

```

1175

```

501  CGGGGAAAAT  TATGAAACGA  CAGGAGAATA  TCGGGTGTGT  TGGCAACCAG
551  ACGGTTCCGT  ATTTGATGCG  GCGGGGCGCG  GGAAAATCGG  GGAAGATGTT
601  TATGAGCATT  GCCTCGGGTG  TTATCAGATG  GCCCAGGTAT  ATTTGGCGAA
651  ATACCGGGAT  GTCGCGAATG  ACGAGCAGAA  GGTTTGGGAC  TTCCGCAAAG
701  AGAGCAACCG  AATTGCGTCG  GACTCGCGCA  ATTCTGTGTT  TTATCAGAA
751  ATGCGGGAAT  TGATGCCCCG  AGGGATGAAG  GCGAACAGTC  TTGTGGTCGG
801  CTATGATGCG  GACGGTCTGC  CGCAAAAAGT  CTATTGGAGT  TTCGACAATG
851  GAAAAAACG  CCAGAGTTTC  GAATATTATT  TGAAAAACGG  AAATCTTTT
901  ATTGCACAAT  CTTGACGGT  AGCATTGAAA  GCGGATGGCG  TAACGGCGGA
951  TATGCAGACC  TATCATGCGC  AACAGACGTG  GTATTTGGAT  GCGGGGCGGA
1001  TTGTCCGCGA  AGAGAAACAG  GGAGACAGAC  TGCCTGATTT  TCCTTTGAAC
1051  TTGGAAAATT  TGGAAAAGA  GGTGCGCCGT  TATGCAGAGG  CTGCGGCGAG
1101  ACGTTCGGGC  GGCAGGCGCG  ACCTTTCTCA  CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2460; ORF 728>:

**m728.pep**

```

1  MFKKFKPVLL  SFFALVFAFW  LGTGIAYEIN  PRWFLSDTAT  EVPKNPNAFV
51  AKLARLFRNA  DRAVVIVKES  IRTEENLAGT  VDDGPLQSEK  DYLAALAIRLS
101  RLKEKAKWFH  VTEQEHGKEV  WLDYHIGEGG  LVAVSLSQRS  PEAFFVNAEYL
151  YRNDRPFSVN  VYGGTVHGEN  YETTGEYRVV  WQPDGSVFDA  AGRGKIGEDV
201  YEHCLGICYM  AQVYLAKYRD  VANDEQKVD  FRKESNRIAS  DSRNSVFYQN
251  MRELMPRGMK  ANSLVVGYDA  DGLPQKVYWS  FDNGKKRQSF  EYYLKNGNLF
301  IAQSSVALK  ADGVTADMQT  YHAQQTWYLD  GGRIVREEKQ  GDRLPDFPLN
351  LENLEKEVRR  YAEAAARRSG  GRRDLSH*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 728 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF728.a) from *N. gonorrhoeae*:

**m728 / g728**

	10	20	30	40	50	60
m728.pep	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVVPKNPNAFVAKLARLFRNA					
g728	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVVPENPNAFVAKLARLFRNA					
	10	20	30	40	50	60
m728.pep	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
g728	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV					
	70	80	90	100	110	120
m728.pep	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
g728	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV					
	70	80	90	100	110	120
m728.pep	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV					
g728	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTAHGENYETTGEYRVV					
	130	140	150	160	170	180
m728.pep	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV					
g728	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTAHGENYETTGEYRVV					
	130	140	150	160	170	180
m728.pep	WQPDGSVFDAAGRGKIGEDVYEHCLGICYMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
g728	WQPDGSVFDAAGRGKIGEDVYEHCLGICYMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
	190	200	210	220	230	240
m728.pep	WQPDGSVFDAAGRGKIGEDVYEHCLGICYMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
g728	WQPDGSVFDAAGRGKIGEDVYEHCLGICYMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
	190	200	210	220	230	240
m728.pep	DSRNSVFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF					
g728	DSRDYVFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF					
	250	260	270	280	290	300
m728.pep	DSRNSVFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF					
g728	DSRDYVFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF					
	250	260	270	280	290	300
m728.pep	IAQSSVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
g728	IAQSSVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
m728.pep	IAQSSVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
g728	IAQSSVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					

1176

```

g728      IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIIREEKQGDRLPDFPLNLEDLEKEVSR
           310      320      330      340      350      360

           370
m728.pep  YAEAAARRSGRRDLSHX
           |||||
g728      YAEAAARRSGRRGLSHX
           370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2461>:

```

a728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51  TGCTTTTGG CTGGGAACGG GTATTGCCA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAAATCCGA ATGCTTTTGT GGCGAAACTT
151 GCCCGCCTGT TCCGAAATGC CGACAGGCG GTTGTTCATCG TGAAGGAATC
201 GATGAGGACG GAGGAAAGTC TTGCCGAGC TGTGGATGAC GGTCCGTTGC
251 AGTCGGAGAA GGATTATCTT GCACTCGCTG TCCGGCTCAG TCGTTTGAAA
301 GAAAAGGCGA AATGGTTTCA CGTAACGGAG CAGGAACATG GGGAAGAGGT
351 TTGGCTGGAT TACTATATCG GCGAGGCGG TTTGGTTGCG GTTTCGCTTT
401 CGCAACGCTC GCCGGAAGCG TTTGTTAATG CCGAATATCT GTATCGGAAC
451 GATCGTCCGT TTTCTGTAAA TGTGTACGGC GGAACGGTTC ACGGGGAAAA
501 TTATGAAACG ACAGGAGAAT ATCGGGTTGT TTGGCAACCG GACGGTTCGG
551 TATTTGATGC GTCGGGCGC GGGAAAATCG GGGAAGATGT TTATGAGCAT
601 TGCCTCGGGT GTTATCAGAT GGCCAGGTA TATTGGCGA AATATCGGGA
651 TGTCGCGAAT GATGAGCAGA AGGTTTGGGA CTTCCGCGAA GAGAGTAACC
701 GGATTGCGTC GGA CTGCGC GATTCTGTGT TTTATCAGAA TATGCGGGAA
751 TTGATGCCCC GAGGGATGAA GGCAAACAGT CTTGTGGTCG GCTATGATGC
801 GGACGGTCTG CCGCAGAAAG TCTATTGGAG TTTCGACAAT GGGAAAAAAC
851 GCCAGAGTTT CGAATATTAT TTGAAAAACG GAAATCTTTT TATTGCACAA
901 TCTTCGACGG TAGCATTGAA AGCGGATGGC GTAACGGCGG ATATGCAGAC
951 CTATCATGCG CAACAGACGT GGTATTTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTTGAA CTTGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
1101 CGCAGGCGC GACCTTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2462; ORF 728.a>:

```

a728.pep
1  MFKKFKPVLL SFFALVFVFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51  ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGCYQMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL PQKVYWSFDN GKQRQSFEYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGRR DLSH*

a728 / m728      96.3% identity in 377 aa overlap

           10      20      30      40      50
a728.pep  MFKKFKPVLLSFFALVFVFWLGTGIAYEINPRWFLSDTATE---NPNAFVAKLARLFRNA
           |||||
m728      MFKKFKPVLLSFFALVFVFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA
           10      20      30      40      50      60

           60      70      80      90      100     110
a728.pep  DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLLALAVRLSRLKEKAKWFHVTEQEHGEEV
           |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
m728      DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLLALAIRLSRLKEKAKWFHVTEQEHGKEV
           70      80      90      100     110     120

           120     130     140     150     160     170
a728.pep  WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
           ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
m728      WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
           130     140     150     160     170     180

```

1177

	180	190	200	210	220	230
a728.pep	WQPDGSVFDASGRGKIGEDVYEHCLGQYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m728	WQPDGSVFDAAAGRGKIGEDVYEHCLGQYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
	240	250	260	270	280	290
a728.pep	DSRDSVFYQNMRELMPRGMKANSLVVGADGLPQKVYWSFDNGKKRQSFYEYLLKNGNLF					
m728	DSRNSVFYQNMRELMPRGMKANSLVVGADGLPQKVYWSFDNGKKRQSFYEYLLKNGNLF					
	250	260	270	280	290	300
	300	310	320	330	340	350
a728.pep	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGGRIVREEKQGDRLPDFPLNLEDLEKEVSR					
m728	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
	360	370				
a728.pep	YAEAAARRSGGRRDLSHX					
m728	YAEAAARRSGGRRDLSHX					
		370				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2463>:

## g729.seq

```

1  ATGAATACTA CATTGAAAAC TACCTTGACC TCTGTTGCAG CAGCCTTTGC
51  ATTGTCTGCC TGCACCATGA TTCCTCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCGGAAAC CTTCCAAAAC GACACATCGG TTTCTTCCAT CCGCGCGGTT
151 GATTTGGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAAGTTT GCGTACAGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACAA TACATGATCG AGCGCAACAA CCTCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGGCTCGCGC CAAGGCAGCT TGAGCGGCgg
351 caaTGTCAGC AGCAGCTACA ATGTCTGGACT GGGTGcGGca tCTTACGAAC
401 TCGATCTGTT CgGGCGCGTG CGCagcaacA GcgaagcAGC ACTGcaggGC
451 tATTTTGCCA GCGTTGCCAA CcgcGATGCG GCACATTtGa ttCtGATTGC
501 CACCGTTGCC AAAGCCTATT TCAAcgaGcG TTATGCCGAA AAAGcgatgT
551 CTTTGCGCGCa gcGTGTCTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTGCGGT ACAAGGCAGG CGTGATTtCC GCCGTCGCCC TGCGCCAGCA
651 GGAAGCCTTG ATTGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCa
701 gcCGGAACA GCGCGCAAT GCCTTGGAAC CCTTGATTAA ccGTCCGATA
751 CCCGAagaCC TGCCCGCCGG TTTGCCGTTG GACAagcAGT TTTTGTGTTGA
801 AAAAATGCCT GCCGGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGACA
851 TCCGCGCCGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 gcgCGCGCCg ccTTTTTCCC GTCCATCCGC CTGACCGGAA GCGTCGGTAC
951 GGGTTCTGTC GAATTGGGCG GGCTGTTCAA AAGCGGCACG GCGGTTTGGG
1001 CGTTCGCTCC GTCTATTACC CTGCCGATT TTAATTGGGG AACGAACAAG
1051 GCGAACCTTG ATGTGGCAAA ACTGCGCCAA CAGGCACAAA TTGTGCCTA
1101 TGAATCCGCC GTCCAATCCG CCTTTCAAGA CGTGGCAAAC GCATTGGCGG
1151 CGCGCGAGCA GCTGGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG CTTGGTCGGA CTGCGTTACA AACACGGCGT
1251 ATCCGGCGCG CTCGATTtGC TCGATGCGGA ACGCATCAGC TATTGCGCGG
1301 AAGGTGCGGC TTTGTGCGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CGCTCgacGG CGGATTGAAA CGGGATACCC AAACCGGCAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2464; ORF 729>:

## g729.pep

```

1  MNTTLKTTLT SVAAAFALSA CTMIPOYEQP KVEVAETFQN DTSVSSIRAV
51  DLGWHDFAD PRLQKLIDIA LERNtSLRtA VLNSEIYRKQ YMIERNLLP
101 TLAANANGSR QGSLSGGNVS SSYNVGLGAA SYELDLFGRV RSNSEAAALQG
151 YFASVANRDA AHLILIATVA KAYFNERYAE KAMSLAQRVL KTREETYKLS

```

m729.seq

1	ATGGATACTA	CATTGAAAAC	CACCTTGACT	TCTGTTGCAG	CAGCCTTTGC
51	ATTGTCTGCC	TGCACCATGA	TTCCCAATA	CGAGCAGCCC	AAAGTCGAAG
101	TTGCCGAAAC	GTTCAAAAAC	GATACCGCCG	ACAGCGGCAT	CCGCGCCGTC
151	GATTTAGGTT	GGCATGACTA	TTTTGCCGAC	CCGCGCCTGC	AAAAGCTGAT
201	CGACATCGCA	CTCGAGCGCA	ATACCAAGTT	CGGTACCGCC	GATTGGAACA
251	GCGAAATCTA	CCGCAAACAA	TACATGATTG	AGCGCAACAA	CCTCCTGCCC
301	ACGCTTGCCG	CCAATGCGAA	CGACTCGCGC	CAAGGCAGCT	TGAGCGGCGG
351	CAATGTAAGC	AGCAGCTACA	AAGTCGGACT	GGGTGCGGCA	TCTTACGAAC
401	TCGATCTGTT	CGGGCGTGTA	CGCAGCAGCA	GCGAGGCGGC	ACTGCAAGGC
451	TATTTGCGCA	GCACCGCGAA	CCGCGATGCG	GCACATTTGA	GCGTGATTGC
501	CACCGTTGCC	AAAGCCTATT	TCAACGAACG	TTACGCCGAA	GAAGCGATGT
551	CTTTGGCGCA	ACGTGTTTTG	AAAACGCGCG	AGGAAACCTA	CAAGCTGTCC
601	GAATTACGTT	ACAAGGCAGG	CGTGATTTCG	GCCGTGCCCC	TACGTCAGCA
651	GGAAGCCCTG	ATCGAATCTG	CCAAAGCCCA	TTATGCCCAT	GCCGCGCGCA
701	GCCGCGAACA	GGCGCGCAAT	GCCTTGGCAA	CCTTGATTAA	CCAACCGATA
751	CCCGAAGACC	TGCCTGCCGG	TTTGCCGCTG	GACAAGCAGT	TTTTTGTGTA
801	AAAAC TGCCG	GCCGGTTTGA	GTTCCGAAGT	ATTGCTCGAC	CGTCCCGATA
851	TCCGTCGTGC	CGAACACCGG	CTCAAAACAG	CAAACGCCAA	TATCGGTGCG
901	GCACGCGCGG	CCTTTTTCCC	ATCCATCCGG	CTGACCGGAA	CCGTCCGGTA
951	GGGTTCTGCC	GAATTGGGTG	GGTTGTTCAA	AAGCGGCACG	GGCGTTTGGT
1001	CGTTCGCGCC	GTCTATTACC	CTGCCGATTT	TTACCTGGGG	TACGAACAAG
1051	GCGAACCTTG	ATGTAGCCAA	GCTGCGCCAA	CAGGTACAAA	TCGTTGCCTA
1101	TGAATCCGCG	GTCCAATCCG	CATTTCAGA	CGTGGCAAA	GCATTGGCGG
1151	CGCGCGAGCA	GCTGGATAAA	GCCATTGACG	CTTTAAGCAA	ACAAAGCCGC
1201	GCCTCTAAAG	AAGCGTTGCG	CTTGGTGCGC	CTGCGTTACA	AGCATGGCGT
1251	ATCCGGCGCG	CTCGACTTGC	TCGATGCGGA	ACGCAGCAGC	TATGCGGCGG
1301	AGGTGCGCGC	TTTGTGCGCA	CAACTGACCC	GCGCCGAAAA	CCTTGCCGAT
1351	TTGTACAAGG	CACTCGGCGG	CGGATTGAAA	CGGGATACCC	AAACCGACAA
1401	ATAA				

729. per

1	MDTTLKTTLT	SVAAAFALSA	CTMIPQYEQP	KVEVAETFKN	DTADSGIRAV
51	DLGWHDYFAD	PRLQKLIDIA	LERNTSLRTA	VLNSEIYRKQ	YMIERNLLP
101	TLAANANDRS	QGSLSGGNVS	SSYKVGLGAA	SYELDLFGRV	RSSEEAALQG
151	YFASTANRDA	AHLSLIATVA	KAYFNERYAE	EAMSLAQRVL	KTREETYKLS
201	ELRYKAGVIS	AVALRQKEAL	IESAKADYAH	AARSREQRAN	ALATLINQPI
251	PEDLPAGLPL	DKQFFVEKLP	AGLSSEVLLD	RPDIRAAEHA	LKQANANIGA
301	ARAAFFPSIR	LTGTVGTGSA	ELGGLFKSGT	GVWSFAPSIT	LPIFTWGTNK
351	ANLDVAKLRQ	QVQIVAYESA	VQSAFQDVAN	ALAAREQLDK	AYDALSKQSR
401	ASKEALRLVG	LDYKHGVSGA	LDLLDAERSS	YAAEGAALSA	QLTRAEANLAD
451	LYKALGGGLK	RDTOTDK*			

ORF 729 shows 95.7% identity over a 467 aa overlap with a predicted ORF (ORF729.a) from *N. gonorrhoeae*:

m729 / q729 95.7% identity in 467 aa overlap

m729.pep      MDTTLKTTLTSVAAAFALSACTMIPQYEQPKVEVAETFKNDTADSGIRAVDLGWHDYFAD  
 10                      20                      30                      40                      50                      60  
 g729           MNTTLKTTLTSVAAAFALSACTMIPQYEQPKVEVAETFQNDTSVSSIRAVDLGWHDYFAD  
                  10                      20                      30                      40                      50                      60

1179

m729.pep	70	80	90	100	110	120
	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNVS					
g729	70	80	90	100	110	120
	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANGSRQGSLSGGNVS					
m729.pep	130	140	150	160	170	180
	SSYKVLGAASYELDLFGRVRSSEAAALQGYFASTANRDAAHLSLIATVAKAYFNERYAE					
g729	130	140	150	160	170	180
	SSYNVGLGAASYELDLFGRVRSNSEAAALQGYFASVANRDAHLILIATVAKAYFNERYAE					
m729.pep	190	200	210	220	230	240
	EAMSLAQRVLKTREETYKLSELRYKAGVISAVALRQOEALIESAKADYAAHAARSREQARN					
g729	190	200	210	220	230	240
	KAMSLAQRVLKTREETYKLSELRYKAGVISAVALRQOEALIESAKADYAAHAARSREQARN					
m729.pep	250	260	270	280	290	300
	ALATLINQPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
g729	250	260	270	280	290	300
	ALATLINRPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
m729.pep	310	320	330	340	350	360
	ARAAFFPSIRLTGTVGTGSAELGGLFKSGTGVWSFAPSITLPIFTWGTNKANLDVAKLRQ					
g729	310	320	330	340	350	360
	ARAAFFPSIRLTGSVGTGSELGGLFKSGTGVWAFAPSITLPIFTWGTNKANLDVAKLRQ					
m729.pep	370	380	390	400	410	420
	QVQIVAYESAVQSAFQDVANALAAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
g729	370	380	390	400	410	420
	QAQIVAYESAVQSAFQDVANALAAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
m729.pep	430	440	450	460		
	LDLLDAERSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX					
g729	430	440	450	460		
	LDLLDAERISYAEGAALSAQLTRAENLADLYKALDGGGLKRDQTQGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2467>:

a729.seq

```

1  ATGGATACTA CATTGAAAAC CACCTTGACT TCTGTTGCAG CAGCCTTCGC
51  ATTATCCGCC TGCACCATGA TTCCCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCCGAAAC GTTCAAAAAC GATACCGCCG ACAGCGGCAT CCGTGCGGTC
151 GATTTGGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACCGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACAA TACATGATTG AGCGCAACAA CCTCCTGCCC
301 ACGTTTGCCG CCAATGCGAA CGACTCGCGC CAAGGCAGCT TGAGCGGCGG
351 CAATGTAAGC AGCAGCTACA AAGTCGGACT GGGTGCGGCA TCTTACGAAC
401 TCGATCTGTT CGGGCGTGTA CGCAGCAGCA GCGAGGCGGC ACTGCAAGGC
451 TATTTCGCCA GCACCGCCAA CCGCGATGCG GCACATTTGA GCCTGATTGC
501 CACCGTTGCC AAAGCCTATT TCAACGAACG TTATGCCGAA GAAGCGATGT
551 CTTTGCGGCA ACGTGTTTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTACGTT ACAAGGCAGG CGTGATTTCG GCGTCGCCC TACGTCAGCA
651 GGAAGCCCTA ATCGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCA
701 GCCGCGAACA GGCGCGCAAT GCCTTGGCAA CCCTGATTAA CCAACCGATA
751 CCCGACGACC TGCCCGCCGG TTTGCCGTTG GACAAGCAGT TTTTGTGTTGA
801 GAAGCTGCCG GCCGGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGATA
851 TCCGTGCTGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGTGCGG
901 GCCGCGCGCG CCTTTTTCCT ATCCATCCGC CTGACCGGAA GCGTCGATAC
951 GCATTCTGCC GAATTGGGCG GGCTGTTCAA AAGCGGCACC GGCGTTTGGT
1001 TGTTCCGACC TTCCATTACC CTGCCGATTT TTACCTGGGG TACGAACAAG

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1180

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1051 GCGAACCTCG ATGTAGCCAA GCTGCGCCAA CAGGCACAAA TCGTTGCCTA
1101 TGAAGCCGCC GTCCAATCCG CATTTC AAGA CGTGGCAAAC GCATTGACCG
1151 CGCGCGAGCA GTTGGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG TTTGGTCGGT CTGCGTTACA AACACGGCGT
1251 ATCCGCGCGC CTCGACTTGC TCGATGCGGA ACGCAGCAGC TATTCGGCGG
1301 AAGGTGCGGC TTTGTGCGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC AAACCGACAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2468; ORF 729.a>:

```

a729.pep
1  MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV
51  DLGWHDFAD PRLQKLIDIA LERNTSLRTA VLNSEIYRKQ YMIERNNLLP
101 TLAANANDSR QGSLSGGNVS SSKVGLGAA SYELDLFGRV RSSSEAALQG
151 YFASTANRDA AHLSLIATVA KAYFNERYAE EAMSLAQRVL KTREETYKLS
201 ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATLINQPI
251 PDDLPA GLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301 ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK
351 ANLDVAKLRQ QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR
401 ASKEALRLVG LRYKHGVSGA LDLLDAERSS YSAEGAALSA QLTRAENLAD
451 LYKALGGGLK RDTQTDK*

```

a729 / m729 98.1% identity in 467 aa overlap

a729.pep	MDTTLKTTLT	SVAAAFALSA	CTMIPQYEQP	KVEVAETFKN	DTADSGIRAV	DLGWHDFAD
m729	MDTTLKTTLT	SVAAAFALSA	CTMIPQYEQP	KVEVAETFKN	DTADSGIRAV	DLGWHDFAD
a729.pep	PRLQKLIDIA	LERNTSLRTA	VLNSEIYRKQ	YMIERNNLLP	TLAANANDSR	QGSLSGGNVS
m729	PRLQKLIDIA	LERNTSLRTA	VLNSEIYRKQ	YMIERNNLLP	TLAANANDSR	QGSLSGGNVS
a729.pep	SSKVGLGAAS	YELDLFGRV	RSSSEAALQG	YFASTANRDA	AHLSLIATVA	KAYFNERYAE
m729	SSKVGLGAAS	YELDLFGRV	RSSSEAALQG	YFASTANRDA	AHLSLIATVA	KAYFNERYAE
a729.pep	EAMSLAQRVL	KTREETYKLS	ELRYKAGVIS	AVALRQOEAL	IESAKADYAH	AARSREQARN
m729	EAMSLAQRVL	KTREETYKLS	ELRYKAGVIS	AVALRQOEAL	IESAKADYAH	AARSREQARN
a729.pep	ALATLINQPI	PDDLPA GLPL	DKQFFVEKLP	AGLSSEVLLD	RPDIRAAEHA	LKQANANIGA
m729	ALATLINQPI	PDDLPA GLPL	DKQFFVEKLP	AGLSSEVLLD	RPDIRAAEHA	LKQANANIGA
a729.pep	ARAAFFPSIR	LTGSVDTHSA	ELGGLFKSGT	GVWLFAPSIT	LPIFTWGTNK	ANLDVAKLRQ
m729	ARAAFFPSIR	LTGSVDTHSA	ELGGLFKSGT	GVWLFAPSIT	LPIFTWGTNK	ANLDVAKLRQ
a729.pep	QAQIVAYEAA	VQSAFQDVAN	ALTAREQLDK	AYDALSKQSR	ASKEALRLVG	LRYKHGVSGA
m729	QAQIVAYEAA	VQSAFQDVAN	ALTAREQLDK	AYDALSKQSR	ASKEALRLVG	LRYKHGVSGA

1181

	430	440	450	460
a729.pep	LDLLDAERSSYSAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX			
m729	LDLLDAERSSYAAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX			
	430	440	450	460

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2469>:

g730.seq

```

1   GTGAAACCGC TGCGCAGACT GACAAACCTC CTTGCCGCCT GCGCCGTAGC
51  GGCGGTCGCA CTCATACAGC CCGCCCTCGC GGCGGACTTG GCGCAAGACC
101 CGTTCATTAC CGATAACACC CAACGGCAGC ACTACGAACC CGGCGGCAAA
151 TACCACCTCT TCGGCGaCCC GCGCGGCAGC GTTTCGACC GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCACCA GATGGGCAAC CTGCTCATCC
251 AACAGGCGGC AATCCAAGGC AATCTTGGTT ACACCGTCCG CTTTTCGGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
351 AAGCGAAGAA AAAGGCAACG TTGACGACGG CTTTACCGTG TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCCGCCG ATGCCTACGA CGGCCCGAAG
451 GGCGGCAATT ACCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCCGCA GTATCAAAC CAATCCGACC GACACCCGCA
551 GCATCCGGCA ACGCATATTC GACAACTACA ACAACCTCGG CAGCAATTTT
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTTCGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TGTCAACGGC GTCGCCGCCG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGGCG AAGCCTTGGG CATAGGCGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCGA TGCGCAACAT
801 CGCCCCCTTA CCCGCCGAGG GCAAATTCGC CGCCATCGGC GGCTTGGGCA
851 GCGCGGCGGG CTTTGAAAAA AATACGCGCG AAGCCGTTGA CCGGTGGATA
901 CAGGAAAACC CCAATGCCGC CGAAACCGTC GAAGCCCTGG TCAACGTCCT
951 GCCGTTTGCC AAAGTCAAAA ACCTGACAAA GGCGGCAAAA CCGGGGAAGG
1001 CTGCGGTTAG TGGGGATTTT TCTAAATCCT ACACCTGCTC CTTCCACGGC
1051 AGCACCTTGG TCAAAACGGC AGACGGCTAC AAAGCCATTG CCCATATTCA
1101 AGCCGGAGAC CGCGTCCTTT CCAAGGACGA GGCAAGCGGA GAAACGGGAT
1151 ACAAACCCGT TACCGCCCGA TACGGCAATC CGTATCAAGA AACCGTTTAC
1201 ATTGAAGTTT CAGACGGCAT CGGCAACAGC CAAACCCTGA TTTCCAACCG
1251 CATCCACCCG TTTTATTCGG ACGGCAATG GATTAAGCGG GAAGATTTAA
1301 AAGCGGGAAG CCGGCTGTTA TCCGAAAGCG GCAAACCCA AACCGTCCGC
1351 AACATCGTTG TCAAACCAAA ACCGCTCAAA GCCTACAATC TGACCGTTGC
1401 CGATTGGCAT ACCTACTTCG TCAAGGGTAA TCAGGCGGAA ACGGAAGGGG
1451 TTTGGGTTCA TAATGATTGT CCGCCTAAAC CAAAACCAAC CAATCATGCC
1501 CAACAAAGAA AAGAAGAAGC TAAAAACGAT TCTCATCGAA GTGTGGGAGA
1551 TTCCAATCGT GTCGTTTCGC AAGGAAAGCA ATATTTAGAT TCCGACACAG
1601 GAAACCATGT TTATGTAAAA GGAGATAAAG TGTTATTCT AACTCCTGAT
1651 GGAAGACAGG TAACTCAATT TAAGAAGTCG AAAGCCAATA CGTCAAAAAG
1701 GGTAAAAAAT GGGAAATGGA CACCAAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2470; ORF 730.ng>:

g730.pep

```

1   VKPLRLRLTNL LAACAVAAVA LIQPALAADL AQDPFITDNT QRQHYEPGGK
51  YHLFGDPRGS VSDRTGKINV IQDYTHQMGN LLIQQAIIQG NLGYTVRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDDGFTV YRLNWEGHEH HPADAYDGPK
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIF DNYNNLGSNF
201 SDRADEANRK MFEHNAKLDR WGNMSEFVNG VAAGALNPF I SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFAAIG GLGSAAGFEK NTREAVDRWI
301 QENPNAAETV EALVNVLPFA KVKNLTKAAK PGKAAVSGDF SKSYTCSFHG
351 STLVKTAGDY KAIAHIQAGD RVLSKDEASG ETGYKPV TAR YGNPYQETVY
401 IEVSDGIGNS QTLISNRIHP FYS DGKWIKA EDLKAGSRL SESGKTQTVR
451 NIVVKPKPLK AYNLTVADWH TYFVKGNQAE TEGVWVHND PPKPKPTNHA
501 QQRKEEAKND SHRSVGDSNR VVREGKQYLD SDTGNHVYVK GDKVVILTPD
551 GRQVTQFKNS KANTSKRVKN GKWTPK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2471>:

m730.seq

```

1   GTGAAACCGC TGCGCAGACT GACAAACCTC CTTGCCGCCT GCGCCGTAGC
51  GGCGGCCGCA CTCATACAGC CCGCCCTCGC GGCGGACTTG GCGCAAGACC

```



1182

```

101 CGTTCATTAC CGATAACGCC CAACGGCAGC ACTACGAACC CGGCGGCAAA
151 TACCACCTCT TCGGCGACCC GCGCGGCAGC GTTTCGACC GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCCACCA GATGGGCAAC CTGCTCATCC
251 AACAGGCAAA CATCAACGGC ACAATCGGCT ACCACACCCG CTTTTCCGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
351 GAGCGAAGAA AAAGGCAACG TTGACGAAGG CTTTACCGTA TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCGCGC ATGCCTACGA CGGCCCGAAG
451 GGCGGCAATT ACCCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCCGCA GTATCAAAC CAATCCGACC GACACCCGCA
551 GCATCCGGCA ACGCATATCC GACAATTACA GCAACCTCGG CAGCAATTTT
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTCGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TATCAACGGC GTCGCCGCCG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGGCG AAGCCTTGGG CATAGGCGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCAA TGCGCAACAT
801 CGCCCCCTTG CCCGCCGAGG GCAAATTCGC CGTCATCGGC GGCTTGGGCA
851 GCGTGGCGGG CTTTGAAAAG AATACGCGCG AAGCCGTTGA CCGGTGGATA
901 CAGGAAAATC CCAATGCCGC CGAAACCGTC GAAGCCGTCT TCAACGTTGC
951 CGCAGCAGCC AAAGTCGCGA AGTTGGCAAA GGCGGCAAAA CCAGGGAAGG
1001 CTGCGGTTAG CGGGGATTTT GCTGATTCTT ATAAAAAGAA ATTGGCTTTG
1051 TCTGATAGTG CGAGACAGTT ATATCAAAAT GCAAAGTATA GAGAAGCTCT
1101 AGATATACAT TATGAAGATT TAATTAGAAG AAAAAGTAT GGTTCATCAA
1151 AATTATTATA CGGCAGAGAA ATTGACGCTG TTACGAATGA TGCTTTAATA
1201 CAAGCCAAAA GAACAATTTT AGCAATAGAT AAACCTAAAA ATTTCTTAAA
1251 TCAAAAAAAT AGAAAGCAAA TTAAAGCAAC CATCGAAGCA GCAAACCAAC
1301 AGGGAAAACG TGCAGAATTT TGGTTTAAAT ACGGTGTTCA TTCACAAGTT
1351 AAGTCATATA TTGAATCAAA AGGCGGCATT GTTAAACAG GTTTAGGAGA
1401 TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2472; ORF 730>:

```

m730.pep
  1 VKPLRRLTNL LAACAVAAAA LIQPALAADL AQDPFITDNA QRQHYEPGGK
 51 YHFGDPRGS VSDRTGKINV IQDYTHQMGN LLIQQANING TIGYHTRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDEGFTV YRLNWEHGEH HPADAYDGP
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIS DNYNSLGSNF
201 SDRADEANRK MFEHNAKLDR WGNMSEFING VAAGALNPMI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFAVIG GLGSVAGFEK NTREAVDRWI
301 QENPNAAETV EAVFNVAAAA KVAKLAKAAK PGKAAVSGDF ADSYKKKLAL
351 SDSARQLYQN AKYREALDIH YEDLIRKTD GSSKFINGRE IDAVTNDALI
401 QAKRTISAID KPKNFLNQKN RKQIKATIEA ANQQGKRAEF WFKYGVHSQV
451 KSYIESKGGI VKTGLGD*

```

g730 / m730 93.0% identity in 344 aa overlap

```

g730.pep      10      20      30      40      50      60
               VKPLRRLTNLLAACAVAAVALIQPALAADLAQDPFITDNTQRQHYEPGGKYHFGDPRGS
m730          10      20      30      40      50      60
               VKPLRRLTNLLAACAVAAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHFGDPRGS

g730.pep      70      80      90      100     110     120
               VSDRTGKINVIQDYTHQMGNLLIQQAAIQGNLGYTVRFSGHGHEEHAPFDNHAADSASEE
m730          70      80      90      100     110     120
               VSDRTGKINVIQDYTHQMGNLLIQQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE

g730.pep     130     140     150     160     170     180
               KGNVDDGFTVYRLNWEHGEHHPADAYDGPKGNNYPKPTGARDEYTYHVNGTARSIKLNPT
m730          130     140     150     160     170     180
               KGNVDEGFTVYRLNWEHGEHHPADAYDGPKGNNYPKPTGARDEYTYHVNGTARSIKLNPT

g730.pep     190     200     210     220     230     240
               DTRSIRQRIFDNYNNLGSNFSRDEANRKMFEHNAKLDRWGNMSEFVNGVAAGALNPMI
m730          190     200     210     220     230     240
               DTRSIRQRISDNYNLSNFSRDEANRKMFEHNAKLDRWGNMSEFINGVAAGALNPMI

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1183

	250	260	270	280	290	300
g730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAAIGGLGSAAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSAAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
g730.pep	QENPNAAETVEALVNVLPFAKVNLTAAKPGKAAVSGDFSYSYCSFHGSTLVKTADGY					
m730	QENPNAAETVEAVFNVAATAAKVAKLAKAAKPGKAAVSGDFADSYKKKLALSDSARQLYQN					
	310	320	330	340	350	360
	370	380	390	400	410	420
g730.pep	KAIAHIQAGDRVLSKDEASGETGYKPVNTARYGNPYQETVYIEVSDGIGNSQTLISNRIHP					
m730	AKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIKPKNFLNQKN					
	370	380	390	400	410	420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2473>:

```

a730.seq
1   GTGAAACCGC TGCGAAGACT CATCAAGCTC CTTGCCGCCT GTGCCGTAGC
51  GCGCGCCGCA CTCATACAGC CCGCCCTCGC GCGCGACTTG GCGCAAGACC
101 CGTTCATTAC CGATAACGCC CAACGCGCAGC ACTACGAACC CGGAGGCAAA
151 TACCACCTCT TCGGCGACCC GCGCGGCAGC GTCTCCGACC GCACCGGTCA
201 AATCAACGTC ATCCAAGACT ATACCCACCG GATGGGCAAC CTGCTCATCC
251 AGCAGGCAAA CATCAACGGC ACAATCGGCT ACCACACCCG CTTTTCGGGA
301 CACGGATACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACACGCG
351 GAGCGAAGAA AAAGGCAACG TTGACGAAGG CTTTACCGTA TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCCGCCG ATGCCTACGA CGGCCCGAAG
451 GCGGGAATT ACCCCAAACC TACGGGTGCA CGCGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCACGCA GCATCAAAC CAATCCGACC GACACCCGCA
551 GCATCCGGCA ACGCATATCC GACAATTACA GCAACCTCGG CAGCAATTTC
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTTCGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TATCAACGGC GTCGCCGCCG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGGCG AAGCCTTGGG CATAGGCGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCAA TGCGCAACAT
801 CGCCCCCTTG CCCGCCGAGG GCAAATTCGC CGTCATCGGC GGCTTGGGCA
851 GCGTGGCGGG CTTTGAAAAA AATACGCGCG AAGCCGTTGA CCGGTGGATA
901 CAGGAAAACC CCAATGCCGC CGAAACCGTC GAAGCCCTGG TCAACGTCCT
951 GCCGTTTGCC AAAGTCAAAA ACCTGACAAA GGCGGCAAAA CCGGGGAAGG
1001 CTGCGGTTAG CGGGGATTTT TCTGCTGCAT ACAATACAAG AACAACTAGA
1051 AAAGTTACTA CAGAAACAGA GGGGTTAAAT AGAATCAGAC AGAACCAGAA
1101 AAATAGTAAT ATACATGAGA AAAATTATGG AAGAGATAAT CCTAATCATA
1151 TTAATGTTTT ATCTGGAAAT TCTATACAAC ATATACTGTA TGGAGATGAA
1201 GCAGGAGGTG GGCATCTTTT TCCTGGCAAA CCTGGTAAGA CAACATTCCC
1251 CCAACATTGG TCAGCCAGTA AAATAACTCA TGAAATTAGT GATATCGTTA
1301 CATCCCCAAA AACGCAATGG TATGCACAGA CTGGAACAGG CGGCAAAATAT
1351 ATTGCTAAAG GAAGACCAGC TAGGTGGGTA TCATATGAAA CGAGAGATGG
1401 AATTCGTATC AGAACAGTTT ATGAACCTGC AACAGGAAAA GTGGTAACGTG
1451 CATTCCCCGA TAGAACCTCT AATCCCAAAT ATAACCCTGT AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2474; ORF 730.a>:

```

a730.pep
1   VKPLRLRIKL LAACAVAAAA LIQPALAADL AQDPFITDNA QRQHYEPGGK
51  YHLEFGDPRGS VSDRTGQINV IQDYTHRMGN LLIQQANING TIGYHTRFSG
101 HGYEEHAPFD NHAADSASEE KGNVDEGFTV YRLNWEGHEH HPADAYDGPKE
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIIS DNYSNLGNSF
201 SDRADEANRK MFEHNAKLDR WGNMSEFING VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFAVIG GLGSAAGFEK NTREAVDRWI
301 QENPNAAETV EALVNVLPFA KVNLTAAK PGKAAVSGDF SAAYNTRTTR
351 KVTTETEGLN RIRQNQNSN IHEKNYGRDN PNHINVLSGN SIQHILYGDE
401 AGGGHLFPKG PGKTTFPQHW SASKITHEIS DIVTSPKTQW YAQTGTGGKY
451 IAKGRPARWV SYETRDGIRI RTVYEPATGK VVTAFFPDRTS NPKYNPVK*

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1184

a730 / m730 88.6% identity in 376 aa overlap

	10	20	30	40	50	60
a730.pep	VKPLRRLIKLLAACAVAAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
m730	VKPLRRLTNLLAACAVAAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
	10	20	30	40	50	60
a730.pep	VSDRTGQINVIQDYTHRMGNLLIQQANINGTIGYHTRFSGHGYEEHAPFDNHAADSASEE					
m730	VSDRTGKINVIQDYTHQMGNLLIQQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
a730.pep	VSDRTGQINVIQDYTHRMGNLLIQQANINGTIGYHTRFSGHGYEEHAPFDNHAADSASEE					
m730	VSDRTGKINVIQDYTHQMGNLLIQQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
a730.pep	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
a730.pep	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
a730.pep	DTRSIRQIRISDNYSNLGNSNFSRDEANRKMFEHNAKLDRWNSMEFINGVAAGALNPFII					
m730	DTRSIRQIRISDNYSNLGNSNFSRDEANRKMFEHNAKLDRWNSMEFINGVAAGALNPFII					
	190	200	210	220	230	240
a730.pep	DTRSIRQIRISDNYSNLGNSNFSRDEANRKMFEHNAKLDRWNSMEFINGVAAGALNPFII					
m730	DTRSIRQIRISDNYSNLGNSNFSRDEANRKMFEHNAKLDRWNSMEFINGVAAGALNPFII					
	190	200	210	220	230	240
a730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSGVAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSGVAGFEKNTREAVDRWI					
	250	260	270	280	290	300
a730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSGVAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSGVAGFEKNTREAVDRWI					
	250	260	270	280	290	300
a730.pep	QENPNAAETVEALVNVLPFAKVKNLTKAAKPGKAAVSGDFSAAYNTRTTRKVTETETGLN					
m730	QENPNAAETVEAVFNVAATAKAKLAKAAKPGKAAVSGDFSADSY-----KKKLALSDSAR					
	310	320	330	340	350	360
a730.pep	QENPNAAETVEALVNVLPFAKVKNLTKAAKPGKAAVSGDFSAAYNTRTTRKVTETETGLN					
m730	QENPNAAETVEAVFNVAATAKAKLAKAAKPGKAAVSGDFSADSY-----KKKLALSDSAR					
	310	320	330	340	350	360
a730.pep	RIRQNQKNSNIHEKNYGRDNPINHINVLSGNSIQHILYGDEAGGGHLFPGKPGKTTFFQHW					
m730	QLYQNAKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIDKPKNF					
	360	370	380	390	400	410
a730.pep	RIRQNQKNSNIHEKNYGRDNPINHINVLSGNSIQHILYGDEAGGGHLFPGKPGKTTFFQHW					
m730	QLYQNAKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIDKPKNF					
	360	370	380	390	400	410

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2475>:

```

g731.seq
1  gatttttcgag  cgttttcatg  CGAGAACGGT  TTGTCTGTGC  GCGTCCGCAA
51  TTTGGACGGC  GGCAAAATCG  CGTTGCGGCT  GGACGGCAGG  CGTGCCGTCC
101 TCTCTTCCGA  CGTTGCCGCA  TCCGGCGAAC  GCTATACCGC  CGAACACGGT
151 TTGTTCGGAA  ACGGAACCGA  GTGGCACCAG  AAAGGCGGCG  AAGCCTTTTT
201 CGGCTTTACC  GATGCCTACG  GCAATTCGGT  CGAAACTTCC  TGCCGCGCCC
251 GTTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2476; ORF 731.ng&gt;:

```

g731.pep
1  DFRAFSCENG  LSVRVRLDGR  GKIALRLDGR  RAVLSSDVAA  SGERYTAEHG
51  LFGNGTEWHQ  KGGEAFFGFT  DAYGNSVETS  CRAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2477>:

```

m731.seq
1  ATGAATATCA  GGTTTTTCGC  GCTGACCGTA  CCGGTTTTGT  CTTTGGCGGC
51  CTGTGCCGTG  CCGGAGGCGT  ATGATGACGG  CGGACGCGGG  CATATGCCGC
101 CCGTTCAAAA  CCAAGCCGGC  ACGGACGATT  TTCGGGCGTT  TTCCTGCGAG
151 AACGGTTTGT  CTGTGCGCGT  CCGCCATTTG  GACAGCGGCA  AAGTCGCGTT
201 GCGGCTGGAC  GGCAGGCGTG  CCGTCTCTC  TTCCGACGTT  GCCGCATCCG

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1185

251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG  
 301 CACCAGAAAG GCGGCGAAGC CTTTTCGGC TTTACCGATG CCTACGGCAA  
 351 TTCGGTCGAA ACTTCCTGCC GCGCCCGTTA A

This corresponds to the amino acid sequence <SEQ ID 2478; ORF 731>:

m731.pep  
 1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TDDFRAFSC  
 51 NGLSVRVRHL DSGKVALRLD GRRAVLSSDV AASGERYTAE HGLFGNATEW  
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR\*

g731/m731 95.2% identity in 84 aa overlap

				10	20	30
g731.pep				DFRAFSCENGLSVRVRNLDGGKIALRLDGR		
m731	LSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCENGLSVRVRHLDSGKVALRLDGR					
	20	30	40	50	60	70
	40	50	60	70	80	
g731.pep	RAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVETSCRARX					
m731	RAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVETSCRARX					
	80	90	100	110	120	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2479>:

a731.seq  
 1 ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTTGT CTTTGGCGGC  
 51 CTGTGCCGTG CCGGAGGCGT ATGATGACGG CGGACGAGGG CATATGCCGC  
 101 CCGTTCAAAA CCAAGCCGCG ACGGCAGATT TTCGGGCATT TTCCTGCGAG  
 151 AACGGTTTGT CTGTGCACGT CCGCCGTTTG GACGGCGGCA GAATCGCGTT  
 201 GCGGTTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG  
 251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG  
 301 CATCAGAAAG GCGGCGAAGC CTTTTCGGC TTTACCGATG CCTACGGCAA  
 351 TTCGGTCGAA ACCTCCTGCC GCGCCCGCTA A

This corresponds to the amino acid sequence <SEQ ID 2480; ORF 731.a>:

a731.pep  
 1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TADFRAFSC  
 51 NGLSVHVRRL DGGRIALRLD GRRAVLSSDV AASGERYTAE HGLFGNGTEW  
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR\*

a731/m731 94.4% identity in 126 aa overlap

		10	20	30	40	50	60
a731.pep	MNIRFFALTVPVL	SLAACAVPEAYDDGGRGHMPPVQNQAGTADFRAFSCENGLSVHVRRL					
m731	MNIRFFALTVPVL	SLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCENGLSVRVRHL					
	10	20	30	40	50	60	
	70	80	90	100	110	120	
a731.pep	DGGRIALRLDGRRAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVE						
	: :						
m731	DSGKVALRLDGRRAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVE						
	70	80	90	100	110	120	
a731.pep	TSCRARX						
m731	TSCRARX						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2481>:

g732.seq  
 1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT  
 51 CAGCGGCGTG GCCGTAAGTC TGGCGGTGCA GGGTTTTGCC GCCGagaagg  
 101 ACGGgcgGGA TAACGAagtC CTGCCGTGC AATCCATCCG TACGATGGCG

1186

```

151 GAGGTTTACG GTCAGATTAA GGCAAACACTAC TATCATGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGTTT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGAGG
401 TGAAAAGCGG CGATTTCATT GTGAAAATCG ATAATGTTTC GACGCGCGGT
451 ATGACGGTCA GCGAAGCGGT GAAAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGTTGTCGC GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCG CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACCGGCG CGGTCGGCGT GTCGGCGGCG TTTCTGCCGT CTGAAGCGGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACGGCATG GACTGAAAG
851 CCGTTCCCGA GGATTATGTG TACGGTATGG GCGGCGACCC TTTGGCGGGT
901 ATTCTTGCCG AGTTGAAAAC GATTCCGATG ACGgtatTGG TcaaTTCGG
951 TTCggcttCC GCGTCGGAGA TTGtgcCGG GCGATTGCAG GACCACAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GTAAAGGTTT GGTTCAGACT
1051 TTGATTCCCTT TGTCCAACGG CAGCGCGGTC AAGTTGACGA CCGCCCTGTA
1101 TTACACGCCG AACGACCGTT CCATTACAGC ACAGGGGATT GTTCCCAGATG
1151 TCgaaGTAAA AGATAAGGAA CGTACTTTTG AAAGCCGCGA GCGGACCTG
1201 GTCGGACACA TCGGCAATCC CTTgggcGCG GAGGATGTGA ACAGTGAAC
1251 CCttgcCGTA CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GCAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTGTG CTTCAAGCGG GATTCCGAAC
1351 CCTGCGAAAG ACGATCAGTT GCGTAAGGCT TTGGATTGG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAA CCGGTTTCAA
1451 ATAAAGATAA AAAAGATAAG AAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2482; ORF 732>:

g732 . pep

```

1 MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDGRDNEV LPVQSIRTMA
51 EVYGOIKANY YHDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGFEGGLGME IGQEDGFVKV VSPIEDTPAE RAEVKSGDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLSRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGDGDM VLKAVPEDYV YGMGGDPLAG
301 IPAELKTIPM TVLVNNGSAS ASEIVAGALQ DHKRAVIVGT QSFKGVSQVT
351 LIPLSNGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RTFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA AKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKKKDK K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2483>:

m732 . seq

```

1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51 CAGCGGCGTG GCCGTCAGTC TGGCGGTGCA GGGTTTTGCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGCTGC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAAACACTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTCGC GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCG CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTGCGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACGGCATG GACTGAAAG
851 CCATTCTCTGA AGATTATGTG TACGGGATGG GCGGCGATTC GTTGGCGGGC
901 ATTCTTGCCG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGGAGA TTGTCGCAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCCTT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CCGCACTGTA

```

1187

```

1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTGT AAAGCCGCGA GGCGGATTGT
1201 GTCGGACACA TCGGCAATCC CTTGGGCGGC GAGGATGTGA ACGGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTGT CTTCAAGGCG GATTCCCAAC
1351 CCTGCCAAAG ACGACCAAGT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GGCGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2484; ORF 732>:

**m732.pep**

```

1  MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51  EVYGQIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTPAE RAGVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDRM VLKAIPEDYV YGMGGDSLAG
301 IPAEKLTIPM TVLVNNGSAS ASEIVAGALQ DHKRAVIVGT QSFSGKSVQT
351 LIPLSNGSAV KLTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNGETLAV PLEKADKPA VKEGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKKDK KDKK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 732 shows 98.2% identity over a 491 aa overlap with a predicted ORF (ORF732.a) from *N. gonorrhoeae*:

**m732/g732** 98.2% identity in 491 aa overlap

	10	20	30	40	50	60
m732.pep	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY					
g732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRDNEVLPVQSIRTMAEVYGOIKANY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	:					
g732	YHDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m732.pep	VSPIEDTPAERAGVKSDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
g732	VSPIEDTPAERAEVKSDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m732.pep	IVVNLTRAIKVKSVRHHLIEPDYGIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
g732	IVVNLTRAIKVKSVRHHLIEPDYGIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m732.pep	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAIPEDYVYGMGGDSLAG					
g732	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDMVLKAVPEDYVYGMGGDPLAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m732.pep	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLSNGSAV					
g732	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLSNGSAV					
	310	320	330	340	350	360

1188

	370	380	390	400	410	420
m732.pep	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNGETLAV					
g732	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERTFESREADLVGHIGNPLGGEDVNSETLAV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
g732	PLEKDADKPAAKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
	430	440	450	460	470	480
	490					
m732.pep	PVS NKDKKDKDKKX					
g732	PVS NKDKKDKKX					
	490					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2485>:

```

a732.seq
1  ATGTCGAAAC CTGTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51  CAGCGCGTG GCCGTCAGTC TGGCGGTGCA GGGTTTGGCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGTGCA AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAAACTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCGGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTTATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTGCG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTG CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGCG GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTCGGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACCGCATG GTACTGAAAG
851 CCGTTCCTGA AGATTATGTG TACGGGATGG GCGGCGATTG GTTGGCGGGC
901 ATTCCTGCCG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGGAGA TTGTCGCAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCTTT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA
1101 TTATACGCCG AACGACCGTT TATTTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTGT AAAGCCGCGA GCGCGGATTG
1201 GTCGGACACA TCGGCAATCC TTTGGGCGGC GAGGATGTGA ACAGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCCAAC
1351 CCTGCCAAAG ACGACCAATT GCGGAAAGCT TTGGATTAGT TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2486; ORF 732.a>:

```

a732.pep
1  MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51  EVYGOIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTAE RAGVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLSRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDRM VLKAVPEDYV YGMGGDSLGA
301 IPAEIKTIPM TVLVNSGSAS ASEIVAGALQ DHKRAIVGT QSFKGSVQT
351 LIPLNSGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVS NKDKKDK KDKK*

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1189

a732/m732 99.6% identity in 494 aa overlap

	10	20	30	40	50	60
a732.pep	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLVPQSIRTMAEVYGGQIKANY					
m732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLVPQSIRTMAEVYGGQIKANY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
m732	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
a732.pep	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
m732	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
	190	200	210	220	230	240
a732.pep	IVVNLTRAIKVKSVRHHLEIPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
m732	IVVNLTRAIKVKSVRHHLEIPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
a732.pep	LDLRDDPGGLLTGAVGVSA AFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAV					
m732	LDLRDDPGGLLTGAVGVSA AFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAV					
	250	260	270	280	290	300
	310	320	330	340	350	360
a732.pep	IPAEELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFGKGSVQTLIPLSNGSAV					
m732	IPAEELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFGKGSVQTLIPLSNGSAV					
	310	320	330	340	350	360
	370	380	390	400	410	420
a732.pep	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
m732	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
	370	380	390	400	410	420
	430	440	450	460	470	480
a732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
m732	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
	430	440	450	460	470	480
	490					
a732.pep	PVSNDKDKDKDKKX					
m732	PVSNDKDKDKDKKX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2487>:

g733.seq

```

1  ATGATGAATC CGAAAACCTT GGGCCGTTTG TCGCTGTGTG CGGCGGTCTT
51 GGCTCTGACC GCCTGCGCCG GCGGCGGGCA TAAAAACCTG TATTATTACG
101 GCGGTTATCC CGATACCGTC TATGAAGGTT TGAAAAACGg cgACACTTCG
151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGCGG AAGCCGCCAA
201 CAAAAAATG AATGCCGCCC CGGGTGCGCA CGCCATTG GGA CTGCTGC

```



1190

251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAATT TGAAGAAGAG  
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC  
 351 CGGtaaAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2488; ORF 733>:

g733.pep

1 MMNPKTLGRL SLCAAVLALT ACAGGGHKNL YYYGGYPDTV YEGLKNDDTS  
 51 LGKQTEKMEK YFAEAANKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE  
 101 KRLFPESGVF MDFLMKTGKG GKR\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2489>:

m733.seq

1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT  
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG  
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG  
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA  
 201 CAAAAAATG AATGCCGCCC CGGGTGCGCA CGCCCATCTG GGAAGTCTGC  
 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG  
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC  
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2490; ORF 733>:

m733.pep

1 MMNPKTLSRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDDTS  
 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE  
 101 KRLFPESGVF MDFLMKTGKG GKR\*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 733 shows 94.3% identity over a 123 aa overlap with a predicted ORF (ORF733.a) from *N. gonorrhoeae*:

m733/g733

	10	20	30	40	50	60
m733.pep	MMNPKTLSRLSLCAAVLALTACGGNGQKSL	YYYGGYPDTVYEGLKNDDTSLGKQTEKMEK				
g733	MMNPKTLGRLSLCAAVLALTACAGGGHKNLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m733.pep	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGA	FRQFEEKRLFPESGVFMDFLMKTGKG				
g733	YFAEAANKKMNAAPGAHAHLGLLLSRSGDKEGA	FRQFEEKRLFPESGVFMDFLMKTGKG				
	70	80	90	100	110	120
m733.pep	GKRX					
g733	GKRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2491>:

a733.seq

1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT  
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG  
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG  
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA  
 201 CAAAAAATG AATGCCGCCC CGGGTGCGCA CGCCCATCTG GGAAGTCTGC  
 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG  
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC  
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2492; ORF 733.a>:

a733.pep

1191

```

1  MMNPKTL SRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDDTS
51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
101 KRLFPESGVF MDFLMKTGKG GKR*

```

a733/m733 100.0% identity in 123 aa overlap

```

              10      20      30      40      50      60
a733.pep      MMNPKTL SRL SLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK
              |||||||
m733          MMNPKTL SRL SLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK
              10      20      30      40      50      60

              70      80      90      100     110     120
a733.pep      YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG
              |||||||
m733          YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG
              70      80      90      100     110     120

a733.pep      GKRX
              ||||
m733          GKRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2493>:

```

g734.seq
1  ATGATGAAAA AGATACTGGC AGTATCGGCA CTATGCCTGA TGA CTGCGGC
51  GGCACAGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGGATGCAAA CGATGTTTTG CAGGTTAAAA CCACAAAAGA AGATTCGGCG
151 AAAAGCGAAG CGTTTGCCGA GTTGGAAGCC TTTTGCAAAG GTCAGGACAC
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT
251 CGCTGAACAA TACCTGTGTC TCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT CGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TCATCAGGTC GCACTCAACC AGTGCATAAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAAACAGTG TATTGCACGT CATCTTCTTA TTACGGCGGG
451 GCTGTTCGCT CCTAATCCA ACACCTGAAA TAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2494; ORF 734.ng&gt;:

```

g734.pep
1  MMKKILAVSA LCLMTAAAOA ADTYGYLAVW QNPQDANDVL QVKTTKEDSA
51  KSEAFAELEA FCKGQDTLAG IAEDEPTGCR SVVSLNNTCV SLAYPKALGA
101 MRVENAVVIT SPRFTSVHGV ALNQCIKKYG AQQQCGLQTV YCTSSSYGG
151 AVRSLIQHLK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2495>:

```

m734.seq (partial)
1  TCGGGCATTG CTGAAGACGA GCCGACCGGA TGCCGGTCGG TCGTGTGCGT
51  GAACAATACC TGTGTCGCGC TGGCATACCC GAAAGCCTTG GGCGCGCTGC
101 GTGTCGACAA CGCCGTCGTG ATTACTTCTC CGCGTTTTAC GAGCGTTCAT
151 CAGGTCGCAC TCAACCAGTG CATCAAAAAA TACGGCGTAC AGGGACAATG
201 CGGCTTGGAA ACAGTGTATT GCACATCTTC TTCTTATTAC GGCGGAACTG
251 TGCCTCTTTT GATTCAAAAT CTCAAATAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2496; ORF 734&gt;:

```

m734.pep (partial)
1  SGIAEDEPTG CRSVSLNNT CVALAYPKAL GALRVDNAVV ITS PRFTSVH
51  QVALNQCIKK YGVQGCGLQ TVYCTSSSY GGTVRSLIQN LK*

```

m734/g734 92.4% identity in 92 aa overlap

```

              10      20      30
m734.pep      SGIAEDEPTGCRSVVSLNNTCVALAYPKAL
              : |||||||
g734          VLQVKTTKEDSAKSEAFAELEAFCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKAL

```

	40	50	60	70	80	90
m734.pep	GALRVDNAVVITSPRET <sup>40</sup> SVHQVALNQC <sup>50</sup> IKKYGVQGC <sup>60</sup> LET <sup>70</sup> VTYCTSS <sup>80</sup> SYGGTV <sup>90</sup> RS <sup>90</sup> LIQN					
g734	GAMRVENAVVITSPRET <sup>40</sup> SVHQVALNQC <sup>50</sup> IKKYGA <sup>60</sup> QGC <sup>70</sup> LET <sup>80</sup> VTYCTSS <sup>90</sup> SYGGAV <sup>90</sup> RS <sup>90</sup> LIQH					
	100	110	120	130	140	150
m734.pep	LKK					
g734	LKK					
	160					

a734.seq

1	ATGATGAAAA	AGATACTGGC	CGTATCGGCA	CTATGCCTGA	TGACTGCGGC
51	GGCACGGGCT	GCCGATACTT	ACGGCTATCT	CGCCGTTTGG	CAGAATCCGC
101	AGAATGCAAA	CGATGTTTTG	CAGGTTAAAA	CCACAAAAGA	AGATTGCAGC
151	AAAAGCGAAG	CGTTTGCCGA	GTTGGAAGCT	TTCTGCAAAG	GTCAGGACAC
201	GCTTGCGGGC	ATTGCCGAAG	ACGAGCCGAC	CGGATGCCGG	TCGGTCGTGT
251	CGCTGAACAA	TACCTGTGTC	GCGCTGGCAT	ACCCGAAAGC	CTTGGGCGCG
301	ATGCGCGTTG	AAAACGCCGT	TGTGATTACT	TCTCCGCGTT	TTACGAGCGT
351	TTATCAGGTC	GCAATCAACC	AGTGCATCAA	AAAATACGGC	GCACAGGGAC
401	AATGCGGCTT	GGAAACAGTG	TATTGCACGT	CTTCTTCTTA	TTACGGGGGA
451	ACTGTGCGCT	CTTTGATTCA	AAATCTCAAA	TAA	

a734.pep

1	<u>MMKKILAVSA</u>	<u>LCLMTAAARA</u>	ADTYGYLAVW	QNPQNANDVL	QVKTTKEDST
51	KSEAFAELEA	FCKGQDTLAG	IAEDEPTGCR	SVVSLNNTCV	ALAYPKALGA
101	MRVENAVVIT	SPRFTSVYQV	ALNQCIKKYG	AQGQCGLETV	YCTSSSYGG
151	TVRSLIQNLK	*			

	10	20	30	40	50	60
a734.pep	MMKKILAVSALCLMTAAARAADTYGYLAVWQNPQNANDVLQVKTTKEDSTKSEAFAELEA					
g734	MMKKILAVSALCLMTAAQAADTYGYLAVWQNPQDANDVLQVKTTKEDSAKSEAFAELEA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a734.pep	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVLAYPKALGAMRVENAVVITSPRFTSVYQV					
g734	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVHQV					
	70	80	90	100	110	120
	130	140	150	160		
a734.pep	ALNQCIKKYGAQGQCGLETVYCTSSSYGGTVRSLIQNLIKX					
g734	ALNQCIKKYGAQGQCGLETVYCTSSSYGGAVRSLIQHLIKX					
	130	140	150	160		

m735.seq		g1		g2	
1	ATGAATCTCG	TGAAACTGCT	GGCGAATAAC	TGGCAACCGA	TTGCCATTAT
51	CGCGCTTGTC	GGCACGGGCT	TGGCTGTGTC	GCACCATCAA	GGCTACAAGT
101	CGGCATTGTC	GAAGCAGCAG	GGCGTCAATC	ACAAGATGGA	GCGCGACAAG
151	GCGCAAGCCC	TGCTGTTGTC	GGCTCAA AAC	TATGCGCGCG	AACTGGA ACT
201	GGCAGCGCGC	GAAGCTAAAA	AATATGAAGT	CAAGGCGCAC	GCTGTCGGGA
251	TGGCTTTGGC	GAAGAAAAAC	CGGGAAGTCA	GCCGCTGTAA	AACGGA AAA T
301	AAAAAGGAAA	TCGAAAATGT	CCTTACTCAA	GACCGTAAAA	ATGCAAGCGG

1193

351 CGGTTGCATT GACGGCTTTG GCTCTCACGG CCTGCAGCTC TACAACCGCG  
 401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2500; ORF 735>:

m735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK  
 51 AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN  
 101 KKEIENVLTQ DRKNASGGCI DGFGSHGLQL YNRALGYGN\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2501>:

a735.seq

1 ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT  
 51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT  
 101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG  
 151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA  
 201 GCGCGGTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCGGCA  
 251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAT  
 301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG  
 351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG  
 401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2502; ORF 735.a>:

a735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK  
 51 AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN  
 101 KKEIENVLTQ DRKNAGGGCI DGFGHHGLQL YKRALGYGN\*

a735/m735 95.7% identity in 139 aa overlap

	10	20	30	40	50	60
a735.pep	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN					
m735	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a735.pep	YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNAGGGCI					
m735	YARELELARA EAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNASGGCI					
	70	80	90	100	110	120
	130	140				
a735.pep	DGFGHHGLQLYKRALGYGNX					
m735	DGFGSHGLQLYNRALGYGNX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2503>:

g736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC  
 51 CTTCCGCAGT ATCAGCTGT TTCTGCTGAA CATTTTGCG AAATCCGGCA  
 101 CGGCTTTCGC CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTGCGCGC  
 151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTCT TCGGTATGGT  
 201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA  
 251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGC CGA AACT GGGTCCCGTG  
 301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GGCGGTGCGA TGACCAGCGA  
 351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG  
 401 CGGTCAACCC CGTCGCCGCG GTGGTTGCCC CGCGTTTTTG GGCGGGCGTG  
 451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCGG GCATTTTCGG  
 501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT  
 551 GGCCGCAGAT GCAGAACAA ATTACGATAC ATTACGATGT AATCAACGGT

1194

```

601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGCGGGT CGATTTTATA
751 TTGACCGCGT GGATGTTTAC AGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2504; ORF 736>:

**g736.pep**

```

1 MNFIRSVGAK TLGLIQSFGS ITLFLNLA KSGTAFARPR LSVRQVYFAG
51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
101 LAAILFASSA GGAMTSEIGL MKTTGQLEAM NVMAVNPVAR VVAPRFWAGV
151 FSMPLLASIF NVAGIFGAYL VGVSWLGLDS GIFWPQMNN ITIHYDVI
201 LIKSAAFGVA VTLIAVHQGF HCIPTSEGIL RASTRTVVSS ALTILAVDFI
251 LTAWMFTD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2505>:

**m736.seq**

```

1 ATGAATTTTA TCCGTTCCTG CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51 CTTCGGCAGT ATCACGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA
101 CGGCTTTCGC CCGTCCGCGC CTGAGCGTGC GCCAAGTGT TTTTGCCGGC
151 GTGCTTTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTTC TCGGTATGGT
201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCCGC GCTTCTCTGT TCGCGAACT GGGTCCCCTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GGCGGTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
401 CGGTCAACCC CGTCGCCCGC GTGGTTGCCC CGCGTTTTTG GGCGGGCGTG
451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCGG GCATTTTCGG
501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
551 GGCCGCAGAT GCAGACAAC ATTACGATAC ATTACGATGT AATCAACGGT
601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGCGGGT CGATTTTATA
751 TTGACCGCGT GGATGTTTAC AGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2506; ORF 736>:

**m736.pep**

```

1 MNFIRSVGAK TLGLIQSLGS ITLFLNLA KSGTAFVRPR LSVRQVYFAG
51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMAVNPVAR VVAPRFWAGV
151 FSMPLLASIF NVAGIFGAYL VGVSWLGLDS GIFWSQMNN ITIHYDVI
201 LIKSAAFGVA VTLIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
251 LTAWMFTD*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 736 shows 97.7% identity over a 258 aa overlap with a predicted ORF (ORF736.ng) from *N. gonorrhoeae*:

**m736/g736**

	10	20	30	40	50	60
m736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNLA KSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
g736	MNFIRSVGAKTLGLIQSFGSITLFLNLA KSGTAFARPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
g736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m736.pep	MKTTEQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					
g736	MKTGQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					

		130	140	150	160	170	180
m736.pep		190	200	210	220	230	240
		GIFWSQM	NNITIHVD	INGLIKSAA	FGVAVTL	IAVHQGFH	CVPTSEGI
g736		GIFWPQM	NNITIHVD	INGLIKSAA	FGVAVTL	IAVHQGFH	CVPTSEGI
		190	200	210	220	230	240
m736.pep		250	259				
		ALTILAVD	FILTAWM	FMTDX			
g736		ALTILAVD	FILTAWM	FMTDX			
		250					

```

a736.seq
1  ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51  TCTCGGCAGT ATCAGCTGCT TTCTGCTGAA TATTCTGGCG AAATCCGGTA
101 CGGCTTTCGT CCGTCCGCGC CTGAGCGTGC CCAAGTGTGA TTTTGCCGGC
151 GTGCTGTCGG TGTTGATTGT TGCCGTTTCA GGGCTGTTTG TCGGCATGGT
201 CTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCCGC GCTTCGCTGT TCGCGAACT GGGTCCGGTG
301 TTGGCGCGCA TTCTGTTTGC CAGCAGCGCG GCGGTTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGAACAGCT CGAAGCGATG AACGTGATGG
401 CGGTAAACCC CGTCGCCCGA GTGGTTGCGC CGCGCTTTTG GCGGGGCGTG
451 TTTTCCATGC CGCTTTTGCG TTCGATTTTC AACGTGGCGG GTATTTTTCG
501 CGCGTATTTG TCGGTTGTAA CCTGGCTGGG CTTGGACAGC GTATTTTCTC
551 GGTCGCAAAT GCAGAACAAC ATCACGATAC ATTACGATGT AATCAACGGT
601 CTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
651 TCAGGGCTTC CACTGCGTCC CGACCTCGGA AGGCATTTTG CGCGCCAGCA
701 CGCGCACGGT GGTTTCGTCC GCCTTGACGA TTTTGGCGGT CGATTTTATA
751 TTGACCGCGT GGATGTTTAC AGATTGA

```

```
a736.pep
1  MNFIRSVGAK  TLGLIQSLGS  ITLFLNILA  KSGTAFVRPR  LSVRQVYFAG
51  VLSVLIVAVS  GLFVGMVLGL  QGYTQLSKFK  SADILGYMVA  ASLLRELGPV
101 LAAILFASSA  GGAMTSEIGL  MKTEQLEAM  NVMAVNPVAR  VVAPRFWAGV
151 FSMPLLASIF  NVAGIFGAYL  VGVTWLGLDS  GIFWSQMNN  ITIHVDVING
201 LIKSAAFGVA  VTLIAVHQGF  HCVPTSEGIL  RASTRVTVSS  ALTILAVDFI
251 LTAWMETD*
```

		10	20	30	40	50	60
a736.pep		MNFIRSVGAKTLGLIQSLGSITLFLNLILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
m736		MNFIRSVGAKTLGLIQSLGSITLFLNLILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
		10	20	30	40	50	60
		70	80	90	100	110	120
a736.pep		GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
m736		GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
		70	80	90	100	110	120
		130	140	150	160	170	180
a736.pep		MKTTEQLEAMNVMVAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLWGLDS					
m736		MKTTEQLEAMNVMVAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLWGLDS					
		130	140	150	160	170	180
		190	200	210	220	230	240
a736.pep		GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					

1196

```

m736      GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS
              190      200      210      220      230      240

              250      259
a736.pep   ALTILAVDFILTAWMFTDX
              |||||
m736      ALTILAVDFILTAWMFTDX
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2509>:

**g737.seq**

```

1   atgaACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51  CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCTT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2510; ORF 737>:

**g737.pep**

```

1   MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51  AQAEEKAARW VGGKITDIDL EHDDGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2511>:

**m737.seq..**

```

1   ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51  CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCTT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2512; ORF 737>:

**m737.pep**

```

1   MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51  AQAEEKAALR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 737 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF737.a) from *N. gonorrhoeae*:

**m737/g737**

```

              10      20      30      40      50      60
m737.pep     MNIKHLLLTSAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISRQAEEKAALR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g737          MNIKHLLLTAAATALLGISAPALAHHDGHGDDDHGHAHQHGKQDKIISRQAEEKAARW
              10      20      30      40      50      60

              70      80      90      100     109
m737.pep     VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||
g737          VGGKITDIDLEHDDGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2513>:

1197

a737.seq  
 1 ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG  
 51 CATTTCGCC CCCGACTCG CCCACCACGA CGGACACGGC GATGACGACC  
 101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAAT CATCAGCCGC  
 151 GCCCAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA  
 201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG  
 251 TC AAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG  
 301 GTGATTTCCT CCCGCCGCGA CGACTGA

This corresponds to the amino acid sequence <SEQ ID 2514; ORF 737.a>:

a737.pep  
 1 MNFKRLLLTAAATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR  
 51 AQA EKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR  
 101 VISSRRDD\*

a737/m737 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a737.pep	MNFKRLLLTAAATALMGISAPALAHHDGHGDDDHGHAHQHSKQDKIISR	AQA EKAALAR				
m737	MNIKHLTSAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISR	AQA EKAALAR				
	10	20	30	40	50	60

	70	80	90	100	109
a737.pep	VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX				
m737	VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX				
	70	80	90	100	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2515>:

g738.seq  
 1 ATGTCCGCTG AAACGACCGT ATCCGGCGCG CGCCCCGCGG CCAAACCTGCC  
 51 GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCATC CCCTTTACCT  
 101 TCGCACTCAG GCTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCG  
 151 GCGGCCGCGC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT  
 201 TGATGTCAA ATCCCGCCA TCAGCTTCCT CCTGTTTGCA ATGCGGCAT  
 251 TTTGGTGGCT TCAGGCACGC CTGATGAACC TGATTTATCC CGGAATGAAC  
 301 GACATCGCCT CTTGGGTTTT CATCTTGCTC GCCGTCAGCG CGTGGGCCTG  
 351 CAAGAGTTTG GTCGCACACT ACGGACAAGA ACGCAtcgtT ACCCTGTTTG  
 401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTcgtCATC  
 451 CAGTTTGCCG GCTGGGAAAA CACCCCTCTG CTCAAAACA TCATCGTTCA  
 501 CAGAGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC  
 551 ACTACCTCAT GTGGGGCATA CTCGCCTCCG CCTACCTCAA CGGACAACGA  
 601 AAAATCCCCG CAGCCCTCGG CGCAATCTGC CTGATTATGC AGACCGCCGT  
 651 TTTAGGTTTG GTCAATTCGC GCACCATCTT GACCTACATA GCCGCCATCG  
 701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGACGG  
 751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT  
 801 TTCCATGAAC GCCATTCTGG AAACCTTTAC AGGCATCCGC TACGAACTG  
 851 CCGTCGAACG CGTCGCCAAC GCGGTTTTCA CAGACTTGCC GCGCCAAAGC  
 901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA  
 951 CGGCTGGAAC AGTTTTGCCC AACAAACCTT CCTGATCAAT GCCGAACAGC  
 1001 ACACCATACA CGACAACCTC CTCAGCACCT TGTTACCCCA TTCCACAAC  
 1051 ATCATCTCTC AACTCCTTGC AGAAATGGGG ATCAGCGGCA CGTCTCTGGT  
 1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGTCCCTGA  
 1151 CCCCCGCATC ACTTTTCTCT CTGTGCGCGC TTGCCGTCAG TATGTGCCAC  
 1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCTTCTCG  
 1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA  
 1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCGC CATATTCGA  
 1351 GGATTGCTGC ACTTGACTG GACATACACC CGGCTGGTTA ACTCCTTTTC  
 1401 CCCCCCGCT GACGACAGTG CAAAACCTT CAACCGGAAA ATCAACGAAC  
 1451 TGCGCTATAT TTCCGCAAAC AGCCCGATGC TGTCCTTTTA TGCCGACTTC  
 1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC  
 1551 GGAAGAAGCA ACCCTCAAAG CACTAAAATA CCGCCCCTAC TCCGCCACCT



1198

```

1601 ACCGCATCGC CCTCTACTTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCAACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAAC TGCCCGTATG GGCACCGCTG CTGCCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CTCCCGGCCA TCCGGAAACA
1801 AAACCCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2516; ORF 738>:

**g738.pep**

```

1 MSAETTVSGA RPAAKLPIYI LPCFLWIGII PFTFALRLKP SPDFYHDAAA
51 AAGLIVLLFL TAGKKLFDVK IPAISFLIFA MAAFWWLOAR LMNLIYPGMN
101 DIASWVFILL AVSAWACKSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWENTPL LQNIIVHRGQ GVIGHIGQRN NLGHYLMWGI LASAYLNGQR
201 KIPAAALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPEW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN AILETFTGIR YETAVERVAN GGFTDLPRQS
301 EWNKALAAFQ SAPIFGHGW N SFAQQTFLIN AEQHTIHDNF LSTLFTHSHN
351 IILQLLAEMG ISGTLLVAAT LLTGIAGLLK RSLTPASLFL LCALAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAESDGI IAFKKAANLG ILTASAAIFA
451 GLLHLDWTYT RLVSFSPAA DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQTWAE EA TLKALKYR PY SATYRIALYL MRQKVAEAK
551 QWMRATQSY Y PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPET
601 KPCK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2517>:

**m738.seq**

```

1 ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACCTGCC
51 GATTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TCGCGCTCAA ACTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCC
151 GCAGCCGGCC TGATTGTCTT GTTGTTCTCT ACGGCAGGAA AAAAAGTGT
201 TGATGTCAA ATCCCGCCA TCAGCTTCCT TCTGTTTGCA ATGGCGCGCT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTGCTC GCCGTCAGCG CGTGGGCCTG
351 CCGGAGCTTG GTCGCACACT TCGGACAAGA ACGCATCGTG ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAAACA TCATCGTTTA
501 CAGCGGGCAA GGCCTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCGCCG CCTACCTCAA CGGACAACGA
601 AAAATCCCCG CCGCCCTCGG CGTAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAACTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCTCATCCTT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGCGCG
751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC TGGCATCCGC TACGAAACTG
851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACTTGCC GCGCCAAATC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCGCA TATTCGGGCA
951 CGGCTGGAAC AGTTTGGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATATA CGACAACCTC CTCAGCAACT TGTTCACCCA TTCCACAAC
1051 ATCGTCTCTC AACTCCTTGC AGAGATGGGA ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTTAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCCTA ATCTGCACGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCTTTCTG
1251 ACTGATGCTC TTCCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTCGCA
1351 GGATGCTGCT ACTTGGAAGT GACATACACC CGGCTGGTTA ACGCCTTTTC
1401 CCCC GCCACT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTT TA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCgTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCACCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2518; ORF 738>:

**m738.pep**

```

1 MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALKLKP SPDFYHDAAA

```

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

m738/q738

	10	20	30	40	50	60
m738.pep	MPAETT	TVSGAHPAAKLPIYILPCFLWIGIVPFTFALKLKPS	PDFYHDA	AAAAAGLIVLLFL		
g738	MSAETT	TVSGARPAAKLPIYILPCFLWIGIIPFTFALRLKPS	PDFYHDA	AAAAAGLIVLLFL		
	10	20	30	40	50	60
m738.pep	70	80	90	100	110	120
g738	TAGKKLFDVKIP	PAISFLLFAMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWAC	RSL			
	70	80	90	100	110	120
m738.pep	130	140	150	160	170	180
g738	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
	130	140	150	160	170	180
m738.pep	190	200	210	220	230	240
g738	NLGHYLMWGILAAAYLNGQRKIPALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
m738.pep	250	260	270	280	290	300
g738	YFRSDKSNRRMTLGLIAAAVFLTALFQFSMNITILETFTGIRYETAVERVANGGFTDLPRQI					
	250	260	270	280	290	300
m738.pep	310	320	330	340	350	360
g738	EWNKALAAAFQSAPIFGHWNSFAQQTFLINAEQHNIIYDNLNLSNLFTHSHNIVLQLLAEMG					
	310	320	330	340	350	360
m738.pep	370	380	390	400	410	420
g738	ISGTLVAATLLTGTIAGLLKRPLTPASFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
m738.pep	430	440	450	460	470	480
g738	FLSPAEEASDGIAPFKKAAANLGILTASAAIFAGLLHLDWTYTRLVNAFSPATDDSAKTLNRK					

1200

	430	440	450	460	470	480
	490	500	510	520	530	540
m738 . pep	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEETLKSLKYRPHSATYRIALYL					
g738	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEETLKALKYRPHSATYRIALYL					
	490	500	510	520	530	540
	550	560	570	580	590	600
m738 . pep	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAAPGHPEA					
g738	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAAPGHPEA					
	550	560	570	580	590	600
m738 . pep	KPCKX					
g738	KPCKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2519>:

```

a738 . seq
1  ATGCCCCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAAC TGCC
51  GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TTGCGCTCAG GCTGCAACCG TCGCCCGACT TTTACCACGA TGCCGCGCCG
151 GCAGCCGGCC TGATTGTCCT GTTGTTCTCT ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCCACCTA TCAGCTTCCT TCTGTTTGCA ATGGCGGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTACTC GCCGTCAGCG CGTGGGCTTG
351 CCGGAGCTTG GTCGCACACT ACGGACAAGA ACGCATCGTT ACCCTGTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAACA TCATTGTTTA
501 CAGCGGGCAA GCGTAATCG GACACATCGG ACAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCGCGG CCTACCTCAA CGGACAACGA
601 AAAATCCCGC CCGCCTTGGG TGCAATCTGC CTGATTATGC AGACCGCGT
651 TTTAGGTTTG GTCAATTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCGTT CGGACAAATC CAACAGGCGG
751 ACGATACTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC CGGCATCCGC TACGAAACCG
851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACCTGCC GCGCCAAATC
901 GAATGGCGCA AAGCCCTCGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
951 CCGCTGGAAC AGTTTGGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATACA CGACAACCTC CTCAGCAACT TGTTACCCA TTCCCACAAC
1051 ATCGTTCTCC AACTCCTTGC AGAGATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCCTG ATCTGCACAC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCCTTCGG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTAACCG CCTCCGCCGC CATATTGCGA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGATGGTTA ACGCCTTTTC
1401 CCCCCCCTAT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCGGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCTATTAC CCTTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCGCCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2520; ORF 738.a>:

```

a738 . pep
1  MPAETTVSGA HPAAKLPYIY LPCFLWIGIV PFTFALRLQP SPDFYHDAAA
51  AAGLIVLLFL TAGKKLFDVK IPPISELLFA MAAFYWLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWEDTPL FQNIIVYSQGV IGVIGHIGQRN NLGHYLMWGI LAAAYLNGQR

```

1201

201 KIPPALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR  
251 TILGIAAAVF LTALFQFSMN TILETFTGIR YETAVERVAN GGFTDLPRQI  
301 EWRKALAAAFQ SAPIFGHGWN SFAQQTFLIN AEQHNHNDNL LSNLFTHSHN  
351 IVLQLLAEMG ISGTLLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH  
401 SMLEYPLWYV YFLIPFGLML FLSPAESDGI AFAKKAANLG ILTASAAIFA  
451 GLLHLDWYTYT RMVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF  
501 SLVNFALPEY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQGVAAEK  
551 QWMRATQSY YPYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA  
601 KPCK\*

a738/m738 98.3% identity in 604 aa overlap

	10	20	30	40	50	60
a738.pep	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALRLQSPDFYHDA	AAAAAGLIVLLFL				
m738	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALRLQSPDFYHDA	AAAAAGLIVLLFL				
	10	20	30	40	50	60
	70	80	90	100	110	120
a738.pep	TAGKKLFDVKIPPISFLLFMAAAFYWLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
m738	TAGKKLFDVKIPAIISFLLFMAAAFYWLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a738.pep	VAHYGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
m738	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
	130	140	150	160	170	180
	190	200	210	220	230	240
a738.pep	NLGHYLMWGILAAAYLNGQRKIPPAALGICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
m738	NLGHYLMWGILAAAYLNGQRKIPPAALGICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
	250	260	270	280	290	300
a738.pep	YFRSDKSNRRRTILGIAAAVFLTALFQFSMNTILETFTGIRYETAVERVANGGFTDLPRQI					
m738	YFRSDKSNRRRTMLGIAAAVFLTALFQFSMNTILETFTGIRYETAVERVANGGFTDLPRQI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a738.pep	EWRKALAAAFQSAPIFGHGWN SFAQQTFLINAEQHNHNDNL LSNLFTHSHNIVLQLLAEMG					
m738	EWKALAAAFQSAPIFGHGWN SFAQQTFLINAEQHNHNDNL LSNLFTHSHNIVLQLLAEMG					
	310	320	330	340	350	360
	370	380	390	400	410	420
a738.pep	ISGTLLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
m738	ISGTLLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
	430	440	450	460	470	480
a738.pep	FLSPAESDGI AFAKKAANLG ILTASAAIFAGLLHLDWYTYTRMVNAFSPATDDSAKTLNRK					
m738	FLSPAESDGI AFAKKAANLG ILTASAAIFAGLLHLDWYTYTRMVNAFSPATDDSAKTLNRK					
	430	440	450	460	470	480
	490	500	510	520	530	540
a738.pep	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEATLKS LKYRPHSATYRIALYL					
m738	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEATLKS LKYRPHSATYRIALYL					
	490	500	510	520	530	540

1202

	550	560	570	580	590	600
a738.pep	MRQ GKVAEAKQWMRATQSYYPYLMPRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
m738	MRQ GKVAEAKQWMRATQSYYPYLMPRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
	550	560	570	580	590	600
a738.pep	KPCKX					
m738	KPCKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2521>:

**g739.seq**

```

1  ATGGCAAAAA AACC GAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACC GC CATCGGCGCA TTGGCAGTAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG AAAAAACCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGCCGTCGGA CAAGATGCCG CCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGAAG AAAGCGGCAG CGGACTGCCG
301 TCCCTGCGG CACCCAGAA AAACCGGGTc AAACCGCGCC CTTCGGATGC
351 GGCCCGGGCA GCCGATTCGT TAACCGGCAC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGCCCCCA TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCGCAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAACA
551 CGCCGGCCAA ACCCCATAAA GAGATTCTCG ACAACCTCTT TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2522; ORF 739>:

**g739.pep**

```

1  MAKKPNKPFR LTPKLLIRAV LLICITAIGA LAVGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGAVG QDAAQPEHHH AASSEPAQPD GTEESGSGLP
101 SPAAPKKNRV KPRPSDAARA AD SLTGTGTQ AENTLKETPV LPTNAPHPEP
151 RKETPEKQAA PKETPKKET PKENHTKPD T PKNTPAKPHK EILDNLFF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2523>:

**m739.seq**

```

1  ATGGCAAAAA AACC GAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCGCCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG AAAAAACCCT TCAAGCCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCTGCGG CACCCAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCGCAG CCCAAAGAAA CGCCCAAGA
501 AAACCATACC AAACCGGACA CCGCGAAAAA CACGCCGCC AAACCCATA
551 AAGAAATTCT CGACAAACTC TTC

```

This corresponds to the amino acid sequence <SEQ ID 2524; ORF 739>:

**m739.pep**

```

1  MAKKPNKPFR LTPKLLIRAV LLICIAAIGA LAIGIVSTFN PNGDKTLQAE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH AASSEPAQPD GTDESGSGLP
101 SPAAPKKNRV KPQPADTAQT DRQPDDAGTQ AENTLKETPV LPTNVRPEP
151 RKETPEKQAA PKETPKENHT KPDTPKNTTP KPHKEILDKL F

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 739 shows 86.3% identity over a 197 aa overlap with a predicted ORF (ORF739.a) from *N. gonorrhoeae*:

m739/g739

1203

	10	20	30	40	50	60
m739.pep	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALVSTFNPNGDKTLQAE PQHTDSPRET					
g739	MAKKPNKPFRLTPKLLIRAVLLICITAIGALVSTFNPNGDKTLQTE PQHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m739.pep	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSAAPKKNRVKQPADTAQT					
g739	EFWLPNGAVGQDAAQPEHHHAASSEPAQPDGTEESGSGLPSAAPKKNRVKPRPSDAARA					
	70	80	90	100	110	120
	130	140	150	160	170	
m739.pep	DRQPDDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKE-----NHTKPD					
g739	ADSLTGTGTQAENTLKETPVLPTNAPHPEPRKETPEKQAQPKETPKEKETPKENHTKPD					
	130	140	150	160	170	180
	180	190				
m739.pep	PKNTPPKPHKEILDKLF					
g739	PKNTPAKPHKEILDNLFX					
	180	190				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2525>:

```

a739.seq
1  ATGGCAAAAA AACC GAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCTCCTCAT
251 CCGCACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAGCACAA GCTGAAAACA
401 CACTCAAAGA AACC CCGTA CTGCCACAA ACGTCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCACAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAAACA
551 CGCCGCCTAA ACCCCATAAA GAAATTCTCG ACAACCTCTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2526; ORF 739.a>:

```

a739.pep
1  MAKKPNKPFRLTPKLLIRAVLLICITAIGA LAIGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH ASSSAPAQPD GTDESGSGLP
101 SPAAPKKNRV KPQADTAQT DRQPDDAGAQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAQ PKETPKEKET PKENHTKPD PKNTPPKPHK EILDNLF*

```

a739/m739 93.9% identity in 197 aa overlap

	10	20	30	40	50	60
a739.pep	MAKKPNKPFRLTPKLLIRAVLLICITAIGALVSTFNPNGDKTLQTE PQHTDSPRET					
m739	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALVSTFNPNGDKTLQAE PQHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
a739.pep	EFWLPNGVVGQDAAQPEHHHASSSAPAQPDGTDESGSGLPSAAPKKNRVKQPADTAQT					
m739	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSAAPKKNRVKQPADTAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
a739.pep	DRQPDDAGAQAE NTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKEKETPKENHTKPD					
m739	DRQPDDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPK-----ENHTKPD					
	130	140	150	160	170	

1204

```

                190
a739.pep      PKNTPPKPKHKEILDNLFX
                |||||
m739          PKNTPPKPKHKEILDKLF
                180    190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2527>:

g740.seq

```

1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTC GCCGTCTGCC TCATCCCCTT
51 GgcgACGCTT GCCGTTTTTCG CCGCCAATcc gccCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTAAa
151 ttcgtgctCT TTGAAACCAT CAAGCATCAT CTTAaacaag gGTTTGATTT
201 GAAACgtcaa ACCATGTTTC TGTATTATCC GATTGTTTGG CTGGTTGTGT
251 ATTTGTTCCA CTATTTCGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2528; ORF 740.ng>:

g740.pep

```

1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KPQHILINGII LACEATFLFK
51 FVLFETIKHH LKQGFDLKRQ TMFLFIPIVL LVVYLFHYFG AF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2529>:

m740.seq

```

1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GCCGTCTGCC TCATCCCGTT
51 GGCGACGCTT GCCGTTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTAAa
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATTT
201 GAAACGTCAA ACTATGTTGC TGTATTATCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2530; ORF 740>:

m740.pep

```

1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KLOHLINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLLFIPIL LIVYLFHYFG AF*

```

m740/g740 93.5% identity in 92 aa overlap

```

                10      20      30      40      50      60
m740.pep      MSRNLLVRWLA VCLIPLATL AVFAANPPED KLOHLINGII LACEATFLFK FVLFDTIKHH
                |||||
g740           MSRNLLVRWLA VCLIPLATL AVFAANPPED KPQHILINGII LACEATFLFK FVLFETIKHH
                10      20      30      40      50      60

                70      80      90
m740.pep      LKQEFDLKRQ TMLLFIPIL LIVYLFHYFG AFX
                |||
g740           LKQGFDLKRQ TMLFIPIVL LVVYLFHYFG AFX
                70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2531>:

a740.seq

```

1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GTCGTCTGCC TGATACCCTT
51 GGCGACGCTT GCCGTTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATTAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTCAAa
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATTT
201 GAAACGTCAA ACTATGTTGC TGTATTATCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2532; ORF 740.a>:

a740.pep

```

1  MSRNLLVRWL VVCLIPLATL AVFAANPPED KPQHILINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLLFIPIL LIVYLFHYFG AF*

```

a740/m740 97.8% identity in 92 aa overlap

```

                10      20      30      40      50      60

```

1205

```

a740.pep  MSRNLLVRWLVLVCLIPLATLAVFAANPPEDKPKQHLINGIILACEATFLFKFVLFDTIKHH
|||||||:|||||||
m740      MSRNLLVRWLAVCLIPLATLAVFAANPPEDKQHLINGIILACEATFLFKFVLFDTIKHH
              10      20      30      40      50      60

              70      80      90
a740.pep  LKQEFDLKRQTMLLFIPIILLIVLYLFHYFGAFX
|||||||
m740      LKQEFDLKRQTMLLFIPIILLIVLYLFHYFGAFX
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2533>:

```

g741.seq
1   GTGAACCGAA CTACCTTCTG CTGCCTTTCT TTGACCGCCG GCCCTGATTC
51  TGACCGCCTG CAGCAGCGGA GGGGCGGAGG CGGTGGTGTC GCCGCCGACA
101 TCGGCACGGG GCTTGCCGAT GCATTAACCG CGCCGCTCGA CCATAAAGAC
151 AAAGGTTTGA AATCCCTAAC ATTGGAAGCC TCCATTCCCC AAAACGGAAC
201 ACTGACCCTG TCGGCACAAG GTGCGGAAAA AACTTTCAAA GCCGCGGGCA
251 AAGACAACAG CCTCAACACG GGCAAACTGA AGAACGACAA AATCAGCCGC
301 TTCGACTTCG TGCAAAAAT CGAAGTGGAC GGACAAACCA TCACACTGGC
351 AAGCGGCGAA TTTCAAATAT ACAAACAGGA TCACTCCGcc gtcgtTgcCC
401 TacgGATTGA AAAATCAAC AACCCTCGACA AAATCGACAG CCTGATAAAC
451 CAACGCTCCT TCCTTGTCAG CGATTGGGGC GGAGAACATA CCGCCTTCAA
501 CCAACTGCCT GACGGCAAAG CCGAGTATCA CGGCAAAGCA TTCAGCTCCG
551 ACGATGCCGA CGGAAACTG ACCTATACCA TAGATTTCGC CGCCAAACAG
601 GGACACGGCA AAATCGAACA CCTGAAAACA CCCGAGCAGA ATGTTGAGCT
651 TGCTCCGCC GAACTCAAAG CAGATGAAAA ATCACACGCC GTCATTTTGG
701 GCGACACGCG CTACGGCGGC GAAGAGAAAG GCACTTACCG CCTCGCCCTT
751 TTCGGCGACC GCGCCCAAGA AATCGCTGGC TCGGCAACCG TGAAGATAGG
801 GGAAAAGGTT CACGAAATCG GCATCGCCGA CAAACAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2534; ORF 741.ng>:

```

g741.pep
1   VNRTTFCCLS LTAGPDSRL QRRGGGGGV AADIGTGLAD ALTAPLDHKD
51  KGLKSLTLEA SIPQNGTLTL SAQGAETFK AGGKDNSLNT GKLKNDKISR
101 FDFVQKIEVD GQTITLASGE FQIYKQDHSA VVALRIEKIN NPKIDSLIN
151 QRSFLVSDLG GEHTAFNQLP DGKAEYHGKA FSSDDADGKL TYTIDFAAKQ
201 GHGKIEHLKT PEQVELASA ELKADEKSHA VILGDTRYGG EEKGTYRLAL
251 FGDRAQEIAG SATVKIGEKV HEIGIADKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2535>:

```

m741.seq
1   GTGAATCGAA CTGCCTTCTG CTGCCTTTCT CTGACCACTG CCCTGATTCT
51  GACCGCCTGC AGCAGCGGAG GGGGTGGTGT CGCCGCCGAC ATCGGTGCGG
101 GGCTTGCCGA TGCACTAACC GCACCGCTCG ACCATAAAGA CAAAGGTTTG
151 CAGTCTTTGA CGCTGGATCA GTCCGTGAGG AAAACGAGA AACTGAAGCT
201 GCGGCACAA GGTGCGGAAA AAATTATGG AAACGGTGAC AGCCTCAATA
251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GTTTCGACTT TATCCGCCAA
301 ATCGAAGTGG ACGGGCAGCT CATTACCTTG GAGAGTGGAG AGTTCCAAGT
351 ATACAAACAA AGCCATTCCG CCTTAACCGC CTTTCAGACC GAGCAAATAC
401 AAGATTCGGA GCATTCCGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
451 GGCGACATAG CGGGCGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
501 CAGGGCGACA TATCGCGGGA CGGCGTTCGG TTCAGACGAT GCCGGCGGAA
551 AACTGACCTA CACCATAGAT TTCGCCGCCA AGCAGGGAAG CGGCAAAATC
601 GAACATTTGA AATCGCCAGA ACTCAATGTC GACCTGGCCG CCGCCGATAT
651 CAAGCCGGAT GGAAAACGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
701 ACCAAGCCGA GAAAGGCAGT TACTCCCTCG GTATCTTTGG CGGAAAAGCC
751 CAGGAAGTTG CCGGCAGCGC GGAAGTGAAA ACCGTAAACG GCATACGCCA
801 TATCGGCCTT GCCGCCAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2536; ORF 741>:

```

m741.pep
1   VNRTAFCCLS LTTALILTAC SSGGGGVAAD IGAGLADALT AFLDHKDKGL
51  QSLTLDQSVR KNEKLKLAAG GAETKYGNND SLNTGKLKND KVSRLFDFIRQ
101 IEVDGQLITL ESGEFQVYKQ SHSALTAFTQ EQIQDSEHSK KMLAKRQFRI

```



1206

151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD AGGKLTYTID FAAKQNGNGKI  
 201 EHLKSPELNV DLAAADIKPD GKRHAVISGS VLYNQAEKGS YSLGIFGGKA  
 251 QEVAGSAEVK TVNGIRHIGL AAKQ\*

m741/g741 61.4% identity in 280 aa overlap

	10	20	30	40	50
m741.pep	VNRTAFCCSLT---	ALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQ			
g741	VNRTTFCCSLTAGPDS	DRLQRRGGGGVAADIGTGLADALTAPLDHKDKGLKSLTLEA			
	10	20	30	40	50
	60	70	80	90	100
m741.pep	SVRKNEKLKLAQA	EKTY---GNGDSLNTGKLKNDKVS	RFD	FIRQIEVDGQLITLES	GE
g741	SIPQNGTLTLSAQA	EKTFKAGGKDNSLNTGKLKNDKIS	RFD	VFQKIEVDGQTITLAS	GE
	70	80	90	100	110
	120	130	140	150	160
m741.pep	FQVYKQSHSALTAFQTE	QIQDSEHSGKMKVAKRQFRIGD	IAGEHTSF	DKLPEGGRATY	RGT
g741	FQIYKQDHS	AVVALRIEINNPKIDSLINQ	RSFLVSDLGGEHTAF	NQLPDG-KAEY	HGK
	130	140	150	160	170
	180	190	200	210	220
m741.pep	AFGSDDAGGKLT	YTIDFAAKQNGNGKIEHLKSP	ELNVDLAAADIKPD	GKRHAVISGS	SVLYN
g741	AFSSDDADGKLT	YTIDFAAKQGHGKIEHLKTPEQ	NVELASAE	LKADEKSHAVILG	DTTRYG
	180	190	200	210	220
	240	250	260	270	
m741.pep	QAEKGSYSLGIFGGKA	QEVAGSAEVKTVNGIRHIGL	AAKQX		
g741	GEEKGTYRLALFGDRA	QEIAGSATVKIGEKVHEIGI	ADKQX		
	240	250	260	270	280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2537>:

a741.seq  
 1 GTGAACCGAA CTGCCTTCTG CTGCCTTTCT TTGACCGCCG CCCTGATTCT  
 51 GACCGCCTGC AGCAGCGGAG GCGGCGGTGT CGCCGCGGAC ATCGGCGCGG  
 101 TGCTTGCCGA TGCACTAACC GCACCGCTCG ACCATAAAGA CAAAAGTTTG  
 151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAACGAGA AACTGAAGCT  
 201 GCGGCGACAA GGTGCGGAAA AAACCTATGG AAACGCGGAC AGCCTCAATA  
 251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GCTTCGACTT TATCCGTCAG  
 301 ATCGAAGTGG ACGGGCAGCT CATTACCTTG GAGAGCGGAG AGTTCCAAGT  
 351 GTACAAACAA AGCCATTCCG CCTTAACCGC CCTTCAGACC GAGCAAGTAC  
 401 AAGATTCGGA GCATTCAGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC  
 451 GGCGATATAG CGGGTGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG  
 501 CAGGGCGACA TATCGCGGGA CGGCATTCGG TTCAGACGAT GCCAGTGGAA  
 551 AACTGACCTA CACCATAGAT TTCGCGGCCA AGCAGGGACA CGGCAAAATC  
 601 GAACATTTGA AATCGCCAGA ACTCAATGTT GACCTGGCCG CCTCCGATAT  
 651 CAAGCCGGAT AAAAAACGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA  
 701 ACCAAGCCGA GAAAGGCAGT TACTCTCTAG GCATCTTTGG CGGGCAAGCC  
 751 CAGGAAGTTG CCGGCAGCGC AGAAGTGGAA ACCGCAAAAC GCATACGCCA  
 801 TATCGGTCTT GCCGCCAAGC AGTAA

This corresponds to the amino acid sequence &lt;SEQ ID 2538; ORF 741.a&gt;:

a741.pep  
 1 VNRTAFCCLS LTAALILTAC SSGGGGVAAD IGAVLADALT APLDHKDKSL  
 51 QSLTLDQSVR KNEKLKLAQA GAETYNGND SLNTGKLKND KVS RFD FIRQ  
 101 IEVDGQLITL ESGEFQVYKQ SHSALTALQT EQVQDSEHSG KMKVAKRQFRI  
 151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD ASGKLTYTID FAAKQGHGKI  
 201 EHLKSPELNV DLAASDIKPD KKRHAVISGS VLYNQAEKGS YSLGIFGGQA  
 251 QEVAGSAEVE TANGIRHIGL AAKQ\*

a741/m741 95.6% identity in 274 aa overlap

1207

	10	20	30	40	50	60
a741.pep	VNRTAFCCLSLTAALILTACSSGGGGVAADIGAVLADALTAPLDHKDKSLQSLTLDQSVR					
m741	VNRTAFCCLSLTTALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a741.pep	KNEKLKLAQAQGAEKTYGNGDSLNTGKLNKDKVSRFDFIRQIEVDGQLITLESGEFQVYKQ					
m741	KNEKLKLAQAQGAEKTYGNGDSLNTGKLNKDKVSRFDFIRQIEVDGQLITLESGEFQVYKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
a741.pep	SHSALTALQTEQVQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPPEGGRATYRGTAFGSDD					
m741	SHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPPEGGRATYRGTAFGSDD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a741.pep	ASGKLTYYTIDFAAKQGHGKIEHLKSPELNVDLAASDIKPKDKRHAIVISGSVLYNQAEEKGS					
m741	AGGKLTYYTIDFAAKQGNKGKIEHLKSPELNVDLAAADIKPDGKRHAIVISGSVLYNQAEEKGS					
	190	200	210	220	230	240
	250	260	270			
a741.pep	YSLGIFGGQAQEVAGSAEVETANGIRHIGLAQKX					
m741	YSLGIFGGKAQEVAGSAEVKTVNGIRHIGLAQKX					
	250	260	270			

g742.seq not found yet

g742.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2539>:

```

m742.seq
1   ATGGTTTACG GCATTGCCGA AGCCGATGCG GGCGACAGCA GTGTGCTTAC
51  TTTGGGCGGC ATGTATCAGA AGAGTAGGGA GGTTCCGTGAT TTTTCGGGCA
101 TTATTTTGCC CTGTGAAAAT CAGAAACTG CCCCCTTCAG TTCAACGCCT
151 GCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
201 TTGGTCGCGG TTAAGTGCCG ACAAATACAA CCTTTTCTCA GGATTCAAAC
251 ATGTGTTTGA CAACGGTTGG CAGCTCAATG CCGAAGTGTC TTATACCAAG
301 AATGAATCCG ATGCGAAGGT GGGGCAGTTT TTTCTGAAAA ACGAATATGC
351 GGCGGGTTTG TCGGGTGAGG ATGCGGTAGG CTTTTTGA CTGAAAAAACG
401 AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATTGGAGAA ACTGAAAGCA
451 TATCGTGATG AAACCGCCAA GGAATACCGG GAGCGCAAAG ACGATTTTGT
501 TAAAAAACCGT TTCGATAATA CTGCTTTCGA ACAGTATCGC AGCCGCCGTG
551 CCGCAGAACG CAAAGCCGGT TTTGACAAGT GTATGAGTGA CCCTTTCGCG
601 CTGGACTTTA TCTGTCAAGG TTCTTGGGGG GATCCGGGCG TTGATGCCGA
651 CAAGGCGGAA TTTGTGCGATA AAGCCCTTGC GAAGGAGGGC ATCTTTAATA
701 ATGCGGCACA ACGTTTTCCTA AACAGCCTGT ATGACTCTTC CTTTAATCGG
751 AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTTGC GGCATACCAA
801 AGACGACCGC CAATGGGGAA TTAACTTGA CCTGACCGGC ACATATGGGC
851 TGTTCGGGCG GGAGCATGAT TTCTTTGTCT GCTATGCCTA CGGTGATGAA
901 AAGATACGTT CGGAATATCT AGAAATCTAC GAACGCCGCT ACAGAGTACG
951 TCCGAATACG GGGGCAACGC ACGCGGTGTA TGCGGGAAGT TGTCAAGAGG
1001 AGCCGGACGG CGATTTGTCTG TCTCCTTTGG TCAGGGGGCA TAAAGAACCC
1051 GATTGGCAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
1101 ATGCAGGAAC GCCAAGAAAA TAAAAACCGA GCCCAAGCTC GATGCCGAAG
1151 GCAAGCAGGT GTATTACTAT GACGAATACA GCGGCAGCCG GACACCGGTA
1201 TATGTCGATG TATATGAGCT GGACGAAAAA GGCAACAAGA TTCAGGAGAC
1251 CAATCCCGAC GGCACGCCCTG CCTTTACCGG TTTTTCGGT ACGGTGCCGG
1301 TTTGGAAAAA CGTCAAAGTG GCAGACGACC ATGTTCTCTG CTTGTATAAC
1351 TACGCCAAAT ACCTCAACAC CAACAAACC CATTTCGTGA CTGCCAGCAC
1401 GCGTTTCAAC GTAACCGGCC GACTGCACCT TTTGGGCGGG CTGCACTACA

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1208

```

1451 CGCGCTATGA GACTTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAGGGCGG ATCAGGACCA
1551 TTACACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGACTT GACACGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCCGC ACAAACTATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTC GCATTGTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTGCTCG ATTTCCGCTA TGTTCCCGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTCGAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAAC GCCGCCGAAG TCAACGCCGA
2001 ACGCCTTGCC AAAAATTCCA GTGCAGACCC GTACAACTTC AGCAATTTC
2051 CACCCGTGCA CATATTCCGT TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGGCGG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCC AAATTGAGCC TCATCGGTAC GAACTTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAACAA
2301 CTTCTACGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

```

This corresponds to the amino acid sequence <SEQ ID 2540; ORF 742>:

```

m742.pep
  1  MVGIAEADA GDSSVLTLGG MYQKSREVPD FSGIILPCEN QKTAPFSSTP
 51  ACNRPLQLPR NTYLGEDWSR LSADKYNLFS GFKHVFNDGW QLNAEVSYTK
101  NESDAKVGQF FLKNEYAAGL SGEDAVGFLT EKNEVIPFEP KDKALEKLKA
151  YRDETAKEYR ERKDDFVKNR FDNTAFEQYR SRRAAERKAG FDKCMSDPFA
201  LDFICQGSWG DPGVDADKAE FVDKALAKEG IFNNAQRFP NSLYDSSFNR
251  KATANRRYSY MPLRHTKDDR QWGIKLDLTG TYGLFGREHD FVGYAYGDE
301  KIRSEYLEIY ERRYRVRPNT GATHGVYAGS CQEEP DGDLS SPLVRGHKEP
351  DWQAYDEKGN RTVYAEECRN AKKIKTEPKL DAEGKQVYYY DEYSGSRTPV
401  YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVPVWKT VKV ADDHVPALYN
451  YAKYLNTNKT HSLTASTRFN VTGRLHLLGG LHYTRYETSQ TKDMPVRYGQ
501  PASDFQTASS IRADQDHYTA KMQGHKLTPY AGITYDLTPQ QSIYGSYTKI
551  FKQQDNVDVS AKTVLPPLVG TNYEVGWKGA FLQGRNLNASF ALFYLEQKNR
601  TVVDFGYVPG AGGKQGSFQT VAKPIGVVS RGAEFELSGE LNEWDKVFAG
651  YTYNKSRYKN AAEVNAERLA KNSSADPYNF SNFTPVHIFR FGTSFHIPNT
701  GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
751  GRTYFENNYN RTRGANNFYG EPRTVSMKLD WQF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2541>:

```

a742.seq
  1  ATGGTTTACG GCATTGCCGA AGCCGATGCG GGCGACAGCA GTGTGCTTAC
 51  TTTGGGCGGC ATGTATCAGA AGAGTAGGGA GGTTCCTGAT TTTTCGGGCA
101  TTATTTTGTC CTGTGAAAAT CAGAAAACCTG CCCCCTTCAG TTCAACGCCCT
151  GCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
201  TTGGTCGCGG TTGAGTGCTG ACAAATACAA CCTTTTCTCA GGTTTCAAAC
251  ATGTGTTTGA CAACGGTTGG CAGCTCAATG CCGAAGTGTC TTATACCAAG
301  AATGAATCCG ATGCGAAGGT GGGGCACTTT TTTCTGAAAA ACGAACATGC
351  GGCGGGTTTG TCAGATGAGG ATGCGGTAGG CTTTTTGACC GAAAAAACG
401  AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATTGGAGAA ACTGAAAGCA
451  TATCGTGACG AAACCGCCAA GGAATACCGT GAGCGCAAAG ACGATTTTGT
501  TAAAAACCGT TTCGATAATA CTGCTTTCGA GCAGTACCGC AGCCGCCGTC
551  CCGCAGAACG CAAAGCCGGT TTTGACGAGT GTATGAGTGC CCCTTTTGCG
601  CTGGACTTTA TCTGTCAAGG TTCTTGCGGG GATCCGGGTG TTGATGCCGA
651  CAAGTCGGAA TTTGTCGATA AAGCCCTTGC GAAGGAAGGC ATCTTTAATA
701  ATGCGGCACA ACGTTTCCA AACAGCCTGT ATGACTCTTC CTTTAATCGG
751  AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTTGC GGCATACCAA
801  AGACGACCGC CAATGGGGAA TTAACTTGA CCTGACCGGC ACATATGGGC
851  TGTTCGGGCG GGAGCATGAT TTCTTTGTCT GCTATGCCTA CGGCGATGAA
901  AAGATACGTT CCGAATATCT GGAAATCTAC GAACGCCGCC ACAGAGTACG
951  TCCGAATACA GGGGCAACGC ACGGCGTGTA TGCGGGAAAG TGTCAGGGGG
1001 AGCCGGACGG TGATTTGTCT TCTCCTTTGG TCAGGGGGCA TAAAGAACCC
1051 GATTGGCAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
1101 ATGCAGGAAT GCCAAGAAAA TAAAAACCGA GCCCAAGCTC GATGCCGAAG
1151 GCAAGCAGGT GTATTACTAT GACGAATACA GCGGCAGCCG GACGCCAGTA

```

a742.pep

1	MVYGIAEADA	GDSSVLTGG	MYQKSREVPD	FSGIILSCEN	QKTAPFSSTP
51	ACNRPLQLPR	NTYLGEDWSR	LSADKYNLFS	GFKHVFNDGW	QLNAEVSYTK
101	NESDAKVGQF	FLKNEHAAGL	SDEDAVGFLT	EKNEVIPFEP	KDKALEKLKA
151	YRDETAKEYR	ERKDDFVKNR	FDNTAFEQYR	SRNAAEKARG	FDECMSAPFA
201	LDFICQGSWG	DPGVDADKSE	FVDKALAKEG	IFRNAAQRF	NSLYDSSFN
251	KATANRRYSY	MPLRHTKDDR	QWGIKLDTLG	TYGLFGREHD	FFVGYAYGDE
301	KIRSEYLEIY	ERRHRVRPNT	GATHGVYAGS	CQGEPDGDL	SPLVRGHKEP
351	DWQAYDEKGN	RTVYAEECRN	AKKIKTEPKL	DAEGQVYYY	DEYSGSRTPV
401	YVDVYELDEK	GNKIQETNPD	GTPAFTGFSG	TVPVWTKVVK	ADDHVPALYN
451	YAKYLTNTKT	HSLTAGTRFN	VTGRLLHLLG	LHTRYETSSQ	TKDMPVRYGQ
501	PASDFNTASS	IKADQPHYTA	KMQGHKLTPY	AGITYDLTPQ	QSIYGSYTKI
551	FKQQDNVDVS	AKTVLPPLVG	TNYEVGWKGA	FLQGRNLNASF	ALFYLEQKNR
601	TVVDFGVVPG	AGGKQGSFQT	VAKPIGKVV	RGAEFELSGE	LNEDWKVFAG
651	YTYNKSRYKA	AAEVNAERLA	KNTGADPYNF	SNFTPVHIFR	FGTSFHIPNT
701	GLTVGGGVSA	QSGTSSLYNI	RQGGYGLIDG	FVRYELGKHA	KLSLIGTNLN
751	GRTYFENNYN	RTRGANNFYG	EPRTVSMKLD	WOF*	

	10	20	30	40	50	60
a742.pep	MVYGIAEADAGDSSVLT	LGGM	YQKSREVP	DFSGIILSCENQKTAPFSSTPACNR	RFLQLPR	
m742	MVYGIAEADAGDSSVLT	LGGM	YQKSREVP	DFSGIILPCENQKTAPFSSTPACNR	RFLQLPR	
	10	20	30	40	50	60
	70	80	90	100	110	120
a742.pep	NTYLGEDWSRLSADKYNLF	SGFKHVFDNGWQLNAEVSYTKNESDAKVGQFFLKNEHAAGL				
m742	NTYLGEDWSRLSADKYNLF	SGFKHVFDNGWQLNAEVSYTKNESDAKVGQFFLKNEYAAGL				
	70	80	90	100	110	120
	130	140	150	160	170	180
a742.pep	SDEDAVGFLTEKNEVIPFEPKDKALEK	LKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR				
m742	SGEDAVGFLTEKNEVIPFEPKDKALEK	LKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR				
	130	140	150	160	170	180
	190	200	210	220	230	240
a742.pep	SRRAAERKAGFDECMSAPFALDFICOGSWGDP	GVDDADKSEFVDKALAKEGIFNNA	AORF			



1211

ferric-pseudobactin receptor precursor - *Pseudomonas putida* >gi|45723 (X56605)  
 pseudobactin uptake protein [*Pseudomonas putida*]Length = 819  
 Score = 152 bits (381), Expect = 6e-36  
 Identities = 110/356 (30%), Positives = 170/356 (46%), Gaps = 55/356 (15%)

Query: 436 KTVKVADDDHV-PALYNYAKYLNNTKTHSLTAGTRFNVTGRLHLLGGLHYTRYETSQTKDM 494  
 +T K DD + P + +Y +N+ +RFN+T LHL+ G + Y  
 Sbjct: 511 QTPKPGDDEIIPGI----QYNISNRQSGYFVASRFNLTDLHLILGARASNYRFDYAL-- 564

Query: 495 PVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTPYAGITYDLTPQQSIYGSYTKIFKQQ 554  
 R G + ++ ++ +TPYAGI YDLT +QS+Y SYT IFK Q  
 Sbjct: 565 -WRIGNEPAPYKM-----VERGVVTPYAGIVYDLTNEQSVYASYTDIFKPQ 609

Query: 555 DNVDVSAKTVLPPLVGTNYEVGWKGAFLOGRNLNASFALFYLEQKNRTVVDFGYVPGAGGK 614  
 +NVD++ K L P VG NYE+GWKG FL+GRLNA+ AL+ +++ N VP +GG  
 Sbjct: 610 NNVDITGKP-LDPEVGKNYELGWKGFELEGRLNANIALYMKRDNLAESTNEVVPDSGGL 668

Query: 615 QGSFQTVAKPIGKVVSRGAEFELSGELNEDWKVFAGYTYNKSRYKNAAEVNAERLAKNTG 674  
 S + + ++G + ELSGE+ W VF GY++ ++  
 Sbjct: 669 IAS-----RAVDGAETKGVDELSEVLPGWNVFTGYSHTRTE-----D 707

Query: 675 ADPYNFSNFTPVHIFRFGTSFHIPN--TGLTVGGGVSAQSGTS---SLYN--IROGGYGL 727  
 AD + P+ FRF ++ +P LT+GGGV+ S ++ + YN + Q Y +  
 Sbjct: 708 ADGKRLTPQLPMDTFREWNTYRLPGWEKLTLLGGGVNWNKSTLNFARYNSHVTQDDYFV 767

Query: 728 IDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLDWQF 783  
 RY + + +L N+ + Y Y G+ YG PR ++ L + F  
 Sbjct: 768 TSLMARYRINESLAATLNVNNIFDKKY----YAGMAGSYGHYGAPRNATVTLRYDF 819

g743.seq not found yet

g743.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2543>:

m743.seq  
 1 ATGAATCAAA ATCATTTTTTC ACTTAAATTT CTGACCGTTA TGCTGTTATC  
 51 GGCTTACGGT GGTTCCTTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA  
 101 ATACCGTCAG TCTGGATACG GTCAATGTAC GCGGCTCTCA TGCTTTGTTG  
 151 GGCAAGACCG AAAAGACCCG TTCTTATACG ATAGATCGGA TGTCACCCGC  
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA  
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA  
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC  
 351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA  
 401 TGACCGTCAA TGTTCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG  
 451 TCTCCGAGTA CCGATTGGC GGTATTGAC CATATTGAAG TTGTACGGGG  
 501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGAGGA ACCGTCAATT  
 551 TGATCCGTAA GTGA

This corresponds to the amino acid sequence <SEQ ID 2544; ORF 743>:

m743.pep  
 1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALL  
 51 GKTEKTRSYT IDRMSTATGM RIAGKDTPQS VSVITRSRLD DKAHVHLEEA  
 101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGMTVNVAG RSGYTAKIDV  
 151 SPSTDLAVYD HIEVVRGATG LTQSNSEPGG TVNLIRK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2545>:

a743.seq  
 1 ATGAATCAAA ATCATTTTTTC ACTTAAATTT CTGACCGTTA TGCTGTTATC  
 51 GGCTTACGGT GGTTCCTTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA  
 101 ATACCGTCAG TTTGGATACG GTCAATGTAC GCGGCTCTCA TGCTCTGTGCG  
 151 GGCAAGACCG AGAAGACCCG TTCTTATACG ATAGATCGGA TGTCACCCGC  
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA  
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA  
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC

1212

```

351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401 TTACCGTCAA TGTTGCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
451 TCTCCGAGTA CCGATTGGC GGTTTATGAC CATATTGAAG TTGTACGGGG
501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGTGGA ACCGTCAATT
551 TGATCCGTAA GCGA

```

This corresponds to the amino acid sequence <SEQ ID 2546; ORF 743.a>:

```

a743.pep
  1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALS
 51 GKTEKTRSYT IDRMSTATGM RIAGKDTPQS VSVITRSLD DKAHVHLEEA
101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGITVNVAG RSGYTAKIDV
151 SPSTDLAVYD HIEVVRGATG LTQSNSEPGG TVNLIRKR

```

a743/m743 98.9% identity in 187 aa overlap

```

              10      20      30      40      50      60
a743.pep    MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALSGKTEKTRSYT
              |||||
m743        MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALLGKTEKTRSYT
              10      20      30      40      50      60

              70      80      90      100     110     120
a743.pep    IDRMSTATGMRIAGKDTPQSVSVITRSLDDKAVHGLEEAMKNTTGVNVVRDSSLQTRFL
              |||||
m743        IDRMSTATGMRIAGKDTPQSVSVITRSLDDKAVHGLEEAMKNTTGVNVVRDSSLQTRFL
              70      80      90      100     110     120

              130     140     150     160     170     180
a743.pep    SRGFYIDQIGEDGITVNVAGRSYGTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGG
              |||||
m743        SRGFYIDQIGEDGMTVNVAGRSYGTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGG
              130     140     150     160     170     180

a743.pep    TVNLIRKR
              |||||
m743        TVNLIRKX

```

g744.seq not found yet

g744.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2547>:

```

m744.seq
  1 ATGAAACCGT TAAAAACATT AGAATTGGGA TTTGTGGATG CTGCAAACTA
 51 CAGAAGAAGA GAAAATAAAG ATTTATTTAA CCGAATATTT GTAAAAGGAG
101 AATATTGGGA TGAATTATGT GAACCAAATA TTTGTTTTT AATCGGAGAA
151 AAGGGAAC TGAAAGACAGC ATATGCTGTT TATTTAACTA ATAACCTCTA
201 TAAAAACATA CATGCCACTA CTAAGTTTGT TCGTGAAACC GATTATTCAA
251 AATTTATTCA GCTAAAGAAA GCAAGACACT TAACTGTTTC AGATTTTACA
301 AGTATTGGGA AAGTCATTTT ATATCTGTTG ATATCAAATC AAATCAAATG
351 TAAAGAAAAC GGAATATTAT CTTCAATATT TAATAAATTT AAAGCCTTAG
401 ATGAGGCTAT AAATGAATAT TATTATGGCG CTTTGATCC GGAAATTGTA
451 CAAGCAATAA CTTTAATAGA AAATCAAAA GAAGCTGCGG AAATGATTTT
501 TGGAAAATTT GTTAACTAG GTGAAGAGGA ATCCCAACAA ATAACCTTTA
551 CAGAAAGTAA ATTCCAAGCA AATTAGGTT TTATTGAAAG AAAATTTAAA
601 GATGCTTTAT CTCAGTTAAA GCTAAAAGAT AATCATATTT TGTTTATGTA
651 TGGGATAGAT ATTAGACCAT CACAGATTCC ATTTGATGAA TATCATGAGT
701 GTGTAAAAGG TCTTGCTAAC GCCATATGGA TGTAAATAA TGATATCTTC
751 CCTTCCATTA AAGATAGTAA GGAAGGATG AGAGTTGTGT TATTGATTAG
801 ACCTGATATC TTTGATTCAT TAGGTTTACA AAATCAAAAT ACCAACTTC
851 AAGATAATTC AGTATTTTGA GACTGGAGGA CGGATTATAA ATCTTATAGA
901 AGTTCAAAGA TTTTGGCGT TTTTGATCAT CTTTGAGAA CCCAGCAAGA
951 AAAACAAGAT AGTTTAGAAA AAGGCAACTC ATGGGATTAT TATTTCCAT
1001 GGAATGCTCC TAATTACAT GATGAGTATA AAAATTTAAC TTCATTAT
1051 AGCTTCTTAA GAAAAATCGTA TTATCGACCT CGCGATATTC TTCAGATGCT
1101 TACTTTGCTA CAAAAAATA AGAAAAGTAA GGAAGATTAT GTCGTAGCAG
1151 AAGATTTTGA TAATACTTCT TTTCAAAGAG AATACTCGAT ATATTTACTT
1201 GGTGAAATCA AAGATCATCT TTTGTTTTAT TATAGTCAA GTGATTATCA
1251 AAATTTCTCG AAATTTTTTG AATTTTAAA CGGGAAGAT AGATTTAAAT

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1213

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1301 ATAGTGATTT TTTAAAAGCA TTTGAACGTT TGAAAAAGCA CTTACAAACA
1351 ACATCAGTGG AAATACCTAA ATTTATGAGT ACTGCTAATG AGTTTTTGCA
1401 ATTTTTATTT GACTTGAATG TTATTGCTTA TTAGATAAAC CCAGAAGATG
1451 AAACGAAACC ATATATCCAT TGGTGCTTTA AAGATAGAAA TTATGCAAAT
1501 ATTTCTCCTA AAATAAAAAC TGAAACTGAA TATTTAATAT TTTCAGGATT
1551 ATCAAAAGCC CTTGATGTTG GTACTCCATT TAAGAACAAA CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2548; ORF 744>:

m744.pep

```

1 MKPLKLTLEFG FVDAANYRRR ENKDLFNRIK VKGEYLDLCL EPNISFLIGE
51 KGTGKTAYAV YLTNNFYKNI HATTKFVRET DYSKFIQLKK ARHLTVSDFT
101 SIWKVILYLL ISNQIKKEN GILSSIFNKF KALDEAINEY YGAFDPEIV
151 QAITLIENSK EAAEMIFGKF VKLGEESQO ITFTESKFQA NLGFIERKFK
201 DALSQLKLKD NHILFIDGID IRPSQIPFDE YHECVKGLAN AIWMLNNDIF
251 PSIKDSKGRM RVVLLIRPDI FDSLGLQONQ TKLQDNVSVL DWRTDYKSYR
301 SSKIFGVFDH LLRTQQEKQD SLEKGNWDY YFPWNAPNLH DEYKNLTSFI
351 SFLRKSYYRP RDILQMLTLL QKNKKSKEY VVAEDFDNTS FOREYSIYLL
401 GEIKDHLLFY YSQSDYQNFL KFFEFLNGKD RFKYSDFLKA FERLKKHLQT
451 TSVEIPKEMS TANEFLQFLF DLNVIAYLDN PEDETKPYIH WCFKDRNYAN
501 ISPKIKTETE YLIFSGLSKA LDVGTPEFNK Q*

```

g745.seq not found yet

g745.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2549>:

m745.seq

```

1 ATGTTTTGGC AACTGACCGT TGTTCAGTA ACCGCCGTCA TTGCACTGGG
51 GACAATATTC ATCAATAAGA AAACCTCAAA GCAAAAGGCG ACATTAGATG
101 TTATTTTGAA TGATTACCAA GATGCACAAT TTGTAGAAGC CGACAATCAT
151 ATTTGCGCTT ATATTCGCGG CACGGCAGTT GACGACAACA ACGCGCGGAT
201 CGACCTGTAT GAAATTTATC AAAATAAGGG CGGACAATGG GAAAAAGAGA
251 GAGGGCATT ACTTACCGTA ATCAATCGGC ACGAGTTTGA TCGGTGCGCA
301 ATCAACTCGG GAGTATTGGA TGAGGATTTG TTTAAACGGC TGCATTGCAC
351 CAACTTCATA AAATTGTGGA ATGCAGTTTC GCCTCTTGTT ATGAAAATAC
401 GCGAAGAAGA ACGCAAAGAC ACAATATTTA GAGAGTTGGA AATTTTGTTT
451 GCATTATGGA AAGCAAACCC CTTAAAGGCA TCTGATTTGT GA

```

This corresponds to the amino acid sequence <SEQ ID 2550; ORF 745>:

m745.pep

```

1 MFWQLTVVSV TAVIALGTIF INKKTSKQKA TLDVILNDYQ DAQFVEADNH
51 ISPYIRGTAV DDNNARIDLY EIYQNKGGQW EKERGHLLTV INRHEFYACA
101 INSGVLDEDL FKRLHCTNFI KLWNAVSPV MKIREEERKD TIFRELEILV
151 ALWKANPLKA SDL*

```

a745.seq not found yet

a745.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2551>:

g746.seq

```

1 ATGTCCGAAA ACAAACAAAA CGAAGTCCTG ACCGGTTACG AACAGCTGAA
51 ACGGCGCAAC CGCCGCCGCC TCGTAACGGC AAGCTCCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCACTCAGTT CCGATCCTCG CGACAGCAAT
151 CCCGCACCGC AGGCCGCGCA AACCAGCGCA ACGGAAAGCC AAACGGCAAA
201 CACGGCACAA ACCCTGCCT TGAAATCCGC CGCCGAAAAC GGGGAAACCG
251 CCGCCGACAA ACCGCAGGAC TTGGCAGGCG AAGACAAGCC TTCTGCCGCC
301 GACAGCGAAA TCAGCGAGCC TGAACACGTA GGCGCGCCGC TGGTGCTGAT
351 TAACGACCGG CTCGAAGACA GCAACATCAA AGGTTTGGA GAATCCGAGA
401 AACTGCAACA GGCAGAAACC GCCAAAACCG AACCAGAGCA GGCAAAACAA
451 CGCGTGCCG AAAAAGTGTC GGCAACTGCC GACAGTACGG ATACGGTAGC
501 GGTTGAAAAA CCGAAACGCA CTGCCGAACC CAAACCGCAA AAAGCGGAAC
551 GCACTGCCGA AGCCAAGCCC AAAGCCAAAG AAACCAAAAC CGCCGAAAAA
601 GTTGCCGACA AACCAGAAAC TGCTGCCGAA AAAACCAAAAC CGGATACGGC
651 AAAATCCGAC AGCGCGGTAA AAGAAGCGAA AAAAGCCGAC AAGGCTGAAG
701 GCAAAAAGAC AGCCGAAAAA GACCGTTCGG ACGGCAAAAA ACACGAAACG

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1214

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751 GCGCAAAAAA CCGACAAAGC GGACAAAACC AAAACCGCCG AGAAGGAAAA
801 ATCCGGCAAG GCGGGCAAAA AAGCCGCCAT TCAGGCAGGT TATGCCGAAA
851 AAGAACGCGC CTTGAGCCTC CAGCGCAAAA TGAAGGCGGC GGTATCGAT
901 TCGACCATCA CCGAAATCAT GACCGACAAC GGCAAGTTT ACCGCGTCAA
951 ATCAAGCAAC TATAAAACG CAAGGGATGC CGAACGCGAT TTGAACAAC
1001 TGCGCGTGCA CGGCATCGCC GGCCAGGTAA CGAATGAATA G

```

This corresponds to the amino acid sequence <SEQ ID 2552; ORF 746.ng>:

**g746.pep**

```

1 MSENKQNEVL TGYEQLKRRN RRRLVTASSL VAASCILLAA ALSSDPADSN
51 PAPQAGETGA TESQTANTAQ TPALKSAAEN GETAADKPQD LAGEDKPSAA
101 DSEISEPENV GAPLVLINDR LEDSNIKGLE ESEKLQQAET AKTEPKQAKQ
151 RAAEKVSATA DSTDTVAVEK PKRTAEPKPQ KAERTAEAKP KAKETKTAEK
201 VADKPKTAAE KTKPDTAKSD SAVKEAKKAD KAEGKKTAEK DRSDGKKHET
251 AQKTDKADKT KTAKEKSGK AGKKAATQAG YAEKERALS QRMKAAGID
301 STITEIMTDN GKVYRVKSSN YKNARDAERD LNKL RVHGIA GQVTNE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2553>:

**m746.seq**

```

1 ATGTCCGAAA ACAACAAAA CGAAGTCCTG AGCGGTTACG AACAACTCAA
51 ACGGCGCAAC GCCTGCCGCC TCGTAACGGC AAGTTGCCCTG GTTGCCGCTT
101 CCTGCATCCT GCTGGCAGCC GCCCTCAGTT CCGGCCCTGC CGAACAGACT
151 CCGGGCGAAA CAAGCGCGCT AGAAAAACAAA GCGGCAGGTG CGGCACAAAC
201 CCCTGCCTTG AAATCCGCGC CCGACAAACC GCAGGACTTG GCAGGCGAAG
251 ACAAGCCTTC TGCCGCCGAC AGCGAAATCA GCGAGCCTGA AAACGTAGGC
301 GCGCCGCTGG TCGTGATTAA CGAGCGCTC GAAGACAGCA ACATCAAAGG
351 TTTGGAAGCA TCCGAGAAAC TGCAACAGGC AGAAACCGCC AAAACCGCAC
401 CGAAGCAGGC AAAACAACGC GCTGCCGAAA AAGTGCCGCG AACTGCCGAC
451 AGTACGGATA CGGTAGCGCT TGAAAAACCG AAACGCACTG CCGAAACAAA
501 ACCGCAAAAA GCGGAACGCA CTGCCAAGC CAAGCCCAA GCCAAAGAAA
551 CCAAAACCGC CGAAAAAGTT GCGACAAAC CGAAAACTGC CGCCGAAAAA
601 ACCAAACCGG ATACGGCAAA ATCCGACAGC GCGGTAAAAG AAGCGAAAAA
651 AGCCGACAAG GCTGAAAGCA AAAAAACAGC CGAAAAAGAC CGTTCGGACG
701 GCAAAAAACA CGAAACGGCA CAAAAACCG ACAAGCGGA CAAGACCAA
751 ACCGCCGAGA AGGAAAAATC CGGTAAAAAA GCGCCATTC AGGCAGGTTA
801 TGCCGAAAAA GAACGCGCCT TAAGCCTCCA GCGCAAAATG AAGGCGGCGG
851 GTATCGATTG GACCATCACC GAAATTATGA CCGACAACGG CAAAGTTTAC
901 CGCGTCAAAT CAAGCAACTA TAAAAACGCA AGGGATGCCG AACGCGATTT
951 GAACAAATTG CGCGTACACG GTATCGCCGG TCAGGTAACG AATGAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2554; ORF 746>:

**m746.pep**

```

1 MSENKQNEVL SGYEQLKRRN RRRLVTASCL VAASCILLAA ALSSGPAEQT
51 AGETSGVENK AAGAAQTPAL KSAADKPQDL AGEDKPSAAD SEISEPENVG
101 APLVLINERL EDSNIKGLEA SEKLQQAETA KTAPKQAKQ AAEKVPATAD
151 STDTVAVEKP KRTAETKPKQ AERTAKAPK AKETKTAEKV ADKPKTAEK
201 TKPDTAKSDS AVKEAKKADK AESKKTAEKD RSDGKKHETA QKTDKADTK
251 TAEKEKSGKK AAIQAGYAEK ERALSQRKM KAAGIDSTIT EIMTDNGKVY
301 RVKSSNYKNA RDAERDLNKL RVHGIAGQVT NE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 746 shows 89.9% identity over a 346 aa overlap with a predicted ORF (ORF 746) from *N. gonorrhoeae*:

**m746/g746** 89.9% identity in 346 aa overlap

```

              10      20      30      40      50
m746.pep      MSENKQNEVLSGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQT---AGETSG
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g746           MSENKQNEVL TGYEQLKRRNRRRLVTASSLVAASCILLAAALSSDPADSNPAPQAGETGA
              10      20      30      40      50      60

              60      70      80      90     100     109
m746.pep      VENKAAGAAQTPALKSAA-----DKPQDLAGEDKPSAADSEISEPENVGAPLVLINER
              :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g746           TESQTANTAQTALPKSAAENGETAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDR
              70      80      90     100     110     120

```

1215

```

      110      120      130      140      150      160      169
m746.pep LEDSNIKGLEASEKLQQAETA KTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPQ
      |||||
g746      LEDSNIKGLEESEKLQQAETA KTEPKQAKQRAAEKVSATADSTDTVAVEKPKRTAEPKPQ
      130      140      150      160      170      180

      170      180      190      200      210      220      229
m746.pep KAERTAKAKPKAKETKTAEKVADKPKTAAETKPD TAKSDSAVKEAKKADKAESKKTAEK
      |||||
g746      KAERTAEAKPKAKETKTAEKVADKPKTAAETKPD TAKSDSAVKEAKKADKAEGKKTAEK
      190      200      210      220      230      240

      230      240      250      260      270      280
m746.pep DRSDGKKHETAQKTDKADKTKTAEKEKSGK---KAAIQAGYAEKERALS LQRKMKAAAGID
      |||||
g746      DRSDGKKHETAQKTDKADKTKTAEKEKSGKAGKKA AIIQAGYAEKERALS LQRKMKAAAGID
      250      260      270      280      290      300

      290      300      310      320      330
m746.pep STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
      |||||
g746      STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
      310      320      330      340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2555>:

```

a746.seq
1  ATGTCCGAAA ACAACAAAA CGAAGTCCTG AGCGGTTACG AACAACTCAA
51  ACGGCGCAAC CGCCGCCGCC TCGTAACGGC AAGTTGCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCCCTCAGTT CCGGCCCTGC CGAACAGACT
151 GCCGGCGAAA CAAGCGCGCT AGAAAAACAA GCGGCAGGTG CGGCACAAAC
201 CCCTGCCCTT AAATCCGCCG CCGACAAACC GCAGGACTTG GCAGGCGAAG
251 ACAAGCCTTC TGCCGCCGAC AGCGAAATCA GCGAGCCTGA AAACGTAGGC
301 GCGCCGCTGG TGCTGATTAA CGACCGCCTC GAAGACAGCA ACATCAAAGG
351 TTTGGAAGCA TCCGAGAAAC TGCAACAGGC AGAAACCGCC AAAACCGCAC
401 CGAAGCAGGC AAAACAACGC GCTGCCGAAA AAGTGCCGGC AACTGCCGAC
451 AGTACGGATA CGGTAGCGGT TGAAAAACCG AAACGCACTG CCGAAACAAA
501 ACCGCAAAAA GCGGAACGCA CTGCCAAAGC CAAGCCCAA GCGCAAGAAA
551 CCAAAACCGC CGAAAAAGTT GCCGACAAAC CGAAAACTGC CGCCGAAAAA
601 ACCAAACCGG ATACGGCAAA ATCCGACAGC GCGGTAAAG AAGCGAAAAA
651 AGCCGCAGAG GCTGAAAGCA AAAAAACAGC CGAAAAAGAG CGTTCGGACG
701 GCAAAAAACA CGAAACGGCA CAAAAACCG ACAAAGCGGA CAAGACCAA
751 ACCGCCGAGA AGGAAAAATC CGGTAAAAAA GCGCCATTC AGGCAGGTTA
801 TGCCGAAAAA GAACGCGCCT TAAGCCTCCA GCGCAAAATG AAGGCGGCGG
851 GTATCGATTG GACCATCACC GAAATTATGA CCGACAACGG CAAAGTTTAC
901 CGCGTCAAAT CAAGCAACTA TAAAAACGCA AGGGATGCCG AACCGGATT
951 GAACAAATTG CGCGTACACG GTATCGCCGG TCAGGTAACG AATGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2556; ORF 746.a>:

```

a746.pap
1  MSENKQNEVL SGYEQLKRRN RRLVTASCL VAASCILLAA ALSSGPAEQT
51  AGETSGVENK AAGAAQTPAL KSAADKPQDL AGEDKPSAAD SEISEPENVG
101 APLVLINDRL EDSNIKGLEA SEKLQQAETA KTAPKQAKQR AAEKVPATAD
151 STDTVAVEKP KRTAETKPQK AERTAKAKPK AKETKTAEKV ADKPKTAAEK
201 TKPD TAKSDS AVKEAKKADK AESKKTAEKD RSDGKKHETA QKTDKADKTK
251 TAEKEKSGKK AAIQAGYAEK ERALS LQRKM KAAGIDSTIT EIMTDNGKVY
301 RVKSSNYKNA RDAERDLNKL RVHGIAGQVT NE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 746 shows 99.7% identity over a 332 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a746/m746; 99.7% identity in 332 aa overlap

```

      10      20      30      40      50      60
a746.pap MSENKQNEVL SGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
      |||||
m746      MSENKQNEVL SGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
      10      20      30      40      50      60

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1216

```

          70      80      90      100      110      120
a746.pep  AAGAAQTPALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDRLEDSNIKGLEA
          |||||
m746      AAGAAQTPALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINERLEDSNIKGLEA
          70      80      90      100      110      120

          130      140      150      160      170      180
a746.pep  SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPKQAERTAKAKPK
          |||||
m746      SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPKQAERTAKAKPK
          130      140      150      160      170      180

          190      200      210      220      230      240
a746.pep  AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA
          |||||
m746      AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA
          190      200      210      220      230      240

          250      260      270      280      290      300
a746.pep  QKTDKADKTKTAEKEKSGKKAIIQAGYAEKERALS LQRMKAAGIDSTITEIMTDNGKVY
          |||||
m746      QKTDKADKTKTAEKEKSGKKAIIQAGYAEKERALS LQRMKAAGIDSTITEIMTDNGKVY
          250      260      270      280      290      300

          310      320      330
a746.pep  RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          |||||
m746      RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          310      320      330

```

g747.seq not found yet

g747.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2557>:

```

m747.seq
1   CTGACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGGGTG CTTCCTCCGA TGTCAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTACAAACC
201 CCGTGAGATT GTCTTGACG GTGACAAAC CAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAGCCGCAA CGTTCTATAG TCAATTAAAA
301 TCAAAATAG

```

This corresponds to the amino acid sequence &lt;SEQ ID 2558; ORF 747&gt;:

```

m747.pep
1   LTPWADAYAD LRGKTKVMTT QMGASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPYYR HKTIIKPREI VLDGDKTKMG RSKSNEYGFR VAATFYSQLK
101 SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2559>:

```

a747.seq
1   CTAACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGTGTG CTTCCCGCGA TGTCAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTGCAAACC
201 CCGTGAGATT GTTTTGACG GCGACAAAAC CAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAACGCAA CGTTCTATAG TCAATTAAAA
301 TCAAAGTAG

```

This corresponds to the amino acid sequence &lt;SEQ ID 2560; ORF 747.a&gt;:

```

a747.pep
1   LTPWADAYAD LRGKTKVMTT QMCASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPYYR HKTICKPREI VLDGDKTKMG RSKSNEYGFR VTATFYSQLK
101 SK*

```

Computer analysis of this amino acid sequence gave the following results:

1217

Homology with a predicted ORF from *N. meningitidis*

ORF 747 shows 97.1% identity over a 102 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a747/m747 97.1% identity in 102 aa overlap

```

          10      20      30      40      50      60
a747.pep  LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGWSVGIGLNVGKQLTDSVGLEFDPYYR
          |||
m747      LTPWADAYADLRGKTKVMTTQMGASRDVSKSAKGWSVGIGLNVGKQLTDSVGLEFDPYYR
          10      20      30      40      50      60

          70      80      90     100
a747.pep  HKTICKPREIVLDGDKTKMGRSKSNEYGFRVTATFYSQLKSKX
          |||
m747      HKTIIKPREIVLDGDKTKMGRSKSNEYGFRVAATFYSQLKSKX
          70      80      90     100

```

a747/m80195

gi|150271 (M80195) outer membrane protein [*Neisseria meningitidis*] Length = 272

Score = 59.3 bits (141), Expect = 6e-09

Identities = 29/99 (29%), Positives = 51/99 (51%), Gaps = 4/99 (4%)

```

Query: 1  LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGWSVGIGLNVGKQLTDSVGLEFDPYYR 60
          + PW++ DL + K+ T          +D+++ GW G+G N+GK+L +S +E P+Y+
Sbjct: 174 INPWSEVKFDLNSRYKLNTGVTNLKKDINQKTNGWGFGLGANIGKKLGESASIEAGPFYK 233

```

```

Query: 61 HKTICKPREIVL---DGD-KTKMGRSKSNEYGFRVTATF 95
          +T + E + GD + ++ EYG RV F
Sbjct: 234 QRTYKESGEFSVTTKSGDVSILTIPKTSIREYGLRVGIKF 272

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2561>:

g748.seq

```

1  ATGAGTCAAA ACCAACCCGC ACAACCGACC AAACGCAATC TGTTCAAAAC
51  CGCCCTTGCC GTCGGCGCAA TCGGCGCAAT CGGAGGTTAT TTCGGCGGCA
101 AAAAACAGGG CGAAACCGCC GAACGCACCG CCGAAAAGCCA ACACTCGCCC
151 CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGTATCG TTACGCCGCG
201 GCAGGCGTTT TCCATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251 AGCAGCTGGA AAACCTGTTC CGCACACTGA CCGCCCGCAT CGAGTTTCTC
301 ACCCAAGGCG GAGAATACCA AGACGGCGAC GACAAACTCC CGTCAGCCGG
351 CAGCGGCATT TTGGGTAAAG CCTTCAACCC CGACGGATG ACCGTTACCG
401 TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451 AAAACGGTTC ATTTGCAGGA AATGCGCGAC TTCCCAACG ATAAGCTGCA
501 AAAAAGCTGG TGCAGCGCG ATTTGAGCCT GCAAATCTGC GCCTTCACCC
551 CCGAAACCTG CCAAACCGCC CTGCGCGACA TCATCAACA CACCGCCCAA
601 ACCGCCGTCA TCCGCTGGAG TATCGACGGG TGGCAGCCTA AATCCGAACC
651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTCGAGAC GGCACGGGCA
701 ACCCCAAGGT TTCCGATCCC AAAACCGCCG ACGAGGTTT ATGGACGGGG
751 GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGCGGAAAA ACGGCAGCTA
801 TCAGGCAGTC CGCCTTATCC GCCGCTTTGT CGAGTTTGG GACAGGACGC
851 CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GCGGAAAAA CAGCGGGGCG
901 CCGATGGACG GCAAAAAGA AGCCGACCAA CCGGATTTG CCAAAGACCC
951 CGAGGGTGAT ATCAGGCCCA AAGACAGCCA TATGCGCCTG GCGAATCCGC
1001 GCGATCCCGA ATTCTCAAA AAACACTGCC TCTTCGCGG CGCTACAGC
1051 TATTCTCGCG GACCCGCTC AAGCGGACAG CTTGATGTCG GGCTGGTGT
1101 CGTCTGCTAT CAGGCAAATC TTGCCGACGG TTTCATCTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCGCTG GAAGAATACA TCAGCCCTT CGGCGGGCGG
1201 TATTCTTCG TCTTGCCCGG CGTGGGAAAA GCGGATTCT TGGGACAAGG
1251 GTCGCCGGGC GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2562; ORF 748.ng>:

g748.pep

```

1  MSQNQPAQPT KRNLFKTALA VGAIGAIGGY FGGKKQGETA ERTAESQHSP
51  QAYPCYGEHQ AGIVTPROAF SIMCAFDVTA QSAKQLENLF RTLTARIEFL
101 TQGGYQDGD DKLPASAGSI LGKAFNPDGL TTVGVGSSL FDRFGLKDK
151 KTVHLQEMRD FPNKDLQKSW CDGDLQLQIC AFTPETCQTA LRDIIKHTAQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLTWG
251 VAANSLDEFE WAKNGSYQAV RLIRRFVEFW DRTPLQEQTQ IFGRRKYSGA
301 PMDGKKEADQ PDFAKDPEGD ITPKDSHMRL ANPRDPEFLK KHCLFRAYS
351 YSRGPASSGQ LDVGLVFVCY QANLADGFIF VQNLNGEPL EEYISPFGGG

```

1218

401 YFFVLPGVGK GGFLGQGLPG V\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2563>:

m748.seq

```

1  ATGAGCAAAA AACAAACCCGC ACAACCGACC AGGCGCACTC TTTTAAAAAC
51  CGCGATCGCA GCCGGAGCAG TCGGCGCAAT CGGAGGTTAT CTCGGCGGCA
101 AAAAACAGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA AACTCGCCC
151 CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGCATCG TTACGCCGCA
201 GCAGCGCTTT TCGATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251 AGCAGCTGGA AAACCTGTTC CGCAGCTGA CCGCCCGCAT CGAGTTTCTC
301 ACCCAAGGCG GCGAATACCA AGACGGCGAC GACAAACTTC CGCCAGCCGG
351 CAGCGGCATT TTGGGCAAAG CCTTCAACCC CGACGGGTG ACCGTTACCG
401 TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451 AAACCGGATC ATTTGCAGGA AATGCGCGAC TTCTCCAACG ATAAGCTGCA
501 AAAAAGCTGG TGGCAGGCG ATTTGAGCCT GCAAATCTGT GCCTTACACC
551 CCGAAACCTG CCAAGCCGCC CTGCGCGACA TCATCAAACA CACCGTCCAA
601 ACCGCCGTTA TCCGTGGAG TATCGACGGG TGGCAGCCCA AATCCGAACC
651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTCAGGGAC GGCACGGGCA
701 ACCCAAAGT TTCCGATCCC AAACTGCCG ACGAGGTTT GTGGACGGGG
751 GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGCGAAAA ACGGCAGCTA
801 TCAGGCAGTC CGCCTTATCC GCCACTTTGT CGAGTTTGG GACAGGACGC
851 CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GCGCAAATA CAGCGGTGCG
901 CCGATGGACG GCAAAAAAGA AGCCGACCAA CCGGATTTTG CCAAAGACCC
951 CGAGGGTGAT ATCAGCCCA AAGACAGCCA TATACGCCTG GCGAATCCGC
1001 GCGATCCCGA ATTCTCAA AAACACCGCC TCTCCGCGC GCCTACAGC
1051 TATTCGCGCG GACTCGCCTC AAGCGGACAG CTTGATGTCG GGCTGGTGTT
1101 CGTCTGCTAT CAGGCAAACC TTGCCGACGG ATTCATCTTC GTGCAAAACC
1151 TCTCTAACGG CGAACCGCTG GAAGAATACA TCAGCCCTT CGGCGGCGGC
1201 TATTCTTCG TCTTGCCCGG CGTGAAAAA GCGGCTTTT TGGGGCAAGG
1251 GCTGCTGGGC GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2564; ORF 748>:

m748.pep

```

1  MSKKQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKKQGETA ERTAESQHSP
51  QAYPCYGEHQ AGIVTPQQAF SIMCAFDVTA QSAKQLENLF RLTARIEFL
101 TQGGYQDGD DLPPAGSGI LGKAFNPDGL TVTVGVGSSL FDGRFGLKDK
151 KPIHLQEMRD FSNLKLQKSW CDGDLQLQIC AFTPETQQA LRDIKHTVQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLTG
251 VAANSLDEPE WAKNGSYQAV RLIRHFEVFW DRTPLQEQTD IFGRRKYSGA
301 PMDGKKEADQ PDFAKDPEGD ITPKDSHRL ANPRDPEFLK KHRLFRFRAYS
351 YSRGLASSGQ LDVGLVFVCY QANLADGFIF VQNLNGEPL EYISPFGGG
401 YFFVLPGVEK GGFLGQGLLG V*

```

Computer analysis of this amino acid sequence gave the following results:

#### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 748 shows 95.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. gonorrhoeae*

m748/g748 95.0% identity in 421 aa overlap

	10	20	30	40	50	60
m748.pep	MSKKQPAQPT RRTLFKTAIAAGAVGAIGGYLGKKQGETAERTAESQHSPQAYPCYGEHQ					
g748	MSQNQPAQPTKRNLFTALAVGAIGAIGGYFGKKQGETAERTAESQHSPQAYPCYGEHQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m748.pep	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGYQDGDGDLPPAGSGI					
g748	AGIVTPRQAFSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGYQDGDGDLPSAGSGI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m748.pep	LGKAFNPDGLTVTVGVGSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLQLQIC					
g748	LGKAFNPDGLTVTVGVGSSLFDGRFGLKDKKTVHLQEMRDFPNKLQKSWCDGDLQLQIC					
	130	140	150	160	170	180
	190	200	210	220	230	240
m748.pep	AFTPETQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					

	:           :           :           :
g748	AFTPETCQTALRDIKHTAQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
	190                  200                  210                  220                  230                  240
m748 . pep	KTADEVLWTGVAANSLDEPEWAKNGSYQAVRLIRHFEVFWDRTPLQEQTDFGRRKYSGA
	250                  260                  270                  280                  290                  300
g748	KTADEVLWTGVAANSLDEPEWAKNGSYQAVRLIRRFVEFWDRTPLQEQTDFGRRKYSGA
	250                  260                  270                  280                  290                  300
m748 . pep	PMDGKKKEADQPDKFDPEGDITPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ
	310                  320                  330                  340                  350                  360
g748	PMDGKKKEADQPDKFDPEGDITPKDSHMLANPRDPEFLKKHCLFRRAYSYSRGPASSGQ
	310                  320                  330                  340                  350                  360
m748 . pep	LDVGLVFVCYQANLADGFIFVNLLNGEPLEEYISPFGGGYFFVLPGVGKGFLQGQLLG
	370                  380                  390                  400                  410                  420
g748	LDVGLVFVCYQANLADGFIFVNLLNGEPLEEYISPFGGGYFFVLPGVGKGFLQGQLPG
	370                  380                  390                  400                  410                  420
m748 . pep	VX   VX
q748	

a748.seq

1	ATGAGCAAAA	ACCAACCCGC	ACAACCGACC	AGGCGCACTC	TTTTTAAAC
51	CGCATCGCA	GCTGGAGAC	TCGGCCGAAT	CGGAGGTTAT	CTCGGCGGCA
101	AAAAACGGG	CGAAACCGCC	GAACGACCCG	CCGAAAGCCA	ACACTCGCCC
151	CAAGCCTATC	CTGCTACGG	GAAACATCAG	GCAGGCATCG	TTACGCCGCA
201	GCAGGCGTTT	TCGATTATGT	GCGCCTTCGA	CGTAACCCGC	CAAAGTGCCA
251	AGCAGCTGGA	AAACCTGTTT	CGCACGCTGA	CCGCCCGCAT	CGAGTTTCTG
301	ACCCAAGGGC	GCGAATACCA	AGACGCTGCG	GACAAACTTC	CGGCTAGCCG
351	CAGCGGCATT	TGGGCAAGT	CCTTCAACCC	CGACGGGTAT	ACCGTTACCG
401	TGGGGCTGGG	CAGCAGCTTG	TTTGACGGCC	GGCTCGGACT	CAAAGACAAC
451	AAACCGATT	ATTTCAGGA	AATGCGCGAC	TTTCTCAAAC	ATAAGTCCGA
501	AAAAAGCTGG	TGCGACGGCG	ATTTGAGCCT	GCAATCTGT	GCCTTCACCC
551	CCGAAACCTG	CCAAGCCGCC	CTGCGCAGCA	TCATCAAACA	ACCGTCCAAA
601	ACCGCCGTTA	TCGCGTGGAG	TATCGACGGA	TGGCAGCCTA	AATCCGAAAC
651	CGGCGCGATG	GCGGCGCGCA	ACCTGTTGGG	CTTCCGCGAC	GGCACGGGCA
701	ACCCCAAAGT	TTCCGACCCC	AAAACTCGCG	ACGAGGTTTT	GTTGCGGGGG
751	GTGGCCGCCA	ACAGCCTCCA	GCAACGGGAG	TGGGCGAAAA	AGGCGAGTCA
801	TCAGGCAGTC	CGCCTTATCC	GCCACTTTGT	TGAGTTTGG	GACAGGACGC
851	CGCTTCAAGA	GCAAAACGAC	ATTTTCGGGC	GGCGCAAATA	CAGCGGCGCG
901	CCGATGGACG	GCAAAAAAG	AGCCGACCAA	CCGATTTTGT	CCAAAGACCC
951	CAGGGGAAT	ACCAACGCCA	AAGACAGCCA	TATACGCCTG	GCGAATCCGC
1001	GCGATCCCGA	GTTCTCTTAA	AAACACCCGC	TCTTCCCGCG	CGCCTACAGC
1051	TATTCGCGCG	GACTCGCCTC	AAGCGGACAG	CTTGATGTCG	GGCTGGTGTG
1101	CGTCTGCTAT	CAGGCAAAAC	TGCGGACGG	ATTACATCTC	GTGCAAAACC
1151	TCCTCAACGG	CBAACCGGTG	GAAGAATACA	TCAGCCCCCT	CGGCGCGCGC
1201	TATTTCTTCG	CTTGCCCGG	CGTGAAAAAA	GGCGGCTTTT	TGGGGCAAGG
1251	GCTGCTGGGC	GTATAA			

a748.pap

1	MSKNQPAQPT	RRTLFKTAIA	AGAVGAIGGY	LGGKKRGETA	ERTAESQHSF
51	QAYPCYGEHG	AGVTPPQAF	STMCAPFDVA	QSAQKLENLF	RTLTAIRLEFL
101	TQGGEGYDGD	DLKPPAGSGI	LGKAFFNDVT	TVTVGVGSSL	FDGFRGLKDK
151	KPIHLQEMRD	FSNDKLQKSW	CDGDLSLQIC	AFTPETCQAA	LRDIIKHTVQ
201	TAIVRWSIDG	WQPKSEPGAM	AARNLLGFDR	GTGNPKVSDP	KTADEVLWTG
251	VANRSLDEPE	WAKNGSYQAV	RLIRHFVEFW	DRTLPLQEOTD	IFGRRKLSGA
301	PMDGKKEADQ	PDFAKDPEN	TTPKDSHIRL	ANPRDPEFLK	KHRLFRRAYS
351	YSRGLASSG	LDVGLVFLCY	QANLADGFIF	VQNLNGEPL	E EYISPFGGG
401	YFFVLPGVEK	GGFLGOGLLV	V*		

Computer analysis of this amino acid sequence gave the following results:

1220

Homology with a predicted ORF from *N meningitidis*

ORF 748 shows 99.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. meningitidis*:

a748/m748 99.0% identity in 421 aa overlap

	10	20	30	40	50	60
a748.pep	MSKNQPAQPTRRTLFKTAIAAGAVGAIGGYLGKKRGETAERTAESQHSFPQAYPCYGEHQ					
m748	MSKKQPAQPTRRTLFKTAIAAGAVGAIGGYLGKKQGETAERTAESQHSFPQAYPCYGEHQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
a748.pep	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLTAIEFLTQGGEYQDGDCLKPPAGSGI					
m748	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLTAIEFLTQGGEYQDGDCLKPPAGSGI					
	70	80	90	100	110	120
	130	140	150	160	170	180
a748.pep	LGKAFNPDGLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLSQLIC					
m748	LGKAFNPDGLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLSQLIC					
	130	140	150	160	170	180
	190	200	210	220	230	240
a748.pep	AFTPETCQAALRDIIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
m748	AFTPETCQAALRDIIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
	190	200	210	220	230	240
	250	260	270	280	290	300
a748.pep	KTADEVLTWGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLEQETDIFGRRKYSGA					
m748	KTADEVLTWGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLEQETDIFGRRKYSGA					
	250	260	270	280	290	300
	310	320	330	340	350	360
a748.pep	PMDGKKEADQPDFAKDPEGNTTPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ					
m748	PMDGKKEADQPDFAKDPEGDITPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ					
	310	320	330	340	350	360
	370	380	390	400	410	420
a748.pep	LDVGLVFVCYQANLADGFI FVQNLNNGEPL E EYISPFGGGYFFVLP GVEKGGFLGQGLLG					
m748	LDVGLVFVCYQANLADGFI FVQNLNNGEPL E EYISPFGGGYFFVLP GVEKGGFLGQGLLG					
	370	380	390	400	410	420
a748.pep	VX					
m748	VX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2567>:

g749.seq

```

1  ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTGGGTTT
51  GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCCGCGCCG GCCCGGTCCG
101 GTGAGACCCA ATCCGCCAAC GAAGCGGTT CGGTCGGTAT CGCCGTCAAC
151 GACAATGCTT GCGAACCGAT GAATCTGACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AGGGCGTGAT GGTGGTGGAC GAACGCGAAA ATATCGCCCC GGGGCTTTCC
301 GACAAAATGA CCGTAAccct GCTGCCGGGC GAATACGAAA TGACCTGCGG
351 CCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAGCCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTGGAAA AACTGCCCCA ACCGCTCGCC
451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG CGGCGAAAAC
501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGCCACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGTGTG AAGACGACTT
651 CAAAGACGGT GCGAAAAGAT CCGGGTTTAC CGGCTTCCAC CGTATCGAAC
701 ACGCCCTTTG GGTGGA AAAA GACGTATCCG GCGTGAAGGA AACC GCGGCC
751 AAATGATGA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC

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1221

```

801 Gttccctccg GGCAAGTGG TCGGCGGCGC GTCCGAAGT ATTGAAGAAG
851 CGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCgttaCAG CCACACCGAT
901 TTGAGCGACT TCCAAGCTAA TGCGGACGGA TCTAAAAAAA TCGTCGATTT
951 GTTCCGTCGG TTGATTGAGG CCAAAAAACA AGCCTTGTTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGCACCAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGAGC GAAGCCGACC GCAAAGCATT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2568; ORF 749.ng>:

g749.pep

```

1 MRKFNLTLALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGI AVN
51 DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPQPLA
151 DYKAYVQGEV KELAAKTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
201 ELFSELDPVI DATEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRILGLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2569>:

m749.seq

```

1 ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51 GACCCGCTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCAGTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCGAT GGAAGTACC GTGCCGAGCG GACAGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGCGGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCCT GTTGCCGGGC GAATACGAAA TGAATTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTGGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAAC
501 CAAAACTTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTAC CGGCTTTCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAGTATGAT CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAAGT ATTGAAGAAG
851 TGGCGGCGAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT
951 GTTCCGTCGG CTGATCGAGG CCAAAAAACA AGCCTTGTTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2570; ORF 749>:

m749.pep

```

1 MRKFNLTLALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSI AVN
51 DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRILGLK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 749 shows 96.1% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. gonorrhoeae*

m749/g749 96.1% identity in 388 aa overlap

```

          10      20      30      40      50      60
m749.pep  MRKFNLTLALSVMALGLTACQPPEAEKAAPAAASGEAQTANEGGSVSI AVNDNACEPMELT
          |||
g749      MRKFNLTLALSVMALGLTACQPPEAEKAAPAAASGETQSANEGGSVGI AVNDNACEPMNLT
          10      20      30      40      50      60

```



1222

	70	80	90	100	110	120
m749.pep	VPSGQVVFNIKNNSGRKLEWEILKGVMMVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
g749	VPSGQVVFNIKNNSGRKLEWEILKGVMMVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m749.pep	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
g749	NPRGKLVVADSGFKDTANEADLEKLPOPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m749.pep	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
g749	KAKSLFAATRVHYERIEPIAELFSELDPVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
g749	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEAAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m749.pep	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTD TNFKOVNEILAKYRTKDG FETYDKLG					
g749	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTD TNFKOVNEILAKYRTKDG FETYDKLS					
	310	320	330	340	350	360
	370	380	389			
m749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
g749	EADRKALQAPINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2571>:

```

a749.seq
1   ATGAGAAAT TCAATTGAC CGCATTGTC GTGATGCTG CCTTAGGTTT
51  GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCAGTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCAGAT GGAAC TGACC GTGCCGAGCG GACAGGTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAATGA CCGTCACCTT GTTGCCGGGC GAATACGAAA TGACTTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTTGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTATGTTCA AGGCGAAGTC AAAGAGCTGG TGGCGAAAC
501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAATCGA CCCCGTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTAC CGGCTTCCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAGTATGTA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAATG ATGAAGAAG
851 TGGCGGGCAG TAAATCAGC GCGGAAGAAG ACCGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCGAAAAAAA TCGTCGATTT
951 GTTCCGTCGG TTGATCGAGA CCAAAAACAA AGCCTTGTTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2572; ORF 749.a>:

```

a749.pep
1   MRKFNLTALS VMLALGLTAC QPPEAEKAAP AASGEAQ TAN EGGSVSI AVN
51  DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGVMMVD ERENIA PGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANE A DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD

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1223

301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK  
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 749 shows 99.7% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. meningitidis*:

a749/m749 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
a749.pep	MRKFNL	TALSVML	LGLTACQ	PPEAEKA	APPAASGE	AQTANEGGS
m749	MRKFNL	TALSVML	LGLTACQ	PPEAEKA	APPAASGE	AQTANEGGS
	70	80	90	100	110	120
a749.pep	VPSGQV	VFNKNNS	GRKLEWE	ILKGV	MVDERENI	APGLSDKMT
m749	VPSGQV	VFNKNNS	GRKLEWE	ILKGV	MVDERENI	APGLSDKMT
	130	140	150	160	170	180
a749.pep	NPRGKL	VVTDSG	FKDTANE	ADLEKLS	QPLADYK	AYVQGEVK
m749	NPRGKL	VVTDSG	FKDTANE	ADLEKLS	QPLADYK	AYVQGEVK
	190	200	210	220	230	240
a749.pep	KAKSLF	ADTRVH	YERIEPI	AE	LFSELD	PVIDAREDD
m749	KAKSLF	ADTRVH	YERIEPI	AE	LFSELD	PVIDAREDD
	250	260	270	280	290	300
a749.pep	DVSGVK	EIAAKL	MTDVEA	LQKEID	ALAFPPG	KVVGGA
m749	DVSGVK	EIAAKL	MTDVEA	LQKEID	ALAFPPG	KVVGGA
	310	320	330	340	350	360
a749.pep	LSDFQAN	VDGSKK	IVDLFR	PLIETKN	KALLEK	TDNFKQV
m749	LSDFQAN	VDGSKK	IVDLFR	PLIETKN	KALLEK	TDNFKQV
	370	380	389			
a749.pep	EADRKA	LQASIN	ALAEDLA	QLRGIL	GLKX	
m749	EADRKA	LQASIN	ALAEDLA	QLRGIL	GLKX	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2573>:

g750.seq

```

1  GTGAAACCGC GTTTTATG GGCAGcctGC GCCGTCTGC CGGCCGCCTG
51  TTCGCCCCGA CCTGCCGCCG AAAAAACTGT ATccgCCGCA TCCCAAGCCG
101 CATCCACACC TGTGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC
151 GTTGTGCCGA AGAATCCCGA ACgcgtcgcc gtgtAcgaCt ggGCGGCGTt
201 ggaTACGTG ACCGAGCCGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG
251 TCGCGGTGGA CTATTGCGAG CCTGCATTG ACAAGGCGGC AACGGTGGGG
301 ACGCTGTTTG AGCCCGATTG CGAATCCCTG CACCGCCACA ATCCGCAGTT
351 TGTCATTACC GCGGGGCCGG GTGCGGAAGC GTATGAACAG TTGGCGAAAA
401 ACGCGACCAC CATAGATTG ACGGTGGACA ACGGCAATAT CCGCACCAGC
451 GCGGAGAAGC AGATGGAGAC CCTGTCGCGG ATTTTCGGTA AGGAAGCGCG
501 CGTGGCGGAA TTGAATGCGC AGATTGACGC GCTGTTCCGC CAAAAGCGCG
551 AAGCCGCCAA AGGCAAAGGA CGCGGGCTGG TGCTGTCCGT TACAGGCAAC
601 AAGGTGTCCG CTTTCGGCAC GCAATCGCGG TTGGCAAGTT GGATACACGG
651 CGACATCGGC CTGCCGCCG TGGACGAATC TTTACGCAAC GAAGGGCACG
701 GGCAGCCCGT TTCCTTCGAA TACATCAAAG AGAAAAACCC CGGCTGGATT
751 TTCATCATCG ACCGCACCGC CGCCATCGGG CAGGAAGGGC CGGCTGCCGT

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1224

```

801 GGAAGTGTG GATAACGCGC TGGTATGCGG CACGAACGCT TGGAAGCGCA
851 AGCAAATCAT CGTCATGCCCT GCCGCGAACT ACATTGTGCG GGGCGGCGCG
901 CGGCAGTTGA TACAGGCGGC GGAACAGTTG AAGGCGGCGT TTGAAAAGGC
951 AGAACCCGTT GCGGCGCAGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2574; ORF 750.ng>:

g750.pep

```

1 VKPRFYWAAC AVLPAACSPE PAAEKTVSAA SQAASTPVAT LTVPTARGDA
51 VVPKNPERVA VYDWAALDTL TEPGVNVGAT TAPVRVDYLQ PAFDKAATVG
101 TLFEPDCESL HRRNPQFVIT GGPGAEEYEQ LAKNATTIDL TVDNGNIRTS
151 GEKQMETLSR IFGKEARVAE LNAQIDALFA QKREAAKGKG RGLVLSVTGN
201 KVSAGFTQSR LASWIHGDIG LPPVDESLRN EGHGQPVSEF YIKEKNPGWI
251 FIIDRTAAIG QEGPAAVEVL DNALVCGTNA WKRKQIIVMP AANYIVAGGA
301 RQLIQAAEQL KAAFEKAEPV AAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2575>:

m750.seq

```

1 GTGAAACCGC GTTTTATTG GGCAGCCTGC GCCGTCTCTG TGACCGCCTG
51 TTCGCCCCGAA CCTGCCGCCG AAAAACTGT ATCCGCCGCA TCCGCATCTG
101 CCGCCACGCT GACCGTGCCG ACCGCGCGGG GCGATGCCGT TGTGCCGAAG
151 AATCCCGAAC CGCTCGCCGT GTACGACTGG GCGGCGTTGG ATACGCTGAC
201 CGAATTGGGC GTGAATGTGG GCGCAACCAC CGCGCCGGTG CGCGTGGATT
251 ATTTGCAGCC TGCATTTGAC AAGGCGGCAA CGGTGGGGAC GCTGTTTCGAG
301 CCGGATTACG AAGCCCTGCA CGCTACAAT CCTCAGCTTG TCATTACCGG
351 CGGGCCGGGC GCGGAAGCGT ATGAACAGTT AGCGAAAAAC GCGACCACCA
401 TAGATCTGAC GGTGGACAAC GGCAATATCC GCACCAGCGG CGAAAAGCAG
451 ATGGAGACCT TGGCGCGGAT TTTCGGCAAG GAAGCGCGCG CGGCGGAATT
501 GAAGGCGCAG ATTGACGCGC TGTTCCGCCA AACGCGCGAA GCCGCCAAG
551 GCAAAGGACG CGGCTGGTG CTGTCGGTTA CGGCAACAA GGTGTCCGCC
601 TTCGGCACGC AGTCGCGGTT GGCAAGTTGG ATACACGGCG ACATCGGCCT
651 ACCGCCTGTA GACGAATCTT TACGCAACGA GGGGCACGGG CAGCCTGTTT
701 CCTTCGAATA CATCAAAGAG AAAAACCCCG ATTGGATTTT CATCATCGAC
751 CGTACCGCCG CCATCGGGCA GGAAGGGCCG GCGGCTGTG AAGTATTGGA
801 TAACGCGCTG TACGCGGCA CGAACGCTTG GAAGCGCAAG CAATCATCG
851 TCATGCCCTG CGCGAACTAC ATTGTCGCGG GCGGCGCGCG GCAGTTGATT
901 CAGGCGGGCG AGCAGTTGAA GGCGGCGTTT AAAAAGGCAG AACCCGTTGC
951 GCGGGGGA AAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2576; ORF 750>:

m750.pep

```

1 VKPRFYWAAC AVLLTACSPE PAAEKTVSAA SASAATLTVP TARGDAVVPK
51 NPERVAVYDW AALDTLTEL VNVGATTAPV RVDYLQPAFD KAATVGTLEF
101 PDYEALHRYN PQLVITGGPG AEAYEQLAKN ATTIDLTVDN GNIRTSGEKQ
151 METLARIFGK EARRAELKAO IDALFAQTRE AAKGKGRGLV LSVTGNKVSA
201 FGTQSRLASW IHGDIGLPPV DESLRNEGHG QPVSEFYIKE KNPDWIFIID
251 RTAAIGQEGP AAVEVLDNAL VRGTNAWKRK QIIVMPAANY IVAGGARQLI
301 QAAEQLKAAF KKAEPVAAGK K*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 750 shows 93.8% identity over a 322 aa overlap with a predicted ORF (ORF 750) from *N. gonorrhoeae*

m750/g750 93.8% identity in 322 aa overlap

```

          10      20      30      40      50
m750.pep  VKPRFYWAACAVLLTACSPEPAAEKTVSAAASASA-----ATLTVPPTARGDAVVPKNPERVA
          |||||  :|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g750      VKPRFYWAACAVLPAACSPEPAAEKTVSAAASQAASTPVATLTVPPTARGDAVVPKNPERVA
          10      20      30      40      50      60

          60      70      80      90      100     110
m750.pep  VYDWAALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLEFPDYEALHRYNPQLVIT
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g750      VYDWAALDTLLEPGNVGATTAPVRVDYLQPAFDKAATVGTLEFPDCESLHRRNPQFVIT
          70      80      90      100     110     120

          120     130     140     150     160     170
m750.pep  GGPGAEEYEQAKNATTIDLTVDNGNIRTSGEKQMETLARIFGKEARAAELKAQIDALFA
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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g750      GGPGAEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLSRIFGKEARVAELNAQIDALFA
           130         140         150         160         170         180

           180         190         200         210         220         230
m750.pep  QTREAAKGKGRGLVLSVTGNKVSAFGTQSRLASWIHGDIGLPPVDESIRNEGHGQPVSF
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g750      QKREAAKGKGRGLVLSVTGNKVSAFGTQSRLASWIHGDIGLPPVDESIRNEGHGQPVSF
           190         200         210         220         230         240

           240         250         260         270         280         290
m750.pep  YIKEKNPDWIFIIDRTAAIGQEGPAAVEVLNDAIVRGTNAWKRKQIIVMPAANYIVAGGA
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g750      YIKEKNPGWIFIIDRTAAIGQEGPAAVEVLNDAIVCGTNAWKRKQIIVMPAANYIVAGGA
           250         260         270         280         290         300

           300         310         320
m750.pep  RQLIQAAEQLKAAFEKAPVAAGKKX
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g750      RQLIQAAEQLKAAFEKAPVAAQX
           310         320

```

```
a750.seq
1 GTGAAACCGC GTTTTTATTG GGCAGCCTGC GCCGTCCTGC TGACCCGCTG
51 TTCGCCCGAA CCTGCGCGCC AAAAACCTGT ATCCGCCCGCA TCCGCACTCG
101 CGCCACACAT GACCGGTGCC GGCATGCCGT TGTGCCGAAG
151 AATCCCGAAC GCGTCGCCCT GTACGACTGG GCGGCGTTGG ATACGCTGAC
201 CGAATTGGGT GTGAATGTGG GCGCAACCAC CGCGCGGGTG CCGCTGGATT
251 ATTTGCAGCC TGCAATTGAC AAGCGCGCAA CGGTGGGGAC GTGTGTCGAG
301 CCCGATTACG AAGCCCTGCA CCGCTACAAT CCTCAGCTTG TCATTACCGG
351 CGGGCCGGGG GCGGAAGCGT ATGAACAAGT GGGCAAAAAA GCGACCACCA
401 TAGATCTGAC GGTGGACAAT TTTCAATATCC GCACCAGCGG CGAAAAAGCA
451 ATGGAGACCT TGGCGCGGAT GTTCGGGAAG GAAGCGCGCG GCGCGGAATT
501 GAAGGCGCAG ATTGACGCGC TGTTCGCCCA AACGCGCGAA GCCGCCAAAG
551 GCAAAAGGAC GCGGCTGGTG CTGTGCGTTA CGGGCAACAA GGTGTCGCGC
601 TTCGGCACGC AGTCGCGGTT GCGAAGTTGG ATACACGGCG ACATCGCCTT
651 ACCGCTGTGA GACGAATCTT TACGCAACGA GGGGCACGGG CACGCTGTTT
701 CCTTCGAATA CATCAAAGAG AAAAACCCCG ATTGGATTTT CATCATCGAC
751 CGTACCGCGG GTATCGGGCA GGAAGGCGCG GCGGCTGTGC AAGTATTGGA
801 TAACGCGCTG CTACGCGGCA CGAACCGTTG GAAGCGCAAG AAGATCATCG
851 TCATGCGCTG CGCGAACTAC ATTGTCGCGG GCGGCTCGCG GCAGTTGATT
901 CAGGCGGGCG AGCAGTTGAA GGAGGCGGTT GAAAAGGCGA AACCCGTTGC
951 GGCGGGGAAA GAGTAG
```

```
a750.pep
1 VKPRFYWAAC AVLLTACSP E PAAEKTVSAA SASAATLTVP TARGDAVVEK
51 NPERVAVYDW AALDTLTTEL G PNVGATTAPV RVDYLQPAFD KAATVGTLFE
101 PDYEALHRYN PQLVITGGPG AEAYEQLAKN ATTIDLTVDN GNIRTSGEKQ
151 METLARIFGK EARAELKQA I DALFAQTR E AAKKGKGRGLV LSNVTGNKVID
201 FGTQSRLASW IHGDIQLPPV DESLRNEHG H QPVSFEYKE K PNDWIFIID
251 RTAAIQGEGP AAEVEVDNAL VRGTNAWKRR QIIVMPAANY IVAGGSRQLI
301 QAAEOLKEAF EAKEPVAAGK E*
```

ORF 750 shows 98.8% identity over a 321 aa overlap with a predicted ORF (ORF 750) from *N. meningitidis*:

	10	20	30	40	50	60
a750.pep	VKPRFYWAACAVLLTACSPEPAAEKTVSAASASAATLTVP	TARGDAVV	PKNPERVA	VYDW		
m750	VKPRFYWAACAVLLTACSPEPAAEKTVSAASASAATLTVP	TARGDAVV	PKNPERVA	VYDW		
	10	20	30	40	50	60
	70	80	90	100	110	120
a750.pep	AAALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGT	LFEPDYEALHRYNPQ	LVI	TGGPG		
m750	AAALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGT	LFEPDYEALHRYNPQ	LVI	TGGPG		

1226

	70	80	90	100	110	120
	130	140	150	160	170	180
a750.pep	AEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARI FGKEARAAELKAQIDALFAQTRE					
m750	AEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARI FGKEARAAELKAQIDALFAQTRE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a750.pep	AAKGKGRGLVLSVTGNKVS AFGTQSRLASWIHGDI GLPPVDESLRNEGHGQPVSF EYIKE					
m750	AAKGKGRGLVLSVTGNKVS AFGTQSRLASWIHGDI GLPPVDESLRNEGHGQPVSF EYIKE					
	190	200	210	220	230	240
	250	260	270	280	290	300
a750.pep	KNPDWIFIIDRTAAIGQEGPAAVEVL DNALVRGTNAWKRKQIIVMPAANYIVAGGSRQLI					
m750	KNPDWIFIIDRTAAIGQEGPAAVEVL DNALVRGTNAWKRKQIIVMPAANYIVAGGARQLI					
	250	260	270	280	290	300
	310	320				
a750.pep	QAAEQLKEAFKAEPVAAAGKEX					
m750	QAAEQLKAAFKKAEPVAAAGKKX					
	310	320				

g751.seq not found yet

g751.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2579>:

```

m751.seq..
1  ATGGCTTGGA GTATGTTTGC CACAACCCAA GCCGATAGAG CGGTAAGGTC
51  TGCAACTGCA CCTAAAGAAA TGTGGTTCCA TAAGAAGATA ATAGATGAAA
101 AAACAGGTAA AGTATCCTTT GATACCAGAC AAATTGGGTC ATTGAATGAT
151 TTAAGCAAGG AAGAACTGGC AAGCATTCAA GACACAAATG GCAAAGTTAT
201 TACTGTGTCT AATCCTGGTA TTTTCAATAA TCGAGAAGAT TCATTAAGCA
251 ACGCAGCAAA ACAAAATCGT AATAGTACAA ACGGTAGTGG TGTTATTGCA
301 GTCATGAATC TCCCAACAGG GAAATATAAA TCTGATTCTA ATAACAAAAT
351 AAAAGATTTT TTATGGCTCG GTTCAAGTCT TGTTCCTGAA CTGATGTATG
401 TCGGTTACGA CCAATTAAAT AATAAAGTGT TCCAAGGCTA TTTACCCAAA
451 ACCAATTCAG AAAAAGTGAA TCAAGATATT TATCGAGAGG TTCAAAAAAT
501 GGGTAACGGC TGGTCGGTTG ATACCAGTAA TCACAGTCGT GGGGGAATTA
551 CAGCAAGCGT TTCCTTAAAA GATTGGGTAA ACAATCAAAA ACAAAATGGC
601 ATTGCCCCAA TCAGAAAAGC ACGTTTCTAT GGTACAGCCA CAAATGTGCA
651 GAATGATTAC GCCGATGTTT TACAGAAAAA CGGCTATACC TATACGGGTG
701 CAGACGGCAA AACTTATAAC AGCGGATCCT ACTCAATCGT GCATGATAAA
751 GATTTTGTGG GGAACAAATG GATACCTTTC TTGCTAGGAA CCAATGACAC
801 CACACAAGGT ACATGTAAGG GGTGTGCTA TTCGCATAGC AGTTATTTTG
851 CGGAGGTGCC AAAAGCAGGT ACAAAGAAT TTGATGACTA TGTA AAAATA
901 TGGGGTGAAG TTGAATATGA CGCTCAAGGT AAGCCAATTA ACAAATCTAA
951 ACCCATACTG GTAGAACCAA ACAAACAAA AGATAATGAA AAATATGAAA
1001 AAGAAGCTTT CTA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2580; ORF 751&gt;:

```

m751.pep..
1  MAWSMFATTQ ADRAVRSATA PKEMWFHKKI IDEKTGKVSF DTRQIWSLND
51  LSKEELASIQ DTNGKVITVS NPGIFNNRED SLSNAAQNR NSTNGSGVIA
101 VMNPPTGKYK SDSNNKIKDF LWLGSSLVSE LMYVGYDQLN NKVFQGYLPK
151 TNSEKLNQDI YREVQKMGNG WSVDTSNHSR GGITASVSLK DWVNNQKQNG
201 IAPIRKARFY GTATNVQNDY ADVLQKNGYT YTGADGKTYN SGSYSIVHDK
251 DFGVGNKWI PF LLGTNDTTQG TCKGLCYSHS SYFAEVPKAG TKEFDDYVKI
301 WGEVEYDAQG KPINKSKPIL VEPNKT KDNE KYEKEAF*

```

a751.seq not found yet

a751.pep not found yet

1227

g752.seq not found yet

g752.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2581>:

m752.seq..

```

1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCCTT
101 CCGCAAACAA TCCTGATATA GACATTCCTG ATTTTCTTAC TGAAATCAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTCTG CATTCCTGAC TCTTTCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAGAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTGTC ACCGCATTGC
651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTCGATTTT CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTGGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTCATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTG GAGCACTACA TTTCCGACAA ACAAACACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGCGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAAAGC
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTT GAGTAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTAGAGTA TGTGCTCCT CAGGATTAT TGGAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence &lt;SEQ ID 2582; ORF 752&gt;:

m752.pep

```

1  MKISRPPEFT LLQEQYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51  DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAKESRK KIQKPIDFPF
101 EHQWFICIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151 EEAITSQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDLHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFH PVVQAILHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351 DLTIFYIYYQC DIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
451 SGNALEYVAP QDLLERLEKK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2583>:

m752-1.seq

```

1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCCTT
101 CCGCAAACAA TCCTGATATA GACATTCCTG ATTTTCTTAC TGAAATCAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTCTG CATTCCTGAC TCTTTCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAGAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTGTC ACCGCATTGC

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1228

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651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTCATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTC GAGCACTACA TTTCCGACAA AAAAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTG GAGTAAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTTGCTCCT CAGGATTTAT TGAAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2584; ORF 752-1>:

m752-1.pep

```

1 MKISRPPEFT LLQEQYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51 DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101 EHGFWFCEPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151 EEAITSAQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDHRIATSN AIENKAEPGO FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFIH PVVQAIILHE LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351 DLTYFIYYQC DIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
451 SGNALFYVAP QDLLERLEKK *

```

a752.seq not found yet

a752.pep not found yet

g753.seq not found yet

g753.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2585>:

m753.seq

```

1 ATGCCCATCA CTCCACCCTT AAACATCATC TCTCCTAAAC TCTACCCCAA
51 TGAACAATGG AACGAAAGCG AAGCACTCGG TGCCATCACT TGGCTATGGT
101 ATCAGTCGCC TACGCATCGC CAAGTACCTA TTGTGGAGAT GATGACGTAT
151 ATATTGCCTG TGTTAAAAAA CGGGCAGTTC GCTTTGTTTT GCAAGGGTAC
201 CCAACCAATC GGTATATCT CATGGGCTTA TTTTGATGAA GTGGCGCAGG
251 CGCATTATTT AGAATCTGAC CGCCATTTGC GTGACAACAG CGATTGGAAC
301 TGTGGCGACA ATATTTGGCT GATTCAATGG TTTGCGCCAT TGGGACACAG
351 TCATCAAATG CGCTCAGCTG TCGCCAGTT ATTTCTTAGT ACGACAGTAC
401 GCGCCTTGTA TCATAAAGGG AGCGATAAGG GTTTGAGAAT TTTAACTTTT
451 AAAACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2586; ORF 753>:

m753.pep

```

1 MPITPPLNII SPKLYPNEQW NESEALGAIT WLWYQSPTHR QVPIVEMMTY
51 ILPVLKNGQF ALFCKGTQPI GYISWAYFDE VAQAHYLESD RHLRDNDSWN
101 CGDNIWLIQW FAPLGHSHQM RSAVRQLFPS TTVRALYHKG SDKGLRILTF
151 KT*

```

a753.seq not found yet

a753.pep not found yet

g754.seq not found yet

1229

g754.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2587>:

```

m754.seq
1  ATGATGAAGT CTATCCTCAC CGTATCCGGA AATCGTATGC GTAAACCCAG
51  AATCACCTAT TTGGATGTTT GGGCAAACGA TGAAAGAATC GGTACTTTGG
101 AAAAGGGGGC CATGTATCGG TTGCATACG ACAATCCCAA TTCTTCGTTG
151 CTGGGCCTGC ATTATCAAGA CAGAAGCAAG GTATATATCA GCAACAATAT
201 GCCGCATATC TTTGCACAGT ATTTTCCGGA AGGCTTTTGT GATGCACACA
251 TCACAAGCAA ATATGCTTTT CATGATGCGC CTTTTGAAGA CAATGAGATG
301 CTGCGCTTGG CAATTCTGTG CAGAGAGACT TTGGGTCGGA TACATGTGCG
351 CTGTAATGAC CCGCTTTTTA ATGAATGGAT TGACGGGTTG GAGATGAAAA
401 ATCCAAGAAT ATTGACTGAA CGGGATTGTC TGGGCATAAA TGCCCGACAG
451 GTTTTTCAGC AATATATGGC AGAAATCTTC CATCACGGCC GTTTCGTCAG
501 TGTATCCGGG ATACAGCAGA AGATGTCCTT AGATGCCATC CGCAGAAATA
551 CCAAGCAAAC TGCCTCATAT ATTGCCAAAG GTTTTGATGC ATCCGAATAT
601 CCTTGCTTGG CTGCCAATGA ATTTTATGTC ATGCAGACCA TCAAACAAGC
651 CGGCATTGCC GTTGCACAGA CCAGCCTGTC GGAAGATTCA TCAGTCTTAT
701 TGGTACGTCG GTTTGATGTC AGTGAACAGG GTTATTTTTT AGGGATGGAA
751 GACTTTACCA GTCTGCGCCA GTATTCGGTA GAAGATAAAT ATAAAGGCAG
801 TTATGCGGCT ATTGCACAGA TTATCCGACA GATATCCGGC AGACCAGATG
851 AAGATTTAAT CCATTTCTTT AATCAGCTTG CTGCCAGTTG CATATTGAAA
901 AACGCGATG CACACCTCAA AAATTTTTCG TACTCTATC ATGACGAATA
951 CGATGTTTCG CTTGCACCTG TCTATGATGT ATTGGATACA TCAATATACA
1001 GGGTTGGAAC ACAAGGAATT TTTGATGCTT ATGACGATAC GCTGGCATTG
1051 AACCTGACTA ACCACGGTAA GAAAACATAT CCTTCCAAGA ATACATTGTT
1101 GGATTTTGCT GAGAAATATT GCGATTGGG AAGAGAAGAT GCATCCTTTA
1151 TGATAGATAC AATCGTTCAA GCTAAAGAAC AGGTTCTTGT TAAATACTCG
1201 GATGTATTGC GTGAGAATGA ATGGTTGGCG CAGAAGTGGC ATTTTATCCC
1251 GGATGAAAAT GAAGAAGGTC TACCGTTTAC ATTCCGGTAG

```

This corresponds to the amino acid sequence &lt;SEQ ID 2588; ORF 754&gt;:

```

m754.pep
1  MMKSILTVSG NRMRKPRITY LDVWANDER I GTLEKGAMYR FAYDNPNSSL
51  LGLHYQDRSK VYISNNMPHI FAQYFPEGFL DAHITSKYAF HDAPFEDNEM
101 LRLAILCRET LGRIHVRCND PLFNEWIDGL EMKNPRILTE RDLLGINARQ
151 VFQQYMAEIF HHGRFVSVSG IQQKMSLDAI RRNTKQTASY IAKGFDASEY
201 PCLAANEFLC MQTIKQAGIA VAQTSLS EDS SVLLVRRFDV SEQGYFLGME
251 DFTSLRQYSV EDKYKGSYAA IAQIIRQISG RPDEDLIHFF NQLAASCILK
301 NGDAHLKNFS VLYHDEYDVR LAPVYDVLD T SIYRVGTQGI FDAYDDTLAL
351 NLTNHGKPTY PSKNTLLDFA EKYCDLGRED ASFMIDTIVQ AKEQVLVKYS
401 DVLRENEWLA QKWHFIPDEN EEGLPFTFR*

```

a754.seq not found yet

a754.pep not found yet

g755.seq not found yet

g755.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2589>:

```

m755.seq..
1  ATGAGCCGTT ACCTGATTAC CTTTGATATG GATACCAACT GCCTGAAAGA
51  CAATTACCAC GGAAATAACT ATACCAATGC CTACTCCGAT ATTAACCAAC
101 TCTTGGCTAG ACATGGATTT GAGAACATTC AGGGCAGTGT TTATCTAGGC
151 CGTGAAGGCA TCAGTGAAGC ACACGGAACA ATAGCCATTC AGGAACTGAC
201 CGCTCGGTTT GATTGGTTT ACTCCTGTAT TTCAAACATT AAGTTTACC
251 GCCTTGAAAG TGATTTGAAC GCACAATTA TCGCTGATGG TGTGTATCAA
301 GCCAAACAGG CTTTCCTTCA ACGTGTGTA CAACTTCGTA TATCCCTAAC
351 AGAAGCTGGA TTGTCTGATG AGCAAATCAA TCAGGTTCTG GAAAAACAGA
401 AATTGGAATT GGAAAGTCCT AACCTGAAAT TAAATTAA

```



1230

This corresponds to the amino acid sequence <SEQ ID 2590; ORF 755>:

m755.pep..

```

1  MSRYLITFDM DTNCLKDNYH GNNYTNAYSD IKTILARHGF ENIQGSVYLG
51  REGISEAHGT IAIQELTARF DWFYSCISNI KFYRLES DLN AQFIADGVYQ
101 AKQAF LQRVE QLRISL TEAG LSDEQINQVL EKQKFELESP NLKLN*
```

a755.seq not found yet

a755.pep not found yet

g756.seq not found yet

g756.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2591>:

m756.seq

```

1  ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
51  CAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTTGCGA AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCTGTC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2592; ORF 756>:

m756.pep

```

1  MTANFAQTLV EIQDSLRYRVV STVQYGGDNL KRLTADKRKQ YELNFKISEG
51  STRVESDFKE TLVRFGDML QDMPKIRSA TLVALTTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DVFQIGRRSY
151 SREDISEANR RAERVPYGAE LVSDGNFTAV LSDIGD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2593>:

a756.seq

```

1  ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
51  NAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTTGCGA AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCTGTC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2594; ORF 756.a>:

a756.pep

```

1  MTANFAQTLV EIQDSLXRVV STVQYGGDNL KRLTADKRKQ YELNFKISEG
51  STRVESDFKE TLVRFGDML QDMPKIRSA TLVALTTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DVFQIGRRSY
151 SREDISEANR RAERVPYGAE LVSDGNFTAV LSDIGD*
```

m756 / a756 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
m756.pep	MTANFAQTLVEIQDSLXRVVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
a756	MTANFAQTLVEIQDSLXRVVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
	10	20	30	40	50	60

1231

```

              70      80      90      100      110      120
m756.pep      TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a756           TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD
              70      80      90      100      110      120

              130      140      150      160      170      180
m756.pep      RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVYPYGAELVSDGNFTAV
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a756           RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVYPYGAELVSDGNFTAV
              130      140      150      160      170      180

m756.pep      LSDIGDX
              ||||||
a756           LSDIGDX

```

g757.seq not found yet

g757.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2595>:

```

m757.seq
1  ATGAAAATAC TCGCTTTATT AATTGCCGCT ACCTGTGCTT TATCTGCGTG
51  TGGCAGCCAA TCTGAAGAAC AACCGGCATC TGCACAACCC CAAGAGCAGG
101 CACAATCCGA ATTA AAAACC ATGCCGGTAA GCTATACCGA CTATCAATCA
151 GCAGCCAATA AAGGGCTGAA TGACCAAAAA ACCGGTCTGA CCCTTCCTGA
201 ACATGTTGTC CCTATCGACA ATGCGGAAGG AAAGAATCTG CTGCATGACT
251 TTTCAGACGG CCTCACAATC TTAACCGTTG ATACCGATAA AGCCGACAAA
301 ATTACTGCTG TCCGAGTAGT CTGGAATACA GATGCAATGC CTCAAAAAGC
351 GGAAAACTG TCCAAAGCTG CCGCAGCCTT GATTGCGGCA ACCGCTCCGG
401 AAGACCGCAC AATGCTGCGT GATACCGCGG ACCAAATCGA AATGGCGATT
451 GACAGCCATA ATGCGCAAAA AGAGCCAACC CGAGAATGGG CGCGTGTTGG
501 GATTGCTTAT AAAGTCACTG TTACCAATTT ACCGAGCGTG GTTTTGACGG
551 CAAAAGCTGA GTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2596; ORF 757&gt;:

```

m757.pep (lipoprotein)
1  MKILALLIAA TCALSACGSQ SEEQPASAQP QEQAQSELKT MPVSYTDYQS
51  AANKGLNDQK TGLTLPEHVV PIDNAEGKNL LHDPSDGLTI LTVDTDKADK
101 ITAVRVVWNT DAMPKAEKL SKAAAALIAA TAPEDRTMLR DTGDQIEMAI
151 DSHNAQKEPT REWARGGIAY KVTVTNLPVS VLTAKAE*

```

a757.seq not found yet

a757.pep not found yet

g758.seq not found yet

g758.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2597>:

```

m758.seq
1  ATGAACAATC TGACCGTGTT TACCCGTTTC GATACCGATT TGGCGACGCT
51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101 AGGGCAAAC TGTGAAATC CCCGTCTGCT ACGGCGGCGA ATACGGCCCG
151 GATTTGCGCG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CCGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCCGTCG GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTGAA TCCGCCGACC
451 CTGCTGGCGG CGGTGACCA AGTCCGCTTT GTTGACAGAA GGATTGAGCC
501 ATGA

```

1232

This corresponds to the amino acid sequence <SEQ ID 2598; ORF 758>:

```
m758.pep
  1 MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGEYGP
 51 DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101 RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPPT
151 LLAAGDQVRF VAERIEP*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2599>:

```
a758.seq
  1 ATGAACAATC TGACCGTGTT CACCCGTTTC GATACCGATT TGGCGACGCT
 51 TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101 AGGGCAAACCT GGTGGAAATT CCCGTCTGCT ACGGCGGCGA ATACGGCCCCG
151 GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CTGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTTGCA CACGCCCCGC
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGCAGAAA GGATTGAGCC
501 ATGA
```

This corresponds to the amino acid sequence <SEQ ID 2600; ORF 758.a>:

```
a758.pep..
  1 MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGEYGP
 51 DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101 RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPPT
151 LLAAGDQVRF VAERIEP*
```

m758 / a758 100.0% identity in 167 aa overlap

m758.pep	10	20	30	40	50	60
	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGEYGPDLAEVAAFHQ					
a758	10	20	30	40	50	60
	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGEYGPDLAEVAAFHQ					
m758.pep	70	80	90	100	110	120
	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPA GSVGIGGSQT					
a758	70	80	90	100	110	120
	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPA GSVGIGGSQT					
m758.pep	130	140	150	160		
	GVYPFASPGGWQIIGRTELP LFRADLNPPPTLLAAGDQVRFVAERIEPX					
a758	130	140	150	160		
	GVYPFASPGGWQIIGRTELP LFRADLNPPPTLLAAGDQVRFVAERIEPX					

g759.seq not found yet

g759.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2601>:

```
m759.seq
  1 ATGCGCTTCA CACACACCAC CCCATTTTGT TCCGTATTGT CCACCCTCGG
 51 TCTTTTGGCC GTTCCCCCTG CTTACTCATC CATTGTCCGC AACGATGTCG
101 ATTACCAATA TTTTCGCGAC TTTGCCGAAA ATAAAGGCGC GTTCAACCGTA
151 GGTGCAAGCA ATATTTCCAT CCAAGACAAG CAAGGCAAAA TATTAGGCAG
201 GGTTCCTCAAC GGCATCCCCA TGCCCGACTT CCGCGTCAGC AACCGCCAAA
251 CCGCCATCGC CACCCTGGTT CACCCCAAT ACGTCAACAG TGTCAAACAC
301 AACGTCGGCT ACGGTTCCAT ACAATTCGGC AACGACACCC AAAATCCAGA
351 AGAACAAGCC TATACCTACC GCCTCGTATC ACGCAACCCG CACCCGACT
401 ACGACTACCA CCTCCCCCGC CTCAACAAAC TGGTTACCGA AATCTCACCT
```

451	ACCGCACTCA	GCAGCGTACC	CTTGCTTGGA	AACGGCCAGC	CAAAGGCCAA
501	TGCTTACCTC	GATACCGACC	GCTTCCCCTA	CTTTGTACGA	CTCGGCTCAG
551	GCACGCAACA	AGTCCGCAAA	GCAGACGGCA	CGCGTACACG	AACCGCCCCG
601	GCATACCAAT	ACCTGACCGG	CGGCACGCCG	CTGAAAGTAT	TGGGGTTCCA
651	AAACCACGGC	TTACTCGTCG	GCGGCAGCCT	GACCGACCAA	CCCCTTAACA
701	CCTACGCAAT	CGCCGGAGAC	AGCGGTTCCC	CCCTGTTTGC	CTTCGACAAG
751	CATGAAAACC	GCTGGGTGCT	TGCGGGCGTA	CTCAGCACCT	ACGCCGGCTT
801	CGATAATTTT	TTCAACAAAT	ACATCGTCAC	GCAACCCGAA	TTCATCCGTT
851	CCACCATCCG	CCAATACGAA	ACCCGGCTGG	ATGTCGGGCT	GACCACCAAC
901	GAATCATAT	GGCGCGACAA	CGGTAATGGC	AACAGCACCC	TGCAAGGGCT
951	CAACGAACGC	ATCACCTGCG	CCATTGCAAA	CCCTTCGCTT	GCCCCACAAA
1001	ACGACAGCAG	GCACATGCCG	TCTGAAGATG	CCGGCAAAAC	GCTCATCCTA
1051	TCCAGCAGGT	TCGACAACAA	AACACTGATG	CTGGCAGACA	ATATCAACCA
1101	AGGCGCAGGC	GCATTGCAGT	TCGACAGCAA	CTTCACCGTC	GTCGGTAAAA
1151	ACCACACATG	GCAAGGTGCA	GGCGTTATCG	TAGCCGACGG	CAAACGCGTC
1201	TTCTGGCAAG	TCAGCAACCC	CAAAGGCGAC	CGGCTCTCCA	AACTGGGCGC
1251	AGGCACGCTT	ATCGCCAACG	GACAAGGCAT	CAACCAGGGC	GACATCAGCA
1301	TCGGGGAAGG	CACTGTCGTA	CTCGCCCAAA	AAGCTGCTTC	AGACGGCAGC
1351	AAACAAGCAT	TCAACCAAGT	CGGCATCACC	AGCGGCAGGG	GCACGGCCGT
1401	CCTCGCCGAC	AGCCAGCAAA	TCAAACCCGA	AAACCTCTAT	TTGGGCTTCA
1451	GGGCGGGACG	GCTCGACCTC	AACGGCAACA	ACCTTGCCCT	TACCCATATC
1501	CGCCATGCGG	ACGGCGGCGC	GCAAATCGTC	AATCACAACC	CTGACCAAGC
1551	CGCGACACTG	ACGCTGACCG	GCAACCCCGT	CCTCAGTCCC	GAGCATGTCT
1601	AGTGGGTGCA	ATGGGGCAAC	CGTCCGCAAG	GCAACGCGGC	GGTTTACGAA
1651	TACATCAACC	CGCACCGBAA	CCGTGCGACC	GACTACTTCA	TACTCAAACC
1701	CGGCGGCAAC	CCGCGCGAAT	TTTTTCCGTT	AAATATGAAA	AACTCAACAA
1751	GCTGGCAATT	TATCGGCAAC	AACAGGCAAC	AGGCCGCCGA	ACAAGTCGCC
1801	CAAGCCGAAA	ATGCCCCGCC	CGACCTGATT	ACCTTCGGCG	GATACTTGGG
1851	TGAAAACGCG	CAAACGGGCA	AAGCCGCGCC	GAGTTACAGC	AAAACCAATG
1901	AAGCAGCCAT	AGAAAAAACC	CGCCATATCG	CAAATGCCGC	CGTATACGGC
1951	CGGCCCGAAT	ACCGTTACAA	CGGCGCACTC	AACCTGCACT	ATCGTCCCAA
2001	ACGCAACGAC	AGCACGCTGT	TGCTCAACGG	CGGCATGAAC	CTTAACGGGG
2051	AAGTCTTGAT	TGAGGGCGGC	AATATGATTG	TGTCAGGCAG	GCCCGTACCC
2101	CATGCCTACG	ACCACCAGGC	CAAACGCGAA	CCCGTTCTTG	AAAACGAATG
2151	GACCGACGGC	AGCTTCAAGG	CTGCACGGTT	CACCCTGCGA	AACCATGCCC
2201	GACTGACGGC	AGGGCGCAAT	ACCGCGCATC	TGGACGGCGA	CATAACGCCA
2251	TACGATCTGT	CCGGCATCGA	CCTCGGCTTT	ACCCAAGGCA	AAACACCGGA
2301	ATGCTACCGC	TCCTACCATA	GCGGCAGCAC	CCACTGCACA	CCCAACGCCG
2351	TTTTAAAAGC	CGAAAACTAT	CGTGCACTAC	CTGCAACGCA	AGTACGCGGC
2401	GACATTACCC	TTAACGACCG	TTCAAGAGTC	CGCCTGGGCA	AAGCACACCT
2451	GTACGGCAGC	ATCCGTGCCG	GCAAAGACAC	CGCAGTCCGC	ATGGAAGCAG
2501	ACAGCAACTG	GACACTTTCC	CAGTCCAGCC	ACACCGGCGC	ACTGACGCTT
2551	GACGGCGCAC	AAATTACCCT	GAACCCCGAT	TTGCGCAATA	ATACACACAA
2601	CAACCGCTTC	AACACACTGA	CCGTCAACGG	CACACTTGAC	GGGTTCGGCA
2651	CATTCCGATT	CCTGACCGGC	ATCGTCCGAA	AACAAAATGC	CCCCCCCCTC
2701	AAACTGGAAG	GGGACAGCCG	CGGCGCATTC	CAAATCCACG	TCAAAAACAC
2751	CGGACAAGAA	CCTCAAACAA	CCGAATCGCT	TGCACTTGTT	AGCCTCAATC
2801	CGAAACACAG	CCACCAAGCC	CGATTACACC	TCCAAAACGG	CTATGCCGAT
2851	TTGGGTGCCT	ACCGCTACAT	CCTCCGCAAA	AACAACAACG	GATACAGCCT
2901	GTACAACCCG	CTCAAAGAGG	CCGAACCTCA	AATTGAAGCC	ACGCGTGCGG
2951	AACATGAGCG	CAACCAACAG	GCATACAACC	AATTACAGGC	AACCGACATC
3001	AGCAGACAGG	TTCAACATGA	CTCTGACGCG	ACCAGGCAGG	CACTACAGGC
3051	CTGGCAGAAC	AGTCAAACCG	AACTTGCCCG	CATCGACAGC	CAAGTCCAAT
3101	ATCTGTCCGC	CCAATTGAAA	CAGACAGACC	CGCTGACCGG	CATTCTGACG
3151	CGTGCCCAAA	ACCTGTGTGC	CGCACAAGGA	TACAGTGCCG	ATATCTGCCG
3201	TCAGGTTGCC	AAAGCCGCCG	ACACGAACGA	CCTGACACTC	TTCGAAACCG
3251	AACTGGATAC	GTATATAGAA	CGTGTAAGAA	TGGCCGAATC	CGAACTTGAC
3301	AAAGCACGGC	AAGGCGGCGA	TGCGCAAGCC	GTCGAAACAG	CCCGGCACGC
3351	CTACCTGAAC	GCACTCAACC	GTCTGTCCCG	ACAAATCCAC	AGTTTGAAAA
3401	CCGGCGTTGC	CGGCATCCGT	ATGCCGAACC	TGGCCGAACT	GATCAGCCGG
3451	TCGGCCAACA	CCGCCGTTTC	CGAACAGGCC	GCCTACAATA	CCGGCCGGCA
3501	ACAGGCGGGA	CGCCGCATCG	ACCGCCACCT	TACCGATCCG	CAGCAGCAAA
3551	ACATCTGGCT	GGAAACCGGT	ACGCAACAAA	CCGACTACCA	TAGCGGCACA
3601	CACCGTCCCT	ACCAACAAAC	TACCAACTAT	GCACATATCG	GCATCCAAAC
3651	GGCATCACC	GACCGTCTCA	GTGTCGGTAC	GATTTTAAAC	GATGAGCGCA
3701	CAAACAACCG	TTTTGATGAA	GGCGTATCCG	CCCGAAACCG	CAGCAACGGC

1234

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3751 GCACATCTGT TCGTCAAAGG GGAAAACGGC GCACTCTTTG CCGCGGCAGA
3801 TTTAGGCTAC AGCAACAGCC GTACCCGATT TACCGATTAT GACGGGGCTG
3851 CCGTCCGCCG CCACGCATGG GATGCAGGCA TCAACACCGG CATCAAATC
3901 GATACCGGCA TCAACCTCAG ACCCTATGCC GGCATCCGTA TAAACCGCAG
3951 CAACGGCAAC CCGTACGTAC TCGACGGCGC AGAGATAAAC AGCCCGGCGC
4001 AAATCCAAAC CACATGGCAT GCCGGCATCC GTCTCGATAA AACCGTCGAA
4051 CTGGGTCAAG CCAAGCTGAC CCCCGCCTTC AGCAGCGATT ACTACCATAC
4101 CCGCCAAAAC AGCGGTTCGG CCCTCAGCGT CAACGACCGT ACCTTACTGC
4151 AGCAAGCCGC CCACGGCACA CTGCATACCC TGCAAATCGA CGCCGGATAC
4201 AAAGGCTGGA ACGCCAAACT TCATGCCGCT TACGGCAAAG ACAGCAACAC
4251 CGCCGCCAC AAACAGGCAG GAATCAAAT AGGCTACAAC TGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2602; ORF 759>:

```

m759.pep
  1 MRFTHTFPC SVLSTLGLFA VSPAYSSIVR NDVDYQYFRD FAENKGAFTV
 51 GASNISIQDK QGKILGRVLN GIPMPDFRVS NRQTAIATLV HPQYVNSVKH
101 NVGYGSIQFG NDTQNPEEQA YTYRLVSRNP HPDYDYHLPR LNKLVTEISP
151 TALSSVPLLG NGQPKANAYL DTDREFPYFVR LSGTQQVRK ADGTRTRTAP
201 AYQYLTGGTP LKVLGFQNHG LLVGGSLTDQ PLNTYAIAGD SGSPLFADFCK
251 HENRWVLAVG LSTYAGFDNF FNKYIVTQPE FIRSTIRQYE TRLDVGLTTN
301 ELIWRDNGNG NSTLQGLNER ITLPIANPSL APQNDNRHMP SEDAGKTLLI
351 SSREFDNKTL LADNINQAG ALQFDSNFTV VGKNHTWQGA GVIVADGKRV
401 FWQVSNPKGD RLSKLGLAGT IANGQGINQG DISIGEGTVV LAQKAASDGS
451 KQAFNQVGIT SGRGTAVLAD SQQIKPENLY FGFRGGRDL NGNNLAFTHI
501 RHADGGAQIV NHNPDAQATL TLTGNPVLSP EHVEWVQWGN RPQGNAAVYE
551 YINPHRNRRT DYFILKPGGN PREFFPLNMK NSTSWQFIGN NRQQAEEQVA
601 QAENARPDLI TFGGYLGENA QTGKAAPSYS KTNEAAIEKT RHIANAAVYG
651 RPEYRYNGAL NLHYRPKRTD STLLNNGGMN LNGEVLIEGG NMIVSGRPVP
701 HAYDHQAKRE PVLENEWTDG SFKAARFTLR NHARLTAGRN TAHLDGDITA
751 YDLSGIDLGF TQGTPECYR SYHSGSTHCT PNAVLAENY RALPATQVRG
801 DITLNRSEL RLGAHLYGS IRAGKDTAVR MEADSNWTL SSSHTGALT
851 DGAQITLNPD FANNTHNRF NTLTVNGTLD GFGTFRELTG IVRKQNAAPL
901 KLEGDSRGAF QIHVKNTGQE PQTTESLALV SLNPKHSHQA RFTLQNGYAD
951 LGAYRYILRK NNGYSLYNP LKEAELQIEA TRAEHERNQO AYNQLQATDI
1001 SRQVQHSDA TRQALQAWQN SQTELARIDS QVQYLSAQLK QTDPLTGILT
1051 RAQNLCQAQG YSADICRQVA KAADTNDLTL FETELDTYIE RVEMAESELD
1101 KARQGGDAQA VETARHAYLN ALNRLSRQIH SLKTGVAGIR MPNLAEIISR
1151 SANTAVSEQA AYNTGRQOAG RRIDRHLTDP QQQNIWLETG TQQTDYHSGT
1201 HRPYQQTNY AHIGIQTGIT DRLSVGTILT DERTNNRFDE GVSARNRSNG
1251 AHLFVKGENG ALFAAADLGY SNSRTRFTDY DGAAVRRHAW DAGINTGIKI
1301 DTGINLRPYA GIRINRSNGN RYVLDGAEIN SPAQIQTTWH AGIRLDKTVE
1351 LGQAKLTAPF SSDYYHTRQN SGSALSVNDR TLLQQAAGHT LHTLQIDAGY
1401 KGWNAKLHAA YGKDSNTARH KQAGIKIGYN W*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2603>:

```

g760.seq (partial)
  1 AACAACCGCA ACACCCGTTA CGCCGCATTG GGCAAACCGG TGATGGAAGG
 51 CGTTGAGACC GAAATCAGCG GTGCGATTAC ACCGAAATGG CAAATCCATG
101 CAGGTTACAG CTATCTGCAC AGCCAAATCA AAACCGCCGC CAATCCACGC
151 GACGACGGCA TCTTCCTGCT GGTGCCCAAA CACAGCGCAA ACCTGTGGAC
201 GACTTACCAA GTTACGCCCC GGCTGACCGT CGGCGGCGGC GTGAACGCGA
251 TGAGCGGCAT TACTTCATCT GCAGGGATGC ATGACGGCGG TTATGCCACG
301 TTCGATGCGA TGGCGGCATA CCGCTTCACG CCAAGCTGA AGCTGCAAAT
351 CAATGCCGAC AACATCTTCA ACCGCCATTA CTACGCCCGC GTCGGCGGCA
401 CGAACACCTT TAACATTCCC GGTCGGAGC GCAGCCTGAC GGCAAACCTG
451 CGTTACAGTT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2604; ORF 760.ng>:

```

g760.pep (partial)
  1 NNRNTRYAAL GKRVMGVEV EISGAITPKW QIHAGYSYLH SQIKTAANPR
 51 DDGIFLLVPK HSANLWTTYQ VTPGLTVGGG VNAMSGITSS AGMHAGGYAT
101 FDAMAAYRFT PKLKLQINAD NIFNRHYAR VGGTNTFNIP GSERSLTANL
151 RYSF*

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1235

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2605>:

```
m760.seq
1   ATGGGACAGT TTATGTCAGT TTTCCGCATC AATATGACCG CCGCCACGGT
51  TTTGGCAGCA CTCTCGTCTT CGGTTTTTGC CGCACAAACG GAAGGTTTGG
101 AAACCGTCCA TATTAAGGGT CAGCGTTCTT ACAACGCGAT TGCCACCGAG
151 AAAAAACGGCG ATTACAGCTC GTTTGCCGCC ACCGTCGGTA CAAAAATCCC
201 CGCTTCTTTG CGCGAAATTC CGCAATCCGT CAGCATCATT ACCAACCAGC
251 AGGTCAAAGA CCGCAATGTT GATACGTTTG ACCAGTTGGC ACGCAAAACG
301 CCCGGCCTGC GCGTGTTGAG CAACGACGAC GGACGCTCTT CGGTTTACGC
351 GCGCGGTTAC GAATACAGCG AATACAACAT CGACGGCCTG CCCGCGCAGA
401 TGCAGAGTAT CAACGGCAGC CTGCCCAACC TGTTCCGCTT CGACCGCGTG
451 GAAGTGATGC GCGGGCCGAG CGGACTGTTT GACAGCAGCG GCGAGATGGG
501 CGGCATCGTG AATCTGGTGC GCAAACGCCC GACCAAAGCG TTCCAAGGTC
551 ATGCGGCGGC AGGGTTCGGT ACGCACAAAC AATATAAAGC CGAGGCGGAC
601 GTATCGGGCA GCCTCAATTC AGACGGCAGC GTGCGCGGCC GCGTGATGGC
651 GCAGACCGTC GCGCGCTCTC CGCGTCCCGC CGAGAAAAAC AACC GGCGCG
701 AAACCTTCTA CGCGGCGGCG GATTGGGACA TCAACCCCGA TACGTTTTTG
751 GGCGCGGGCT ATCTTTACCA GCAACGCCGC CTCGCGCCGT ACAACGGCCT
801 GCCTGCCGAT GCCAATAACA AATTACCGTC CCTGCCGCAA CACGTATTTG
851 TCGGCGCGGA TTGGAACAAA TTAAAATGC ACAGCCACGA CGTGTTCCGC
901 GATTGAAAC ATTACTTCGG CAACGGCGGC TACGGCAAAG TCGGTATGCG
951 CTATTCCGAT CGGAAAGCCG ATTCCAATTA TACGTTTGGG GGCAGCAAAAC
1001 TCAACAATAC CGGACAAGCC GACGTAGCGG GTTTGGGTAC GGACATTAAA
1051 CAAAAAGCCT TTGCGGTTGA CGCAAGTTAC AGCCGTCCTG TTGCCTTGGG
1101 CAACACCGCC AACGAATTTG TGATTGGTGC AGACTACAAC CGCTTGCCGA
1151 GTACTAATGA ACAAGGGCGT TCGACTTTGT CAAAAAGCGT CGCTTTAGAT
1201 GGTTCCTCGC CTTTGCCTTA TAACGGCATA CTTCAGAACG CCCGCGCCGG
1251 AAACAAAGGT TTCAATCACT CCGTTACCGA AGAAACCTC GACGAAACCG
1301 GTTTGTATGC CAAGACGGTG TTCCGTCTC TGGAAGGTTT GTCGTTGATT
1351 GCAGGCGGAC GTGTAGGACA TCACAAAATC GAGTCGGGCG ACGGCAAAAC
1401 CCTGCATAAA GCTTCGAAAA CCAAATTTAC AAGCTACGCC GGCGCGGTTT
1451 ACGTATAGA CGGCAGCAAC AGCCTGTACG CTTCCGCCTC CCAACTTAC
1501 ACACCGCAA CCAGCATCGG CACCGACGGC AAGCTGCTCA AACC GCGCGA
1551 AGGCAACCAG TTTGAAATCG GCTACAAAGG CAGCTACATG GACGACCGCC
1601 TCAATACCCG GGTTCCTGTT TACCGCATGA AGGATAAAAA CGCCGCGCGA
1651 CCGCTGGACT CAAACAACAA AAAAAACCGT TACGCCGCAT TGGGCAAACG
1701 CGTGATGGAA GGTGTTGAGA CCGAAATCAG CGGCGCGATG ACACCGAAAT
1751 GGCAATCCA TGCAGGTTAC AGCTACCTGC ACAGCCAAAT CAAAACCGCC
1801 TCCAATTGCG GCGACGAAGG CATCTTCCTG CTGATGCCCA AACACAGCGC
1851 AAACCTGTGG ACGACTTACC AAGTTACGTC CGGGCTGACC ATCGGCGGCG
1901 GCGTGAACGC GATGAGCGGC ATTACTTCAT CTGCAGGGAT ACATGCAGGC
1951 GGTATGCCA CGTTCGATGC GATGGCGGCA TACCGCTTCA CGCCCAAAC
2001 GAAGCTGCAA ATCAACGCCG ACAACATCTT CAACCGCCAT TACTACGCCC
2051 GCGTCGGCAG CGAGAGCACC TTAAACATTC CCGTTCGGA GCGCAGCCTG
2101 ACGGCAAACC TCGGTTACAG TTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2606; ORF 760>:

```
m760.pep
1   MGQFMSVFRI NMTAATVLAA LSSSVFAAQT EGLETVHIKQ QRSYNAIATE
51  KNGDYSSFAA TVGTKIPASL REIPQSVSII TNQQVKDRNV DTFDQLARKT
101 PGLRVLNSDD GRSSVYARGY EYSEYNIDGL PAQMOSINGT LPNLFADFDRV
151 EVMRGPSGLF DSSGEMGGIV NLVRKRPTKA FQGHAAAGFG THKQYKAEAD
201 VSGSLNSDGS VRGRVMAQTV GASPRPAEKN NRRETFYAAA DWDINPDTVL
251 GAGYLYQQR LOPYNGLPAD ANNKLPSLPQ HVFVGADWNK FKMHSHDVFA
301 DLKHYFGNGG YGKVGMRYSR RKADSNYTFA GSKLNNTGQA DVAGLGTDIK
351 QKAFAYVDASY SRPFALGNTA NEFVIGADYN RLRSTNEQGR STLSKSVALD
401 GFRALPYNGI LQNRAGNKG FNHSVTEENL DETGLYAKTV FRPLEGLSLI
451 AGGRVGHKKI ESGDGKTLHK ASKTKFTSYA GAVYDIDGSN SLYASASQLY
501 TPQTSIGTDG KLLKPREGNQ FEIGYKGSYM DDRLNTRVSF YRMKDKNAAA
551 PLDSNNKKTR YAALGKRVME GVETEISGAM TPKWQIHAGY SYLHSQIKTA
601 SNSRDEGIFL LMPKHSANLW TTYQVTSGLT IGGGVNAMSG ITSSAGIHAG
651 GYATFDAMAA YRFTPCLKLQ INADNIFNRH YYARVGSEST FNIPGSERSL
701 TANLRYSF*
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1236

m760 / g760 91.6% identity in 154 aa overlap

	530	540	550	560	570	580
m760.pep	YKGSYMDRLNTRV	SFYRMKDKNAA	PLDSNNKKTRYA	ALGKRVMEGVETE	ISGAMTPKW	
				:		
g760				NNRNTRYAALGKRV	MEGVETEISGAIT	PKW
				10	20	30

	590	600	610	620	630	640
m760.pep	QIHAGYSYLHSQIK	TASNSRDEGIFLL	MPKHSANLWTTYQ	VTSGLTIGGGVNAM	SGITSS	
g760	QIHAGYSYLHSQIK	TAAANPRDDGIFLL	VPKHSANLWTTYQ	VTPLTVGGGVNAM	SGITSS	
	40	50	60	70	80	90

	650	660	670	680	690	700
m760.pep	AGIHAGGYATFDAMA	AYRFTPKLKLQIN	ADNIFNRHYARVG	SESTFNI	PGSERSLTANL	
g760	AGMHAGGYATFDAMA	AYRFTPKLKLQIN	ADNIFNRHYARVG	GTNTFNI	PGSERSLTANL	
	100	110	120	130	140	150

	709
m760.pep	RYSFX
g760	RYSFX

g761.seq not found yet

g761.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2607>:

m761.seq

1	ATGAAAATAT	CATTTCATTT	AGCTTTATTA	CCCACGCTGA	TTATTGCTTC
51	CTTCCCTGTT	GCTGCCGCCG	ATACGCAGGA	CAATGGTGAA	CATTACACCG
101	CCACTCTGCC	CACCGTTTCC	GTGGTCGGAC	AGTCCGACAC	CAGCGTACTC
151	AAAGGCTACA	TCAACTACGA	CGAAGCCGCC	GTTACCCGCA	ACGGACAGCT
201	CATCAAAGAA	ACGCCGAAA	CCATCGATAC	GCTCAATATC	CAGAAAAACA
251	AAAATTACGG	TACGAACGAT	TTGAGTTCCA	TCCTCGAAGG	CAATGCCGGC
301	ATCGACGCTG	CCTACGATAT	GCGCGGTGAA	AGCATTTTCC	TGCGCGGTTT
351	TCAAGCCGAC	GCATCCGATA	TTTACCGCGA	CGGCGTGC GC	GAAAGCGGAC
401	AAGTGCGCCG	CAGTACTGCC	AACATCGAGC	GCGTGGAAAT	CCTGAAAGGC
451	CCGTCTTCCG	TGCTTTACGG	CCGCACCAAC	GGCGGCGGCG	TCATCAACAT
501	GGTCAGCAAA	TACGCCAACT	TCAAACAAAG	CCGCAACATC	GGAGCGGTTT
551	ACGGCTCATG	GGCAAACCGC	AGCCTGAATA	TGGACATTAA	CGAAGTGCTG
601	AACAAAAACG	TCGCCATCCG	TCTCACCGGC	GAAGTCGGGC	GCGCCAATT C
651	GTTCCGCAGC	GGCATAGACA	GCAAAAATGT	CATGGTTTCG	CCCAGCATTA
701	CCGTCAAAC T	CGACAACGGC	TTGAAGTGGA	CGGGGCAATA	CACCTACGAC
751	AATGTGGAGC	GCACGCCC GA	CCGCAGTCCG	ACCAAGTCCG	TGTACGACCG
801	CTTCGGACTG	CCTTACCGCA	TGGGGTTCGC	CCACCGGAAC	GATTTTGTCA
851	AAGACAAGCT	GCAAGTTTGG	CGTTCCGACC	TTGAATACGC	CTTCAACGAC
901	AAATGGCGTG	CCCAATGGCA	GCTCGCCAC	CGCACGGCGG	CGCAGGATTT
951	TGATCATTT C	TATGCAGGCA	GCGAAAATGG	CAACTTAATC	AAACGTAAC T
1001	ACGCCTGGCA	GCAGACCGAC	AACAAAACCC	TGTCGTCCAA	CTTAACGCTC
1051	AACGGCGACT	ACACCATCGG	CCGTTT TGAA	AACCACCTGA	CCGTAGGCAT
1101	GGATTACAGC	CGCGAACACC	GCAACCCGAC	ATTGGGTTTC	AGCAGCGCCT
1151	TTTCCGCCTC	CATCAACCCC	TACGACCGCG	CAAGCTGGCC	GGCTTCGGGC
1201	AGATTGCAGC	CTATTCTGAC	CCAAAACCGC	CACAAAGCCG	ACTCCTACGG
1251	CATCTTTGTG	CAAAACATCT	TCTCCGCCAC	GCCCGATT TG	AAATTCGTCC
1301	TCGGCGGCCG	TTACGACAAA	TACACCTTTA	ATTCCGAAAA	CAAAC TACC
1351	GGCAGCAGCC	GCCAATACAG	CGGACACTCG	TTCAGCCCCA	ACATCGGCGC
1401	AGTGTGGAAC	ATCAATCCCG	TCCACACACT	TTACGCCTCG	TATAACAAAG
1451	GCTTCGCGCC	TTATGGCGGA	CGCGGCGGCT	ATTTGAGCAT	CGATACGTTG
1501	TCTTCCGCGG	TGTTCAACGC	CGACCCCGAG	TACACCCGCC	AATACGAAAC
1551	CGGCGTGAAA	AGCAGTTGGC	TGGACGACCG	CCTCAGCACT	ACGTTGTCTG
1601	CCTACCAAAT	CGAACGCTTC	AATATCCGCT	ACCGCCCCGA	TCCAAAAAAC
1651	AACCCTTATA	TTTATGCGGT	TAGCGGCAAA	CACCGTTTCG	GCGGCGTGGA

1237

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1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT
1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAATACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCGACCG AAAACCTCTA CGGCGAAATC GGCGTAACCG
1901 GTACAGGCAA ACGCTACGGT TACAATCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTAAACGTT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGTAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2608; ORF 761>:

```

m761.pep
  1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
 51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVS K YANFKQSRNI GAVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVYDRFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQT D NKTLSNLT L
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
401 RLQPIILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPAPYG RGGYLSIDTL
501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN
551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGS LGVMQA KVVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT
651 LPGFARVDAM LGWNHKNVNV TFAAANLLNQ KYWRSDSMPG NPRGYTARVN
701 YRF*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2609>:

```

a761.seq
  1 ATGAAAATAT CATTTCATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC
 51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCGCA ACGGACAGCT
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
251 AAAATTACGG CACGAACGAT TTGAGTCCA TCCTCGAAGG CAATGCCGGC
301 ATCGACGCCG CCTACGATAT GCGCGCGCAA AGCATTTCCT TGCGCGGCTT
351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC GAAAGCGGGC
401 AGGTGCGCCG TAGCACCGCC AACATCGAGC GCGTGGAAAT CCTGAAAGGT
451 CCGTCTCCG TGCTTTATGG GCGTACCAAC GGCGGCGGTG TCATCAACAT
501 GGTACGAAA TACGCCAAT TCAAACAAAG CCGTAATATC GGTACGGTTT
551 ATGGTTCGTG GGCAAACCGC AGCCTGAATA TGGACATCAA CGAAGTGCTG
601 AACAAAAACG TCGCCATCCG TCTACCGGC GAAGTCGGGC GCGCCAATTC
651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA
701 CCGTCAAATC CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC
751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG
801 CTTCCGACTG CTTACCGCA TGGGGTTTCG CCACCGGAAC GATTTTGTCA
851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC
901 AAATGGCGTG CCCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATTT
951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAATC
1001 ACGCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCAA CTTAACGCTC
1051 AACGGCGACT ACACCATCGG CCGTTTGTGA AACCACCTGA CCGTAGGCAT
1101 GGATTACAGC CGGAACACC GCAACCGAC ATTGGGTTTC AGCAGCGCCT
1151 TTTCCGCCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC
1201 AGATTGCAGC CTATTCTGAC CAAAACCGC CACAAAGCCG ACTCCTACGG
1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCCGATTG AAATTCGTCC
1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCGGAAAA CAACTCACC
1351 GGCAGCAGC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC
1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAACAAAG
1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CGATACGTTG
1501 TCTTCGCGCG GTTCAACGC CGACCCGAG TACACCCGCC AATACGAAAC
1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG
1601 CTAACCAAT CGAACGCTT AATATCCGCT ACCGCCCGCA TCCAAAAAAC
1651 AACCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCG GCGGCGTGA
1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

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1238

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1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTGAA TAACACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGCGTAACCG
1901 GTACAGGCAA ACGCTACGGT TACGACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC
2051 GTTCGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2610; ORF 761.a>:

```

a761.pep
1  MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
51  KGYINYDEAA VTRNGQLIKE TPQTIOTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVS K YANFKQSRNI GTVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNMVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYRFL PYRMGFHRN DFVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAQQTD NKTLSNLT
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSASFASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KEVLGGRYDK YTFENSENKL
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFAFYGG RGGYLSIDTL
501 SSAFVNADPE YTRQYETGVK SSWLDRLST TLSAYQIERF NIRYRPDPKN
551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRSLGVMQA KVVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YDSRNKEVTT
651 LPGFARVDAM LGWNHKNVNV TFAAANLFNQ KYWRSDSMPG NPRGYTARVN
701 YRF*

```

m761 / a761 99.6% identity in 703 aa overlap

	10	20	30	40	50	60
m761.pep	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA					
a761	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m761.pep	VTRNGQLIKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
a761	VTRNGQLIKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m761.pep	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRNNGGGVINMVS K YANFKQSRNI					
a761	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRNNGGGVINMVS K YANFKQSRNI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m761.pep	GAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNMVSPSITVKLDNG					
a761	GTVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNMVSPSITVKLDNG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m761.pep	LKWTGQYTYDNVERTPDRSP TKSVDYRFLPYRMGFHRNDFVKDKLQVW RSDLEYAFND					
a761	LKWTGQYTYDNVERTPDRSP TKSVDYRFLPYRMGFHRNDFVKDKLQVW RSDLEYAFND					
	250	260	270	280	290	300
	310	320	330	340	350	360
m761.pep	KWRAQWQLAHRTAAQDFDHFYAGSENGNLIK RNYAQQTDNKTLSNLT L NGDYTIGRFE					
a761	KWRAQWQLAHRTAAQDFDHFYAGSENGNLIK RNYAQQTDNKTLSNLT L NGDYTIGRFE					
	310	320	330	340	350	360
	370	380	390	400	410	420

1239

```

m761.pep      NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRQLQPILTQNRHKADSYGIFV
               |||||
a761          NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRQLQPILTQNRHKADSYGIFV
               370      380      390      400      410      420

               430      440      450      460      470      480
m761.pep      QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
               |||||
a761          QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
               430      440      450      460      470      480

               490      500      510      520      530      540
m761.pep      YNKGFPYGGRRGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDDRLSTTLSAYQIERF
               |||||
a761          YNKGFPYGGRRGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDDRLSTTLSAYQIERF
               490      500      510      520      530      540

               550      560      570      580      590      600
m761.pep      NIRYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
               |||||
a761          NIRYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
               550      560      570      580      590      600

               610      620      630      640      650      660
m761.pep      RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYNSRNKEVTTLPGFARVDAM
               |||||
a761          RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYDSRNKEVTTLPGFARVDAM
               610      620      630      640      650      660

               670      680      690      700
m761.pep      LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
               |||||
a761          LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
               670      680      690      700

```

g762.seq Not yet found

g762.pep Not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2611>:

```

m762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTTTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT
301 AGTTTTATGG ACTTTTACTT TTTTTCATA TATTCAGATA ACCTTAGCTA
351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTCTCT
401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2612; ORF 762>:

```

m762.pep
1  MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT
51  LFLLFIFNEF TKSIYMAIIY PILYFFTIKK YYPYSRKVII LLSLALSIYF
101 SFMDYFFFSI YSDNLSYETE PLHLYIPIII NFFSLLVSNF ILSFINK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2613>:

```

a762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTTTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT

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1240

301 AGTTTTATGG ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA  
 351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTTTCT  
 401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

This corresponds to the amino acid sequence <SEQ ID 2614; ORF 762.a>:

a762.pep  
 1 MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT  
 51 LFLLFIFNFV TKSIYMAIIY PILYFFTICK YYPYSRKVII LLSLALSIYF  
 101 SFMDFYFFSI YSDNLSYETE PLHLYIPIII NFFSLLVSNF ILSFINK\*

m762 / a762 100.0% identity in 147 aa overlap

	10	20	30	40	50	60
m762.pep	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
a762	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m762.pep	TKSIYMAIIYPILYFFTICKYYYPYSRKVIIILSLALSIYFSFMDFYFFSIYSDNLSYETE					
a762	TKSIYMAIIYPILYFFTICKYYYPYSRKVIIILSLALSIYFSFMDFYFFSIYSDNLSYETE					
	70	80	90	100	110	120
	130	140				
m762.pep	PLHLYIPIIINFFSLLVSNFILSFINKX					
a762	PLHLYIPIIINFFSLLVSNFILSFINKX					
	130	140				

g763.seq not yet found

g763.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2615>:

m763.seq  
 1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG  
 51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT  
 101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA  
 151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC  
 201 GGCGCAGCAA CATTCCGCTG ATTTTCAAGC GTCCCATAC CAGCGTGATG  
 251 CAGTGCAGCG ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA  
 301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG  
 351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG  
 401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA  
 451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG  
 501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG  
 551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT  
 601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA  
 651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG  
 701 AAAACCAATT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC  
 751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA  
 801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC  
 851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA  
 901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA  
 951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG  
 1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA  
 1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC  
 1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT  
 1151 ATACCGAAAG CCGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT  
 1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA  
 1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC  
 1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT  
 1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA  
 1401 ATAA

This corresponds to the amino acid sequence <SEQ ID 2616; ORF 763>:

**m763.pep**

```

1  MTLNLNMIMO DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNLYT SSAQNNDYHY RGKGMVGVQ LNLPLYTGGE
351 LSGKIHAEAE QYGAAEAQLT ATERHIKLA RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2617>:

**a763.seq**

```

1  ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
51  CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGCGCAGCAA CATTCCGGCTG ATTTTCAAGC GTCCCATTA CAGCGTGATG
251 CAGTGCAGCG ACGGCAACAA CAAGCCAAGG CCGATTTCCT TCCCCATGTA
301 TCCGCCAATG CCAGTACCA GCGCCAGCCG CCATCGATT CTTCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAACCTTA TTTGACCTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
551 AAAAGAGAGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA
651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
701 AAAACAGTGT GAACGACTAC ACCGGCCTGG ACAGCAAACA AATCGAGGCC
751 ATAGATACCG CCAACCTGTT GGCACGTAT CTGCCCAAGC TGGAACGTTA
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
951 CCTTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC
1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT
1201 TTGGAAGACA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
1251 CGGCATCCGC AACCGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCC
1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAACCG TATTTGCGGA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2618; ORF 763.a>:

**a763.pep**

```

1  MTLNLNMIMO DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNLYT SSAQNNDYHY RGKGMVGVQ LNLPLYTGGE
351 LSGKIHAEAE QYGAAEAQLT ATERHIKLA RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

m763 / a763 99.8% identity in 467 aa overlap

```

          10      20      30      40      50      60
m763.pep  MTLNLNMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
          |||
a763      MTLNLNMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
          10      20      30      40      50      60

```

1242

m763.pep	70	80	90	100	110	120
	LPEAWRAAQHSAD	FQASHYQRDAV	RRARQQQAKAA	FLPHV	SANASYQRQPP	SISSTRETQ
a763	LPEAWRAAQHSAD	FQASHYQRDAV	RRARQQQAKAA	FLPHV	SANASYQRQPP	SISSTRETQ
	70	80	90	100	110	120
m763.pep	130	140	150	160	170	180
	GWSVQVGQTLF	DAAKFAQYRQSR	FDTQAAEQRFDA	AREELLKVAES	YFNVLLSRDT	VAA
a763	GWSVQVGQTLF	DAAKFAQYRQSR	FDTQAAEQRFDA	AREELLKVAES	YFNVLLSRDT	VAA
	130	140	150	160	170	180
m763.pep	190	200	210	220	230	240
	HAAEKEAYAQQV	RQAQALFNKGA	ATALDIHEAKA	GYDNALAQEI	AVLAEKQTYE	NQNDY
a763	HAAEKEAYAQQV	RQAQALFNKGA	ATALDIHEAKA	GYDNALAQEI	AVLAEKQTYE	NQNDY
	190	200	210	220	230	240
m763.pep	250	260	270	280	290	300
	TDLDSKQIEAID	TANLLARYLPK	LERYSLDEWQRI	ALSNNHEYRMQ	QALQSSGQAL	RRAA
a763	TGLDSKQIEAID	TANLLARYLPK	LERYSLDEWQRI	ALSNNHEYRMQ	QALQSSGQAL	RRAA
	250	260	270	280	290	300
m763.pep	310	320	330	340	350	360
	QNSRYPTVSAHV	GYQNNLYTSSA	QNNNDYHYRGK	GMSVGVQLNL	PLYTGGELSG	KIHEAEA
a763	QNSRYPTVSAHV	GYQNNLYTSSA	QNNNDYHYRGK	GMSVGVQLNL	PLYTGGELSG	KIHEAEA
	310	320	330	340	350	360
m763.pep	370	380	390	400	410	420
	QYGAAEAQLTAT	ERHIKLAVRQAY	TESGAARYQIMA	QERVLESSRL	KLKSTETGQQ	YGIR
a763	QYGAAEAQLTAT	ERHIKLAVRQAY	TESGAARYQIMA	QERVLESSRL	KLKSTETGQQ	YGIR
	370	380	390	400	410	420
m763.pep	430	440	450	460		
	NRLEVIRARQEVA	QAEQKLAQARY	KFMLAYLRLVK	ESGLGLETVF	AE	
a763	NRLEVIRARQEVA	QAEQKLAQARY	KFMLAYLRLVK	ESGLGLETVF	AE	
	430	440	450	460		

1243

g764.seq not found yet

g764.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2619>:

```
m764.seq
1  ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCTCGATACA TTA
```

51	GCGCAATGTT	TGGGCGGTGC	GCGACCAAGT	GAAACCGCCC	AAACGCACGG
101	CGGAAGAACA	GGCGTTTTTG	CCCGCGCATT	TGGAACGTAC	CGATACGCCG
151	GTCTCTGCCG	CTCCGAAATG	GGCGGCGCGT	TTTATTATGG	CGTTTGC
201	TTTGGCTTTG	TTGTGGTCCT	GGTTCGGCAA	AATCGATATT	GTGGCGGCGG
251	CTTCGGGCAA	AACGGTGTCT	GGCGGGCGCA	GCAAAACCAT	CCAGCCGCTG
301	GAAACGGCGG	TGGTTAAGGC	GGTACATGTG	CGCGACGGGC	AGCATGTGAA
351	ACAGGGAGAA	ACGCTGGCGG	AACTGGAGGC	TGTGGGAACA	GACAGCGATG
401	TGGTGCAGTC	GGAGCAGGCT	TTGCAGGCTG	CCCAATTGTC	CAAACGCGT
451	TATGAAGCGG	TATTGGCGGC	ATTGGAAAGC	CGTACCGTGC	CGCATATCGA
501	TATGGCGCAA	GCACGGTCTT	TAGGTCTCTC	CGATGCCGAT	GTGCAATCGG
551	CGCAGGTGTT	GGCGCAGCAC	CAGTATCAGG	CATGGGCGGC	GCAGGATGCG
601	CAATTGCAGT	CGGCTTTGCG	CGGCCATCAG	GCGGAATTGC	AGTCGGCCAA
651	GGCGCAGGAG	CAGAAGCTGG	TTTCGGTGGG	GGCGATCGAG	CAGCAGAAAA
701	CAGCAGACTA	CCGCCGTTTG	CGGGCCGACA	ATTTTATTTT	GGAACATGCG
751	TTTTTGGAGC	AGCAGAGCAA	ATCGGTCAGC	AATTGGAACG	ATTTGGAAG
801	TACGCGCGGT	CAGATGAGGC	AGATTGAGGC	GGCCATTGCA	CAGGCGGAGC
851	AGAATCGGGT	GCTGAATACG	CAGAACCTGA	AACGCGATAC	GCTGGATGCG
901	CTGCGCCAGG	CAAACGAACA	GATTGACCAA	TACCGCGGCC	AAACGGATAA
951	GGCAAAGCAG	CGGCAGCAGC	TGATGACAAT	ACAGTCGCCT	GCGGACGGCA
1001	CGGTGCAGGA	ATTGGCTACC	TATACGGTGG	GCGGTGTGGT	GCAGGCTGCC
1051	CAAAAAATGA	TGGTGATTGC	GCCCGATGAC	GACAAAATGG	ACGTGGAAGT
1101	TTTGGTATTG	AACAAAGACA	TCGGTTTTGT	GGAACAGGGA	CAGGATGCGG
1151	TGGTGAAGAT	TGAGAGCTTT	CCCTATACGC	GCTACGGTTA	TCTGACGGGC
1201	AAGGTGAAAA	GTGTCAGCCA	TGATGCGGTA	AGCCACGAAC	AGTTGGGCTT
1251	GGTTTATACG	GCGGTGGTGT	CGCTGGACAA	ACATACCTTG	AATATTGACG
1301	GCAAAGCAGT	GAATCTGACG	GCGGGCATGA	ATGTCACGGC	GGAGATTAAA
1351	ACGGGTAAAC	GGCGGGTGCT	GGATTATCTG	TTAAGCCCGC	TGCAAACCAA
1401	ATTGGACGAA	AGCTTTAGGG	AGCGATAG		

This corresponds to the amino acid sequence <SEQ ID 2620; ORF 764>:

```
m764.pep
1  MFFSALKSFL SRYITVWRNV WAVRDQLKPP KRTAEQAF LPAHLELDTPT
```

51	VSAAPKWAAR	FIMAFALLAL	LWSWFGKIDI	VAAASGKTVS	GGRSKTIQPL
101	ETAVVKAVHV	RDGQHVQGE	TLAELEAVGT	DSDVVQSEQA	LQAAQLSKLR
151	YEAVLAALES	RTVPHIDMAQ	ARSLGLSDAD	VQSAQVLAQH	QYQAWAAQDA
201	QLQSALRGHQ	AELQSAKAQE	QKLVSVGAIE	QKKTADYRRL	RADNFISEHA
251	FLEQQSKSVS	NWNDLESTRG	QMRQIQAAIA	QAEQNRVLNT	QNLKRDTLDA
301	LRQANEQIDQ	YRGQTDKAKQ	RQQLMTIQSP	ADGTVQELAT	YTVGGVVQAA
351	QKMMVIAPDD	DKMDVEVLVL	NKDIGFVEQG	QDAVKIESF	PYTRYGYLTG
401	KVKSVSHDAV	SHEQLGLVYT	AVVSLDKHTL	NIDGKAVNLT	AGMNVTAIEK
451	TGKRRVLDYL	LSPLQTKLDE	SFRER*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2621>:

```
a764.seq (partial)
1  ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCCCGCTACA TTACCGTATG
```

51	GCGCAATGTT	TGGGCGGTGC	GCGACCAAGT	GGAACCGCCC	AAACGCACGG
101	CGGAAGAACA	GGCGTTTTTG	CCCGCGCATT	TGGAACGTAC	CGATACGCCG
151	GTCTCTGCCG	CTCCGAAATG	GGCGGCGCGT	TTTATTATGG	CGTTTGC
201	TTTGGCTTTG	TTGTGGTCCT	GGTTCGGCAA	AATCGATATT	GTGGCGGCGG
251	CTTCGGGCAA	AACGGTGTCT	GGCGGGCGCA	GCAAAACCAT	CCAGCCGCTG
301	GAAACGGTGG	TGGTTAAGGC	GGTACATGTG	CGCGACGGGC	AGCATGTGAA
351	ACAGGGAGAA	ACGCTGGCGG	AACTGGAGGC	TGTGGGAACA	GACAGCGATG
401	TGGTGCAGTC	GGAGCAGGCT	TTGCAGGCTG	CCCAATTGTC	CAAACGCGT
451	TATGAAGCGG	TATTGGCGGC	ATTGGAAAGC	CGTACCGTGC	CGCATATCGA
501	TATGGCGCAA	GCACGGTCTT	TAGGTCTCTC	CGATGCCGAT	GTGCAATCGG
551	CGCAGGTGTT	GGCGCAGCAC	CAGTATCAGG	CATGGGCGGC	GCAGGATGCG
601	CAATTGCAGT	CGGCTTTGCG	CGGCCATCAG	GCGGAATTGC	AGTCGGCCAA
651	GGCGCAGGAG	CAGAAGCTGG	TTTCGGTGGG	GGCGATCGAG	CAGCAGAAAA

1244

```

701 CAGCAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAAG
801 TACGCGCGGT CAGATGAGGC AGATTGAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCCACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGGTTGC GCCCGATGAC GACAAAATGG ACGTGGAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGTTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAA

```

This corresponds to the amino acid sequence <SEQ ID 2622; ORF 764.a>:

**a764.pep (partial)**

```

1 MFFSALKSFL SRYITVWRNV WAVRDQLEPP KRTAEQAFLE PAHLELTDTP
51 VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETVVVKAVHV RDGQHVQKQE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSAALRGHQ AELQSAKAQE QKLVSVAIE QQKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVDHDAV SHEQLGLVYT AVVSLDKHTL NIDGK

```

**m764 / a764 99.3% identity in 435 aa overlap**

m764.pep	10	20	30	40	50	60
	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAFLEPAHLELTDTPVSAAPKWAAR					
a764	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAFLEPAHLELTDTPVSAAPKWAAR					
	10	20	30	40	50	60
m764.pep	70	80	90	100	110	120
	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVVKAVHVRDQHVQKQE					
a764	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVVKAVHVRDQHVQKQE					
	70	80	90	100	110	120
m764.pep	130	140	150	160	170	180
	TLAELEAVGTDSDDVVQSEQAALQAAQLSKRLRYEAVLAALESRTVPHIDMAQARSLGLSDAD					
a764	TLAELEAVGTDSDDVVQSEQAALQAAQLSKRLRYEAVLAALESRTVPHIDMAQARSLGLSDAD					
	130	140	150	160	170	180
m764.pep	190	200	210	220	230	240
	VQSAQVLAQHQQYQAWAAQDAQLQSAALRGHQAEQSAKAQEQKLVSVAIEQQKTADYRRL					
a764	VQSAQVLAQHQQYQAWAAQDAQLQSAALRGHQAEQSAKAQEQKLVSVAIEQQKTADYRRL					
	190	200	210	220	230	240
m764.pep	250	260	270	280	290	300
	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIQAAIAQAEQNRVLNTQNLKRDTLDA					
a764	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIQAAIAQAEQNRVLNTQNLKRDTLDA					
	250	260	270	280	290	300
m764.pep	310	320	330	340	350	360
	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVIAPDD					
a764	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVAPDD					
	310	320	330	340	350	360
m764.pep	370	380	390	400	410	420
	DKMDVEVLVLNKDIGFVEQGQDAVVKIESFPYTRYGYLTGKVKSVDHDAVSHEQLGLVYT					

1245

```

a764      |||||
          DKMDVEVLVLNKDIGFVEQGDVAVVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT
          370      380      390      400      410      420

          430      440      450      460      470
m764.pep  AVVSLDKHTLNIDGKAVNLTAGMNVTAETIKTGKRRVLDYLLSPLQTKLDESFRERX
          |||||
a764      AVVSLDKHTLNIDGK
          430

```

g765.seq not yet found

g765.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2623>:

```

m765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTTG GATTCAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCCTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGACGGG TCGTTGCTGA TGTTACGGT CATGATTCCG CCACAATGAA
201 CGCTGCGGGT GCCAAAGATT ATATGAAAAC GGTGAGTTA AACAAAGTCTG
251 CCGGCAATGT CGATAACCACA TCCAGAACAG CCCGCAGGGT GCAGGCAGTA
301 TTTCGACGTA TGCTGCCTTA TGCCGATGCG GCAAATAATA CCAGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAA CGATGAGCTG AACGCGTGGG
401 CAATGCCCGG TGGAAAAATG GCGTTTTATA CGGGGATAGT CGACAAACTC
451 AAGCTGACCG ATGACGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 CGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGCAA ATCTTGACCA
551 ATACGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAT
601 ACTAATCCGG AATTGGTTCGG ATTGGGTATG GATATTTTGG GGACGTACGG
651 TCTTACCTTG CCTTATAGCC GCAGCTTGGA AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCGGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAACACGAC CAAACCGGCT TTATTTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTTGCC GACCGTTATG CCGGTTTATG AGCAAAGTGT CAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGCGTTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2624; ORF 765&gt;:

```

m765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKYEI SFLPSFKRIL CLSAVISVLG
51  ACAVVADVYG HDSATMNAAA AKDYMKTVEL NKSAGNVDTT SRTARRVQAV
101 FRRLPYADA ANNTSHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDDEIAAI MGHEMTHALH EHGKKNVGOQ ILTNTAAQIG TQIILDKKPD
201 TNPELVGLGM DILGTYGLTL PYSRSLEEEA DEGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAITS THPTNNARIE NLKRLLPVLM PVYEQSVRNK
301 GRVNKKRRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2625>:

```

a765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTTG GATTCAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCCTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGACGGG TCGTTGCTGA TGTTACGGT CAGGATTCCG CCACAATGAA
201 TGCTGCGGGT GCCGAAGATT ATATGAAAAC GGTGAGTTG AACAAAGTCTG
251 CCGGCAATGT CGATACTACA TCCAAAACAG CCCGTAGGGT GCAGGCAGTA
301 TTTCGACGTA TGTTGCCTTA TGCCGATGCG GCAAATAATA CCGGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAA CGATGAGCTG AACGCGTGGG
401 CAATGCCCGG CGGAAAAATG GCGTTTTATA CGGGGATAGT CGATAAACTT
451 AAGCTGACCG ATGGCGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 TGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGAAA ATCTTGACTA
551 ATATGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAC
601 ACTAATCCGG AATTGGTTCGG ATTGGGTATG GATATTTTGG GGATGTACGG
651 CATTACCTTG CCTTATAGCC GCAGCTTGGA AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCAGC CGTGTACAG
751 GTTTGGGAAA AAATGAATCA GGAACACGAC CAAACCGGCT TTATTTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTTGCC GACCGTTATG CCGGTTTATG AGCACAGTGT TAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGCGTTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2626; ORF 765.a&gt;:

```

a765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKYEI SFLPSFKRIL CLSAVISVLG

```



1246

```

51  ACTVVADVYG QDSATMNAAA AEDYMKTVEL NKSAGNVDTT SKTARRVQAV
101 FRRMLPYADA ANNTGHHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTGGEIAAI MGHMETHALH EHGKKNVGOK ILTNMAAQIG TQIILDKKPD
201 TNPELVGLGM DILGMYGITL PYSRSLSEEA DEGGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAITs THPTNNARIE NLKRLLPVTM PVYEHsVRNK
301 GRVNKNRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 765 shows 96.18% identity over a 309 aa overlap with a predicted ORF (ORF 765) from *N. meningitidis*:

m765 / a765 96.1% identity in 309 aa overlap

```

              10      20      30      40      50      60
m765.pep      MLRCRPKSVLDSGIFLKFNFLRSKPKYEISFLPSFKRILCLSAVISVLGACAVVADVYG
              |||||
a765           MLRCRPKSVLDSGIFLKFNFLRSKPKYEISFLPSFKRILCLSAVISVLGACTVVADVYG
              10      20      30      40      50      60

              70      80      90      100     110     120
m765.pep      HDSATMNAAAAKDYMKTVELNKSAGNVDTTsRTARRVQAVFRRMLPYADAANNTSHKFDW
              :|||
a765           QDSATMNAAAAEDYMKTVELNKSAGNVDTTsKTARRVQAVFRRMLPYADAANNTGHKFDW
              70      80      90      100     110     120

              130     140     150     160     170     180
m765.pep      KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDDEIAAIMGHEMTHALHEHGKNKVGQQ
              |||||
a765           KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDGEIAAIMGHEMTHALHEHGKNKVGQK
              130     140     150     160     170     180

              190     200     210     220     230     240
m765.pep      ILTNAAQIGTQIILDKKPDTNPVLVGLGMDILGTyGLTLPSYRSLEEEADEGGMMLMAQ
              |||
a765           ILTNAAQIGTQIILDKKPDTNPVLVGLGMDILGMYGITLPSYRSLEEEADEGGMMLMAQ
              190     200     210     220     230     240

              250     260     270     280     290     300
m765.pep      AGYHPAAAVRVWEKMNQENDQNGFIYAITsTHPTNNARIENLKRLLPVTMPVYEQSVRNK
              |||||
a765           AGYHPAAAVRVWEKMNQENDQNGFIYAITsTHPTNNARIENLKRLLPVTMPVYEHsVRNK
              250     260     270     280     290     300

              310
m765.pep      GRVNKKRRRX
              |||||
a765           GRVNKNRRRX
              310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2627>:

g767.seq

```

1  ATGAAGTTTA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTTGTCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCTCTCA AGAACAGCCG GGAAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTTTGGCG TACATTGCCA TCATTTTCGAT CCTTTGTAT TGAAACTGGG
201 CAAGGCATTG CCGTCTGATA CTTATCTGCG GACGGAGCAC GTGGTCTGGC
251 GGCTTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCGGT CAAGCTGTCG
301 GGTTTGAAAT ATCAGGCAAA CTCTGCTGTG TTAAAGCAG TTACGAACA
351 AAAATCCGT TTGGAAAAACA GGGCTGTTCG CGGGAAATGG GCTTTATCTC
401 AAAAAGGTTT TGACGGCAAA AACTGATGC GCGCCTATGA TTCCCCGAA
451 GCTGCCGCCG TCGCATTAAA AATGCAGAAA CTGACGGAAC AATACGGTAT
501 TGACAGCACG CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGATGGCGGC GTTCATACGA TTAAAGAATT GGTGCCCCAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2628; ORF 767.ng>:

g767.pep

```

1  MKFKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIQEQP GKIEVLEFFG
51  YFCVHCHHFD PLLLLKGKAL PSDTYLRTEH VVWRPEMLGL ARMAAAVKLS

```

1247

101 GLKYQANS AV FKA VYE QKIR LENRAVAGKW ALSQKGF DKG KLMRAYDSPE  
 151 AAAVALKMQK LTEQY GIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK  
 201 VREERKRQTP AVQK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2629>:

m767.seq

```

1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCTCTCA AGAACAGTCG GGTAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTTCTGCG TACATTGCCA TCATTTTCGAT CCTTTGTTAT TGAAACTGGG
201 CAAGGCATTG CCGTCTGATG CCTATTTGAG GACGGAGCAC GTGGTCTGGC
251 AGCCTGAAAT GCTCGGTTTG GCTAGGATGG CGGCTGCCGT CAATTTGTCTG
301 GGTTTGAAAT ATCAGGCAAA CCCTGCTGTG TTAAAGCAG TTTACGAACA
351 AAAAATCCGC TTGAAAACA GGTCCGTTGC CGGAAATGG GCTTTGTCTC
401 AAAAAGGCTT TGACGGCAAA AACTGATGC GCGCCTATGA TTCCCCGAA
451 GCTGCCGCG CCGCATTAAA AATGCAGAAA CTGACGGAAC AATACCGCAT
501 CGACAGCAG CGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAACGGCTT TGACGGCGGC GTTCATACGA TTAAAGAATT GGTTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2630; ORF 767>:

m767.pep

```

1 MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQS GKIEVLEFFG
51 YFCVHCHHFD PLLKLGLKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVNLS
101 GLKYQANPAV FKA VYE QKIR LENRSVAGKW ALSQKGF DKG KLMRAYDSPE
151 AAAAALKMQK LTEQYRIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 767 shows 95.8% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. gonorrhoeae*

m767/g767 95.8% identity in 214 aa overlap

	10	20	30	40	50	60
g767.pep	MKFKHLLPLL SAVLSAQAYALTEGEDYLV LDKPIPQEQPGKIEVLEFFGYFCVHCHHFD					
m767	MKLKHLLPLL SAVLSAQAYALTEGEDYLV LDKPIPQEQSGKIEVLEFFGYFCVHCHHFD					
	10	20	30	40	50	60
g767.pep	PLLLKLGKALPSDYLRTHEV VVWRPEMLGLARMAAAVKLSGLKYQANS AVFKAVYE QKIR					
m767	PLLLKLGKALPSDYLRTHEV VVWQPEMLGLARMAAAVNLSGLKYQANPAV FKA VYE QKIR					
	70	80	90	100	110	120
g767.pep	LENRAVAGKW ALSQKGF DGGKLMRAYDSPE AAAVALKMQK LTEQY GIDST PTVIVGGKYR					
m767	LENRSVAGKW ALSQKGF DGGKLMRAYDSPE AAAAALKMQK LTEQY RIDST PTVIVGGKYR					
	130	140	150	160	170	180
g767.pep	VIFNNGFDGG VHTIKELVAK VREERKRQTP AVQKX					
m767	VIFNNGFDGG VHTIKELVAK VREERKRQTP AVQKX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2631>:

a767.seq

```

1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCTCTCA AAAACAGTCG GGCAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTTCTGCG TACATTGCCA TCATTTTCGAT CCTTTGTTAT TGAAATTGGG
201 CAAGGCATTG CCGTCTGATG CCTATTAAAG GACGGAGCAC GTGGTCTGGC
251 AGCCTGAAAT GCTCGGCTCTG GCAAGAAATGG CTGCTGCGGT CAAGCTGTCA
301 GGTTTGAAAT ATCAGGCAAA CCCTGCCGTG TTAAAGCAG TTTACGAACA
351 AAAAATCCGC TTGAAAACA GGTCCGTTGC CGAAAATGG GCTTTGTCTC
401 AAAAAGGCTT TGACGGCAAA AACTGATGC GCGCCTACGA CTCTCTGCG

```

1248

```

451 GCAGCGGCTG CTGCATCAAA AATGCAGCAA TTGACGGAAC AGTACCGCAT
501 CGACAGTACG CCGACCGTTG TCGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGACGGCGGT GTTCATACGA TTAAGAATT GGTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2632; ORF 767.a>:

```

a767.pep
  1 MKLKHLPLLL LSAVLSAQAY ALTEGEDYLV LDKPIPOKQS GKIEVLEFFG
  51 YFCVHCHHFD PLLKLKGKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVKLS
 101 GLKYQANPAV FKAUYEQKIR LENRSVAEKW ALSQKGFQDG KLMRAYDSPA
 151 AAAAASKMQQ LTEQYRIDST PTVVVGKYYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 767 shows 96.7% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. meningitidis*:

m767/a767 96.7% identity in 214 aa overlap

	10	20	30	40	50	60
a767.pep	MKLKHLPLLLSAVLSAQAYALTEGEDYLVLDKPIPOKQSGKIEVLEFFGYFCVHCHHFD					
m767	MKLKHLPLLLSAVLSAQAYALTEGEDYLVLDKPIPOEQSGKIEVLEFFGYFCVHCHHFD					
	10	20	30	40	50	60
	70	80	90	100	110	120
a767.pep	PLLLKLKGKALPSDAYLRTEHVWQPEMLGLARMAAAVKLSGLKYQANPAVFKAVYEKIR					
m767	PLLLKLKGKALPSDAYLRTEHVWQPEMLGLARMAAAVNLSGLKYQANPAVFKAVYEKIR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a767.pep	LENRSVAEKWALSQKGFQDGKLMRAYDSPAAAAASKMQQLTEQYRIDSTPTVVVGKYYR					
m767	LENRSVAGKWALSQKGFQDGKLMRAYDSPAAAAALKMQKLTEQYRIDSTPTVIVVGKYYR					
	130	140	150	160	170	180
	190	200	210			
a767.pep	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
m767	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2633>:

```

g768.seq
  1 ATGAATATCA AACAATTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
  51 TGCCACGCAG GCAGCCCGCG AAAAACCCTG ATCCGCGGCC CAAACCGCGC
 101 AACATTGATC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
 151 GGTCAATTGC ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
 201 CATATACGAA GCCGCGCCCG ACAAAGACAC GCCGGTCAAC CTCTACTGCC
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
 301 TATACAAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAGG
 351 GATGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2634; ORF 768.ng>:

```

g768.pep
  1 MNIKQLITAA LIASAAFATQ AAPQKPVSAQ QTAQHSVWI DVRSEQEFSE
  51 GHLHNAVNIQ VDQIVRRIYE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKKGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2635>:

```

m768.seq
  1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
  51 TGCCACGCAG GCAGCCCGCG AAAAACCCTG ATCCGCGGCC CAAACCGCGC
 101 AACATCCGGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
 151 GGGCATTGTC ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
 201 CATACACGAA GCCGCGCCCG ACAAAGACAC GCCGGTCAAC CTCTACTGCC

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1249

251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT  
 301 TATACAAATG TTGCCAATCA CGGCGGTAT GAAGACCTGC TCAAAAAGG  
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2636; ORF 768>:

m768.pep  
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE  
 51 GHLHNAVNI VDIIVRIHE AAPDKDPVN LYCRSGRAE AALQELKKAG  
 101 YTNVANHGGY EDLLKGMK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 768 shows 96.6% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. gonorrhoeae*

m768/g768 96.6% identity in 119 aa overlap

	10	20	30	40	50	60
g768.pep	MNIKQLITAA	LIASAAFAAQ	AAPQKPVSA	QTAQHSAVWI	DVRSEQEFSE	GHLHNAVNI
m768	MNIKHLITAA	LIASAAFAAQ	AAPQKPVSA	QTAQHSAVWI	DVRSEQEFSE	GHLHNAVNI
	10	20	30	40	50	60
	70	80	90	100	110	120
g768.pep	VDQIVRRIE	AAAPDKDTPV	NLYCRSGRAE	AALQELKKAG	YTNVANHGGY	EDLLKGMKX
m768	VDQIVRRIE	AAAPDKDTPV	NLYCRSGRAE	AALQELKKAG	YTNVANHGGY	EDLLKGMKX
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2637>:

a768.seq  
 1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT  
 51 TGCCGCGCAG GCAGCCCCGC AAAAACCCTG ATCCGCGGCC CAAACGCGC  
 101 AACATTCAGC CGTTTGGATC GATGTCCGCA GCGAACAGGA ATTTAGCGAA  
 151 GGTCAATTGC ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG  
 201 CATACACGAA GCCGCGCCCG ACAAAGACAC GCCGGTCAAC CTCTACTGCC  
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAACTGAA AAAAGCAGGC  
 301 TATACGAATG TTGCCAATCA CGGCGGTAT GAAGACCTGC TCAAAAAGG  
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2638; ORF 768.a>:

a768.pep  
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE  
 51 GHLHNAVNI VDIIVRIHE AAPDKDPVN LYCRSGRAE AALQELKKAG  
 101 YTNVANHGGY EDLLKGMK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 768 shows 99.2% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. meningitidis*:

m768/a768 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
a768.pep	MNIKHLITAA	LIASAAFAAQ	AAPQKPVSA	QTAQHSAVWI	DVRSEQEFSE	GHLHNAVNI
m768	MNIKHLITAA	LIASAAFAAQ	AAPQKPVSA	QTAQHSAVWI	DVRSEQEFSE	GHLHNAVNI
	10	20	30	40	50	60
	70	80	90	100	110	120
a768.pep	VDQIVRRIE	AAAPDKDTPV	NLYCRSGRAE	AALQELKKAG	YTNVANHGGY	EDLLKGMKX
m768	VDQIVRRIE	AAAPDKDTPV	NLYCRSGRAE	AALQELKKAG	YTNVANHGGY	EDLLKGMKX
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2639>:

g769.seq

```

1   TTGATAATGG TTATTTTTTA TTTTATTTT TGTGGGAAGA CATTATGCC
51  TGCACGAAAC AGATGGATGC TGCTGCCTTT ATTGGCAAGC GCGGCATACG
101 CCGAAGaAAC ACCgtgCGAA CCGGATTTGA GAAGCCGTCC CGAGTTCAGG
151 CTTTATGAAG CGGAGGTCAA ACCGATCGAC AGGGAAGAAG TACCGGGGCA
201 GGTGCGGGAA AAAGGAAAAG TTTTGCAGGT TGACGgcGAA ACCCTGCTGA
251 AAAATCCCGA ATTGTTGTCTG CGTGCCATGT ATTCCGCAGT GGTCTCAAAC
301 AATATTGCCG GTATCCGCGT GATTTTGCCG ATTTACCTAC AACAGGCGCG
351 GCAGGATAAG ATGTTGGCAC TTTATGCACA AGGGATTTTG GCGCAGGCAG
401 AGGGCAGGGT GAAGGAGGCG GTTCCCATTT ACCGGGAATT GATTGCCGCC
451 CAACCCGACG CGCCCGCCGT CCGTATGCGT TTGGCGGCGG CATTGTTTGA
501 AGACAGGCAG AACGAGGCGG CGGCAGACCA GTTCGACCGC CTGAAAACAG
551 AAGATCTGCC GCCGCAGCTT ATGGAGCAGG TCGAGCTGTA CCGCAAGGCA
601 TTGCGCGAAC GCGATGCGTG GAAGGTAAAC GCGGGTTTCA GCGTTACCCG
651 CGAACACAAT ATCAACCAAG CCCCAGAAAC GCAGCAGTAC GGCAATTGGA
701 CTTTCCCGAA ACAGGTGGAC GGCACGGCAG TCAATTACCG GTTCGGCGCG
751 GAGAAAAAAT GGTGCTGAA AAACGGCTGG TACACGACGG CGGGCGGCGA
801 CGTGTCGGC AGGGTTTATC CGGGGAATAA GAAATTCAAC GATATGACGG
851 CAGGTGTTTC CGCGGCGCATC GGTTTTGCCG ACCGGCGTAA AGATGTCGGG
901 CTGGCAGTGT TCCACGAACG CCGCACCTAC GGCAACGACG CTTATTCTTA
951 CGCCAACGGC GCACGCCTTT ATTTCAACCG TTGGCAAACC CCGAGATGGC
1001 AACGCTGTC TTCGGCGGAG TGGGGCGGTT TGAAGAATAC GCGCCGGGCG
1051 CGTTCCGACA ATACCCATTG GCAAATTTCC AATTGCGTGG TGTTTTACCG
1101 GAATGCGCGC CAATATTGGA CGGGCGGTTT GGATTTTAC CCGGAGCGCA
1151 ACCCCGCCGA CCGTGGCGAC AATTTCAACC GTTACGGCCT GCGCTTTGCC
1201 TCGGGGCGAG AATGGGGCGG CAGCGGCTGT TCTTCGCTGT TCCGCCTCGG
1251 CGTGGCGAAA CGGCATTATG AAAAACCCGG CTTCTTCAGC AGTTTTAAAG
1301 GGGAAAGGCG CAGGGATAAA GAATCGGACA CATCCTTGAG CCTTTGGCAC
1351 CGGGCATTGC ATTTCAAAGG CATCACGCCG CGCTGACGCG TGTCGCACCG
1401 CGAAACGTGG AGCAACGATG TGTTTAACGA ATACGAGAAA AACAGGGCGT
1451 TTGTCGAGTT TAACAAAACG TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2640; ORF 769.ng>:

g769.pep

```

1   LIMVIFYFYF CGKTFMPARN RWMLLPLLAS AAYAEETPCE PDLRSRPEFR
51  LHEAEVKPID REKVPQVRE KGVLVQVDGE TLLKNPELLS RAMYSAVVSN
101 NIAGIRVILP IYLQARQDK MLALYAQGIL AQAEGRVKEA VSHYRELIAA
151 QPDAPAVRMR LAAALFEDRQ NEAAADQFDR LKTEDLPPQL MEQVELYRKA
201 LREERDAWKVN GGSFVTRHN INQAPKQQY GNWTFPKQVD GTAVNYRFGA
251 EKKWSLKNGW YTTAGGDVSG RVYPGNKKFN DMTAGVSGGI GFADRRKDVG
301 LAVFHERRTY GNDAYSANG ARLYFNRWQT PRWQTLSSAE WGRLLKNTRRA
351 RSDNTHLQIS NSLVFYRNAR QYWTGGLDFY RERNPADRGD NFNRYGLRFA
401 WGQEWGGSGL SSLFRLGVAK RHYEKPGFFS SFGERRRDK ESDTSLSLWH
451 RALHFKGITP RLTLSHRETW SNOVFNEYEK NRAFVEFNKT F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2641>:

m769.seq

```

1   TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCTTTTATT GGCAGGCGCG GCATATGCGG
101 AAGAAACACC GCGCGAACCG GATTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC GATCGACAGG GAGAAGGTGC CGGGGCAGGT
201 GCGGGA AAAA GGAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GTTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGCGC CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCATTACC GGAATTGAT TGCCGCCCAA
451 CCGGACGCGC CCGCGTCCG TATGCGTTTG GCGGCAGCAT TGTGTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCCTG AAGGCGGAAA
551 ACCTGCCGCC CGAGCTGATG GAGCAGGTGC AGCTGTACCG CAAGGCATTG
601 CGCGAACGCG ATGCGTGGAA GGTAATGGC GGCTTCAGCG TCACCCGCGA
651 ACACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CCGCTGGTAC ACGACGGCGG GCGGCGACGT
801 GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCGTTTCCGG CGGCATCGGT TTTGCCGACC GGCAGCAAAG TGCCGGGCTG
901 GCAGTGTTCC ACGAACGCCG CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCTTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 CGTTGTCTTC GGCAGGAGTG GGGCGTTTGA AGAATACGCG CCGGGCGCGT
1051 TCCGACAATA CCAATTTGCA AATTCCAAT TCGCTGGTGT TTTACCGGAA
1101 TCGCGGCCAA TATTGGATGG GCGGTTTGGG TTTTACCAGC GAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCCTGCG CTTTGCCTGG
1201 GGCAGGAAT GGGGCGGCGG CCGCTGTCT TCGCTGTTGC GCCTCGGCGC

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1251

```

1251 GGC GAAACGG CATTATGAAA AACCCGGCTT TTTCAGCGGT TTAAAGGGG
1301 AAAGGCGCAG GGATAAGAA TTGAACACAT CCTTGAGCCT TTGGCACC GG
1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACC GCGA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
1451 TCGAGTTTAA TAAACGTTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2642; ORF 769>:

m769.pep

```

1  LIMVIFYFCG KTFMPARNRW MLLLPLLSA AYAEETPREP DLRSRPEFRL
51  HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIAAQ
151 PDAPAVRMRL AAALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTRHNI NQAPKRQQYG KWTFFPKQVDG TAVNYRLGAE
251 KKWSLKNWY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNRWQTP KWQTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGDLDFYR ERNPADRGDN FNRYGLRFAW
401 GQEWGGGSL SLLRLGAAKR HYEKPGFFSG FKGERRRDK LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDVFNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 769 shows 95.1% identity over a 492 aa overlap with a predicted ORF (ORF 769) from *N. gonorrhoeae*

m769/g769 95.1% identity in 492 aa overlap

```

g769.pep      10      20      30      40      50      59
LIMVIFYFYFCGKTFMPARNRWMLL-PLLSAAYAEETPCEPDLRSRPEFRLHEAEVKPI
|||||
m769          10      20      30      40      50
LIMVIFY--FCGKTFMPARNRWMLLPLLSAAYAEETPREPDLRSRPEFRLHEAEVKPI

g769.pep      60      70      80      90     100     110     119
DREKVPQGVREK GKVLQVDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQD
|||||
m769          60      70      80      90     100     110
DREKVPQGVREK GKVLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQD

g769.pep      120     130     140     150     160     170     179
KMLALYAQGILAQAEGRVKEAVSHYRELIAAQPDAPAVRMRLAAALFEDRQNEAADQFD
|||||
m769          120     130     140     150     160     170
KMLALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVRMRLAAALFENRQNEAADQFD

g769.pep      180     190     200     210     220     230     239
RLKTEDLPPQLMEQVELYRKALRERDAWKVNGGFSVTRHNIINQAPKQQYGNWTFPKQV
|||||
m769          180     190     200     210     220     230
RLKAENLPPQLMEQVELYRKALRERDAWKVNGGFSVTRHNIINQAPKQQYGNWTFPKQV

g769.pep      240     250     260     270     280     290     299
DGTAVNYRFGAEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDV
|||||
m769          240     250     260     270     280     290
DGTAVNYRLGAEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDA

g769.pep      300     310     320     330     340     350     359
GLAVFHERRTYGNDAYSANGARLYFNRWQTPRWQTLSSAEWGRGLKNTRRARSNDNTHLQI
|||||
m769          300     310     320     330     340     350
GLAVFHERRTYGNDAYSANGARLYFNRWQTPRWQTLSSAEWGRGLKNTRRARSNDNTHLQI

g769.pep      360     370     380     390     400     410     419
SNSLVFYRNARQYWTGGLDFYRERNPADRGDNFNRYGLRFAWQEWGGGSLSSFLRLGVA
|||||
m769          360     370     380     390     400     410
SNSLVFYRNARQYWMGGDLDFYRERNPADRGDNFNRYGLRFAWQEWGGGSLSSFLRLGAA

g769.pep      420     430     440     450     460     470     479
KRHYEKP GFFSFKGERRRDKESDTSLSLWHRALHFKGITPRLTLSHRETWSNDVFNEYE
|||||

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1252

```

m769      KRHYEKPGFSSGFKGERRRDKE LNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYE
          420      430      440      450      460      470

          480      490
g769.pep  KNRA FVEFNKTFX
          |||||
m769      KNRA FVEFNKTFX
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2643>:

```

a769.seq
1  TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACCG GATTTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC AATCGACAGG GAGAAGGTAC CGGGGCAGGT
201 GCGGGAAAAA GAAAAAGTTT TGCAGATTGA CCGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GCTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTACC GGAATTGAT TGTGCGCCAA
451 CCGGACGCGC CCGCCGTCGG TATGCGTTTG GCGCGGCGAT TGTGTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
601 CCGGAACGCG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TTACCCGCGA
651 ACACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGGCGG CCGGCGACGT
801 GTCCGCGAGG GTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCCTTTCCGG CCGCATCGGT TTTGCCGACC GCGCGAAAGA TGCCGGGCTG
901 GCAGTGTTCC ACGAACGCGC CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA GCCTTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 CGTTGTCTTC GCGGAGTGG GGGCGTTTGA AGAATACGCG CCGGGCGCGT
1051 TCCGACAATA CCCATTGCA AATTTCCAAT TCGCTGGTGT TTTACCGGAA
1101 TCGCGGCCAA TATTGGATGG GCGGTTTGA TTTTACC GCAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCCTGCG CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCG CCGCCTGTCT TCGCTGTTGC GCCTCGGCGC
1251 GGGGAAACGG CATTATGAAA AACCCGGCTT TTTACGCGGT TTTAAAGGGG
1301 AAAGGCGCAG GGATAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCAG
1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCGCGA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CCGGCGTTTG
1451 TCGAGTTTAA TAAACGTTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2644; ORF 769.a>:

```

a769.pep
1  LIMVIFYFCG KTFMPARNRW MLLPLLASA AYAETPREP DLRSRPEFRL
51  HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIVAQ
151 PDAPAVRMRL AAALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTREHNI NQAPKRQYQG KWTFFPKQVDG TAVNYRLGAE
251 KKWSLKNGWY TTAGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRYTG NDAYSYTNGA RLYFNWQTP KWQTLSSAEW GR LKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW
401 GQEWGSGSL SLLRLGAAGR HYEKPGFSSG FKGERRRDKE LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDFVNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 769 shows 99.8% identity over a 490 aa overlap with a predicted ORF (ORF 769) from *N. meningitidis*:

m769/a769 99.8% identity in 490 aa overlap

```

          10      20      30      40      50      60
a769.pep  LIMVIFYFCGKTFMPARNRWMLLLPLLASAAYAETPREPDLRSRPEFRLHEAEVKPIDR
          |||||
m769      LIMVIFYFCGKTFMPARNRWMLLLPLLASAAYAETPREPDLRSRPEFRLHEAEVKPIDR
          10      20      30      40      50      60

          70      80      90      100     110     120
a769.pep  EKVPQVREK GKVLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKM

```

1253

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|||||
m769      EKVPGQVREKGVLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKM
              70      80      90      100     110     120

              130      140      150      160      170      180
a769.pep   LALYAQGILAQADGRVKEAISHYRELIVAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
|||||
m769      LALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
              130      140      150      160      170      180

              190      200      210      220      230      240
a769.pep   KAENLPPQLMEQVELYRKALRERDAWKVNGGFSVTREHNINQAPKRQOYGKWTFFPKQVDG
|||||
m769      KAENLPPQLMEQVELYRKALRERDAWKVNGGFSVTREHNINQAPKRQOYGKWTFFPKQVDG
              190      200      210      220      230      240

              250      260      270      280      290      300
a769.pep   TAVNYRLGAEEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
|||||
m769      TAVNYRLGAEEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
              250      260      270      280      290      300

              310      320      330      340      350      360
a769.pep   AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRCLKNTRRARSNDTHLQISN
|||||
m769      AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRCLKNTRRARSNDTHLQISN
              310      320      330      340      350      360

              370      380      390      400      410      420
a769.pep   SLVFYRNARQYWMGGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGGSGLSLLRLGAAGR
|||||
m769      SLVFYRNARQYWMGGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGGSGLSLLRLGAAGR
              370      380      390      400      410      420

              430      440      450      460      470      480
a769.pep   HYEKPGFFSFGKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYEKN
|||||
m769      HYEKPGFFSFGKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYEKN
              430      440      450      460      470      480

              490
a769.pep   RAFVEFNKTFX
|||||
m769      RAFVEFNKTFX
              490

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2645>:

```

g770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCCGA CTGCCTGCGG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATGT
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTCGACGA TCCCACGTT
151 CAAGGGGTTG CCGTGTATAT TTCGTATGCA AAAAAAGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGT TCGTGCGTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTCA AGCGCGGTAC GGGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAGCCTT CGCCTATTG GTTTACAGCG
401 ATAAAAATCGT CCAAGGATCG CCGAAAAATT CCTTAAGCGC GGTTTCCTGT
451 TCGGCAGCG GCATACCGCA AACCGACGGG GTGCAAGCGG ATACTTCCGG
501 CAAACTGCTT GCCGGCGCCT GCATTATTC CAACCCGATA AAAAATCCCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2646; ORF 770.ng>:

```

g770.pep
1  MNRLLLLSAA VLPTACGSGE TDKIGRASTV FNMLGKNDR I EVEGFDDPDV
51  QGVACYISYA KGGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKRGTFGA FKSQRIVRY DPKRKAFAYL VYSDKIVQGS PKNSLSAVSC
151 FGSGIPQTDG VQADTSGKLL AGACIISNPI KNPDKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2647>:

```

m770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCGG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC

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1254

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101 TGGGCAAAAA CGACCGTATC GAAGTGGAAG GATTTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGC GTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTCA AACACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAAATCTCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2648; ORF 770>:

m770.pep

```

1 MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR IVEGFDDPDV
51 QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKHGASFA FKSRIQIVRY DPKRKTFAYL VYSDKIIQGS PKNSLSAVSC
151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENLDRK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 770 shows 93.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. gonorrhoeae*

m770/g770 93.5% identity in 186 aa overlap

```

g770.pep      10      20      30      40      50      60
MNRLLLLSAAVLPTACGSGETDKIGRASTVFNMLGKNDRIVEGFDDPDVQGVACYISYA
|||||
m770          10      20      30      40      50      60
MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIVEGFDDPDVQGVACYISYA
|||||

g770.pep      70      80      90      100     110     120
KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKKEVFKRGTGFAGFKSRQIVRY
|||||
m770          70      80      90      100     110     120
KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKKEVFKHGASFAFKSRQIVRY
|||||

g770.pep      130     140     150     160     170     180
DPKRKAFAVLVYSDKIVQSPKNSLSAVSCFGSGIPQTDGVDQADTSGKLLAGACIISNPI
|||||
m770          130     140     150     160     170     180
DPKRKTFAVLVYSDKIIQSPKNSLSAVSCFGGGIPQTDGVDQADTSGNLLAGACMISNPI
|||||

g770.pep      KNPDKRX
               :| ||||
m770          ENLDRKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2649>:

a770.seq

```

1 ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCGG
51 CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC
101 TGGGCAAAAA CGACCGTATC GAAGTGGAAG GATTTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGC GTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTCA AACACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAAATCCCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2650; ORF 770.a>:

a770.pep

```

1 MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR IVEGFDDPDV
51 QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKHGASFA FKSRIQIVRY DPKRKTFAYL VYSDKIIQGS PKNSLSAVSC

```

1255

151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENPDKR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 770 shows 99.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. meningitidis*:

m770/a770 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
a770.pep	MNRL	LLLSAAVLLTACGS	GETDKIGRASTVFNILGKN	DRIEVEGFDDPDVQGV	ACYISYA	
m770	MNRL	LLLSAAVLLTACGS	GETDKIGRASTVFNILGKN	DRIEVEGFDDPDVQGV	ACYISYA	
	70	80	90	100	110	120
a770.pep	KKGGLKEMVNLEEDAS	DASVSCVQTASSISFDE	TAVRKPKFVKHGASFA	FKSRQIVRYY		
m770	KKGGLKEMVNLEEDAS	DASVSCVQTASSISFDE	TAVRKPKFVKHGASFA	FKSRQIVRYY		
	130	140	150	160	170	180
a770.pep	DPKRKTFAVLVYS	DKIIQGSFKNLSAVSC	FGGGIPQTDG	VQADTSGNLLAGAC	MISNPI	
m770	DPKRKTFAVLVYS	DKIIQGSFKNLSAVSC	FGGGIPQTDG	VQADTSGNLLAGAC	MISNPI	
a770.pep	ENPDKRX					
m770	ENLDKRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2651>:

g771.seq

1	ATGGATTAT	TATCGGTTT	CCACAAATAC	CGTCTGAAAT	ATGCGGTGGC
51	GGTGCTGACG	ATGCTGCTTT	TGGCGGCAGT	CGGGCTGCAC	GCTTCCGTAT
101	ATCGCACCTT	CACGCCGAA	AACATCCGCA	GCCGCCTCCA	ACAAAGCATT
151	GCCCATACCC	ACCGGAAAAT	CTCGTTTGAT	GCGGATATAC	GGCGCAGGCT
201	TCTGCCCCGC	CCGACCGTCA	TCCTGAAAAA	CCTGACCATT	ACCGAACCCG
251	ACGGCGGCCG	GGTCGCCGTT	TCCGTCAAAG	AAACCAAAAT	CGGATTGAGC
301	TGGAAAAACC	TGTGGTCGGA	TCGGATACAG	GTTGAAAAAT	GGGTGGTTTC
351	GGGTGCCGAT	CTTGCCCTGA	CGCGCGACAG	AAACGGCGCT	TGGAACATCC
401	AAGACCTGTT	CGACGGCGCG	AAACACTCCG	CCTCAGTCAA	CCGCATTATC
451	GTCGAAAACA	GCACCGTCCG	CCTCAATTTT	CTGCAGCAAC	AGCTTATCCT
501	GAAGGAAATC	AGCCTCAACC	TGCAATCCCC	CGATTTCGTC	GGGCAGCAGT
551	TTGAAAAGTT	GGGCATACTG	GTTTGGAGAA	AGCTGTCCGT	CCCGTGGAAA
601	AGCAGGGGGC	TGTTCCCTTC	AGACGGCATC	GGCACGCCCG	AAATCTCACC
651	GTTCCATTTT	GAAAGTTCCA	CTTCGCTGGA	CGGACACGGC	ATCACCATT
701	GCACCACCGG	CAGCCCTTCT	GTCCGCTTCA	ACGCCGGCGG	AGCGGATGCC
751	GCCGGCCTCG	GCCTGCGTGC	AGACACTTCC	TTCCGCAACC	TCCACCTGAC
801	CGCGCAAATC	CCCGCACTGG	CACTCAAAAA	CAACAGCATC	AAAACCGGCA
851	CGGTCAACGG	CACGTTTACC	GCCGGCGGCG	AATATGCCCG	ATGGGACGGT
901	TCGTTCAAAC	TCGACAAAGC	CAACCTGCAC	TCCGGCATCG	CCAACATCGG
951	CAACGCCGAA	ATCTCCGGCA	GCTTCAAAAC	ACCGCGCCTT	CAAACCAATT
1001	TCTCCCTCGG	CTCGCCGTTG	GTTTGGAGTC	GGGACAACGG	GCTGGACGCC
1051	CCGCGCCTGC	ACATATCGAC	CCTTCAGGAT	ACCGTCGACC	GCCTGCCGCA
1101	ACCCCGTTTC	ATCAGCCGGC	TCGACGGTTC	GCTGTCCATA	CCGAATCTGC
1151	AAAATTGGAA	TGCCGAATTA	AACGGCACAT	TCGACCGCCA	ACCCGTTGCC
1201	GCAAAATTCA	AATATACGCG	GGAAGCGCGA	CCGCACCTGG	AAGCCGCCGC
1251	CGCGCTGCAA	AAATTAACCC	TCGCCCCCTA	TCTTGACGAA	TTTCGGCAAC
1301	AAAACGGCAA	AATATTCCCC	GACATCCTCG	GCAGGCTGTC	CGGCAACGTC
1351	GAGGCACACC	TCAAAATCGG	CAGCATCCAA	CTCCCCGGCT	TGCAACTGGA
1401	CGATATGGAA	ACCTACCTCC	ACGCCGACAA	AGACCATATC	CGGCTCAGCC
1451	GTTTCAAGTC	AGGGCTTTAC	GGCGGCCATA	CCGAAGGCGG	CATCAGCATC
1501	GCCAACACCC	GTCCCGCCAC	TTACCGCCTG	CAACAGAATG	CAAGCAACAT
1551	CCAAATCCAA	CCGCTGCTGC	AAGACCTGTT	CGGCTTCCAC	AGCTTCAGCG
1601	GCAACGGCGA	TGCGGTCATC	GACCTGACCG	CAAGCGGCGA	AAACCGCAAA
1651	CAGCTTATCC	GCTCGCTGCA	AGGCAGCCTG	TCGCTGAATA	TTTCCAACGG
1701	CGCGTGGCAC	GGCATCGATA	TGGACAGCAT	TTTAAAAAAC	GGCCTTTCCG

1256

```

1751 GGAAAAATCTC GGGCAGCACA CCCTTCTACC GATTACAGCT CAACAGCGAA
1801 ATTTTCAGACG GCATCAGCCG CCACATCGAT ACCGAACTCT TCTCCGACAG
1851 CCTCTATGTT ACCAGCAACG GCTATACCAA TCTGGATACG CAGGAATTGT
1901 CTGAAGATGT CCTTATCCGC AACGCCGTCC ATCCGAAAAA CAAACCGATT
1951 CCCCTGAAAA TCACCGGTAC GGTGGACAAG CCGTCCATTA CCGTCGATTA
2001 CGGCAGGCTG ACCGGCGGCA TCAATTCGCG CAAAGAGAAA CAGAAAATCC
2051 TCGAAGACAC CCTGCTGGAA CAATGGCAGT GGCTCAAACC TAAAGAACCG
3051 TAA

```

This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

g771.pep

```

1 MDLLSVFHKY RLKYAVAVLT MLLLAAVGLH ASVYRTFTPE NIRSRLQQSI
51 ANTHRKISFD ADIRRRLLPR PTVILKNLTI TEPDGGRVAV SVKETKIGLS
101 WKNLWSDRIQ VEKVVVSGAD LALTRDRNGA WNIQDLFDGA KHSASVNRRI
151 VENSTVRLNF LQQQLILKEI SLNLQSPDSS GQQFESSGIL VWRKLSVPWK
201 SRGLFLSDGI GTPEISPFHF EASTSLDGHG ITISTTGSPTS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PALALKNNNSI KTGTVNGTFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRL QTNFSLGSPV VWSRDNGLDA
351 PRLHISTLQD TVDRLPQPRF ISRLDGSLSI PNLQNNNAEL NGTFDRQPVA
401 AKFKYTRREGA PHLEAAAAAQ KLNLAAPYLDE FRQNGKIFP DILGRLSGNV
451 EAHLKIGSIQ LPGLQLDDME TYLHADKDHI ALSRFKSGLY GGHTEGGISI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFSNGNDAVI DLTASGENRK
551 QLIRSLQGS LSLNISNGAWH GIDMSILKN GLSGKISGST PFYRFTLNSE
601 ISDGISRHID TELFSDSLYV TSNGYTNLDT QELSEDVLIR NAVHPKNKPI
651 PLKITGTVDK PSITVDYGR L TGGINSRKEK QKILEDTLLE QWQWLKPKPE
701 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2653>:

m771.seq

```

1 ATGGATTTAT TATCGGTTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
51 CGTGCTGACG ATACTGCTTT TGGCGGCAGT CGGGCTGCAC GCTTCCGTAT
101 ATCGCACCTT CACGCCTGAA AACATCCGCA GCCGCCTACA ACAAAAGCATT
151 GCACACACAC ACCGAAAAAT CTCGTTTGAT GCGGACATT AGCGCAGGCT
201 CCTGCCCCGG CCGACCGTCA TCCTGAAAAA CCTGACCATT ACCGAACCGG
251 GCGGCGACCA GACTGCCGTT TCCGTCCAAG AAACCAAAAT CGGATTGAGC
301 TGGAAAAACC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
351 GAGTGCAGGA CTGCGCCTGA CGCGCGACGG GAAAGGTGTT TGGAAACATCC
401 AAGACCTGAT CGACAGCCAA AAACGCCAAG CCTCAGTCAA CCGCATTATC
451 GTCGAAAACA GCACCGTCCG CCTCAATTTT CTCGAGGAAC AGCTTATCCT
501 GAAGGAAATC AACCTCAACC TGCAATCCCC CGATTCTGCG GGGCAGCCGT
551 TTGAAAGTTC GGGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGAAA
601 AGCAGGGGGC TGTTCCTTTC AAACGGCATC GGCCCGCCCG AAATCTCACC
651 GTTCCATTTT GAAGCTTCCA CTTCGCTGGA CGGACACGGC ATTACCATTT
701 CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
751 GCCGGCCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
801 CGCCCAAATC CCCGCGCTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
851 CGCTCAACCG CGCATTTACC GCGGCGCGCG AATATGCCCG ATGGGACGGT
901 TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GCTTCAAAC ACCGCGCCAC CAGACCAACT
1001 TCTCCCTCAA TTGCGCGCTC GTATGGACGG AAAACAAAGG GCTGGACGCG
1051 CCGCGCCTGT ATGTATCGAC CCTTCAGGAT ACCGTCAACC GCCTGCCGCA
1101 ACCCCGTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA AACCGTTGCC
1201 GCGAAATTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCGGT
1251 CGCACTGCAA AAATTGAACC TGACCCCTTA TCTTGACGAC GTGCGGCAAC
1301 AAAACGGCAA AATATTTCCT GACACCTCG CCAAGCTGTC CGGCGACATC
1351 GAGGCGCACG TGAAAATCGG AAAAGTCCAA CTTCGCGGCC TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCCGACAA AGGCCATATC GCGCTCAGCC
1451 GTTTCAAAGT AGGGCTTTAC GCGCGCCATA CCGAAGGCGG CATCAGCATC
1501 GCCAACACCC GTCCCGCCAC TTACCGCTCG CAACAGAATG CAAGCAACAT
1551 CCAAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGCGA CCGGTCATC GACCTGACCG CGGGCGGCGA AACCCGAAAA
1651 GAGCTTATCC GCTCGCTTCA GGGCAGCTCG TCGCTAAATA TTTCCAACGG
1701 TGCATGGCAC GGTATCGACA TGGACAATAT CCTGAAAAAC GGCATTTCGG
1751 GCAAAATGTC CGACAATGCC GCACCCAGCA CACCCTTCCA CCGATTACAG
1801 CTCAACAGCG AAATTTCAGA CGGCATCAGC CGCCACATCG ATACCGAACT
1851 CTTCTCCGAC AGCCTCTATG TTACCAGCAA CGGCTATACC AATCTGGATA
1901 CGCAGGAATT GTCTGAAGAT GTCCTTATCC GCAACGCCGT CCATCCGAAA
1951 AACAAACCGA TTCCCCTGAA AATCACCGGC ACGGTGGACA AACCGTCCAT
2001 TACCGTCCAT TACGGCAGGC TGACCGGCGG CATCAATTCT CGCAAAGAGA
2051 AACAGAAAAT CCTCGAAGAC ACCCTGCTGG AACAATGGCA GTGGCTCAAA
2101 CCTAAAGAAC CGTA

```

This corresponds to the amino acid sequence <SEQ ID 2654; ORF 771>:

```
m771.pep
1 MDLLSVFHKY RLKYAVAVLT ILLAAVGLH ASVYRTFTPE NIRSRLQQSI
51 AHTRKISFD ADIQRRLPR PTVILKNLTI TEPGGDQTAV SVQETKIGLS
101 WKNLWSDQIQ IEKWVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
151 VENSTVRLNF LQEQILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
201 SRGLFSLNGI GPPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PALALRNNSI KIETVNGAFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTV
401 AKFRYTHEDA PHLEAAVALQ KNLNTPYLDV VRQQNGKIFP DTLAKLSGDI
451 EAHKIGKQV LPGLQLDDME TYLHADKQHI ALSRFKSGLY GGHTEGGISI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
551 ELIRSLQGS LNLISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRFT
601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDTOELSED VLIRNAVHPK
651 NKPIPLKITG TVDKPSITVD YGRLTGGIN S RKEKQKILED TLEQWQWLK
701 PKEP*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 771 shows 90.3% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. gonorrhoeae*

```
m771/g771 90.3% identity in 704 aa overlap
10 20 30 40 50 60
g771.pep MDLLSVFHKYRLKYAVAVLTMLLLAAVGLHASVYRTFTPENIRSRLQQSIAHTRKISFD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPENIRSRLQQSIAHTRKISFD
10 20 30 40 50 60

70 80 90 100 110 120
g771.pep ADIRRRLLPRPTVILKNLTITEPDGGRVAVSVKETKIGLSWKNLWSDRIQVEKWVVSAD
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 ADIQRRLPRPTVILKNLTITEPDGQTAVSVQETKIGLSWKNLWSDQIQIEKWVSSAE
70 80 90 100 110 120

130 140 150 160 170 180
g771.pep LALTRDRNGAWNIDLDGAKHSASVNRIIVENSTVRLNLFQQLILKEISLNQSPDSS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNLFQEQILKEINLNQSPDSS
130 140 150 160 170 180

190 200 210 220 230 240
g771.pep GQQFESSGILVWRKLSVPWKSRLGLSDGIGTPEISPFHFEASTSLDGHGITISTTGSPS
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 GQPFESSGILVWGKLSVPWKSRLGLFSLNGIGPPEISPFHFEASTSLDGHGITISTTGSPS
190 200 210 220 230 240

250 260 270 280 290 300
g771.pep VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALKNNSIKTGTVNGTFTAGGEYARWDG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG
250 260 270 280 290 300

310 320 330 340 350 360
g771.pep SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSPVWVRDGLDAPRLHISTLQD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD
310 320 330 340 350 360

370 380 390 400 410 420
g771.pep TVDRLPQPRFISRLDGSLSIPNLQNWNAELNGTFDRQPVAAKFYTRGAPHLEAAVALQ
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 TVNRLPQPRFISRLDGSLSVNLQNWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ
370 380 390 400 410 420

430 440 450 460 470 480
g771.pep KNLNAPYLDEFQNGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDDMETYLHADKQHI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 KNLNTPYLDVVRQQNGKIFPDITLAKLSGDI EAHKIGKQVLPGLQLDDMETYLHADKQHI
```

1258

	430	440	450	460	470	480
	490	500	510	520	530	540
g771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQLLDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQLLDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	
g771.pep	DLTASGENRKQLIRSLQGSLSLNISNGAWHGIDMDSILKNGLSGKISG----STPFYRFT					
m771	DLTAGGETRKLIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRT					
	550	560	570	580	590	600
	600	610	620	630	640	650
g771.pep	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	660	670	680	690	700	
g771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2655>:

a771.seq

1	ATGGATTAT	TATCGGTCTT	CCACAAATAC	CGTCTGAAAT	ATGCGGTAGC
51	CGTGCTGACG	ATACTGCTTT	TGGCGGCAAT	CGGGCTGCAC	GCTTCCGTAT
101	ATCGCATCTT	CACACCTGAA	AACATCCGAA	GCCGCCTCCA	ACAAAGCATT
151	GCCCATACGC	ACCGGAAAT	CTCGTTTAT	GCGGATATAC	AGCGCAGGCT
201	TCTGCCCCCG	CCGACCGTCA	TCCTGAAAAA	CCTGACCATT	ACCGAACCCG
251	GCGGCGACCG	GACTGCCGTT	TCCGTCCAAG	AAACCAAAAT	CGGATTGAGC
301	TGGAAAAACC	TGTGGTCGGA	TCAGATACAG	ATTGAAAAAT	GGGTGGTTTC
351	GAGTGCCGAA	CTGCCCTGA	CGCGCGACGG	GAAAGGTGTT	TGGAACATCC
401	AAGACCTGAT	CGACAGCCAA	AAACGCCAAG	CCTCAGTCAA	CCGCATTATC
451	GTCGAAAAAC	GCACCGTCCG	CCTCAATTTC	CTGCAGGAAC	AGCTTATCCT
501	GAAGGAAATC	AACCTCAACC	TGCAATCCCC	CGATTTCGTC	GGGCAGCCGT
551	TTGAAAGTTC	GGGCATACTG	GTTTGGGGAA	AGCTGTCCGT	CCCGTGGAAA
601	AGCAGGGGGC	TGTTCCCTTC	AGACGGCATC	GGCACGCCCA	AAATCTCACC
651	GTTCCATTTT	GAAGCTTCCA	CTTCGCTGGA	CGGACACGGC	ATTACCATTT
701	CCACCACCGG	CAGCCCTTCT	GTCCGCTTCA	ACGCCGGCGG	AGCGGATGCC
751	GCCGCGCTCG	GCCTGCGTGC	AGACACTTCC	TTCGCAACC	TCCACCTGAC
801	CGCCCAATC	CCTACGCTGG	CACTCAGGAA	CAACAGCATT	AAAATTGAAA
851	CCGTCAACGG	CGCATTATCC	GCCGGCGGCG	AAATATGCCCA	ATGGGACGGT
901	TCGTTCAAAC	TCGACAAAGC	CAACCTGCAC	TCCGGCATCG	CCAACATCGG
951	CAACGCCGAA	ATCTCCGGCA	GCTTCAAAAC	ACCGCGCCAC	CAGACCAACT
1001	TCCTCCCTAA	TTGCCCGCTC	GTATGGACGG	AAAACAAGG	GCTGGACGCG
1051	CCGCGCCTGT	ATGTATCGAC	CCTTCAGGAT	ACCGTCAACC	GCCTGCCGCA
1101	ACCCCGTTTC	ATCAGCCGGC	TCGACGGTTC	GCTGTCCGTA	CCGAATCTGC
1151	AAAATTGGAA	TGCCGAATTA	AACGGCACAT	TCGACCGCCA	AACCGTTGCC
1201	GCGAAATTCA	GATACACACA	TGAAGACGCA	CCGCATCTGG	AAGCCGCCGT
1251	CGCACTGCAA	AAATTGAACC	TGACCCCTTA	TCTTGACGAC	GTGCGGCAAC
1301	AAAACGGCAA	AATATTTCCT	GACACCCTCG	CCAAGCTGTG	CGGCGACATC
1351	GAGGCGCACC	TGAAAATCGG	AAAAGTCCAA	CTTCCCGGCC	TGCAACTGGA
1401	CGATATGGAA	ACCTACCTCC	ACGCCGACAA	AGGCCATATC	GCGCTCAGCC
1451	GTTTCAAGTC	AGGGCTTTAC	GGCGGCCATA	CCGAAGGCGG	CATCAGCATC
1501	GCCAACAGCC	GTCCCGCCAC	TTACCGCCTG	CAACAGAATG	CAAGCAACAT
1551	CCAAATCCAA	CGCTGCTGTC	AAGACCTGTT	CGGCTTCCAC	AGCTTCAGCG
1601	GCAACGGCGA	CGCGGTCATC	GACCTGACCG	CGGGCGGCGA	AACCCGAAAA
1651	GAGCTTATCC	GCTCGCTTCA	GGGCAGCCTG	TCGCTAAATA	TTTCCAACGG
1701	TGCATGGCAC	GGTATCGACA	TGGACAATAT	CCTGAAAAAC	GGCATTTCGG
1751	GCAAACTGTC	CGACAATGCC	GCACCCAGCA	CACCCTTCCA	CCGATTACAG
1801	CTCAACAGCG	AAATTTTCAGA	CGGCATCAGC	CGCCACATCG	ATACCGAATC
1851	CTTCTCCGAC	AGCCTCTATG	TTACCAGCAA	CGGCTATACC	AATCTGGATA
1901	CGCAGGAATT	GTCTGAAGAT	GTCCTTATCC	GCAACGCCGT	CCATCCGAAA
1951	AACAAACCGA	TTCCCTGAA	AATCACCAGT	ACGGTGGACA	AACCGTCCAT
2001	TACCGTCCAT	TACGGCAGGC	TGACCGGCGG	CATCAATTTC	CGCAAGAGA
2051	AACAGAAAAT	CCTCGAAGAC	ACCCTGCTGG	AACAATGGCA	GTGGCTCAAA
2101	CCTAAAGAAC	CGTAA			

This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

1259

a771.pep  
 1 MDLLSVFHKY RLKYAVAVLT ILLLAAGLH ASVYRIFTPE NIRSRLQOSI  
 51 ANTHRKISFD ADIQRLLPR PTVILKNLTI TEPGGDRTAV SVQETKIGLS  
 101 WKNLWSDQIQ IEKVVVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII  
 151 VENSTVRLNF LQEQILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK  
 201 SRGLFLSDGI GTPKISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA  
 251 AGLGLRADTS FRNLHLTAQI PTLALRNNSI KIETVNGAFT AGGEYAQWDG  
 301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA  
 351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTVA  
 401 AKFRYTHEDA PHLEAAVALQ KLNLTPLYDD VRQONGKIFP DTLAKLSGDI  
 451 EAHLKIGKVQ LPGLQLDDME TYLHADKGHI ALSRFKSGLY GGHTGGISI  
 501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFSNGDAVI DLTAGGETRK  
 551 ELIRSLQGS LNLISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRFT  
 601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDTQELSED VLIRNAVHPK  
 651 NKPIPLKITG TVDKPSITVD YGRLTGGIN S RKEKQKILED TLLEQWQWLK  
 701 PKEP\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 771 shows 98.9% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. meningitidis*

m771/a771 98.9% identity in 704 aa overlap

	10	20	30	40	50	60
a771.pep	MDLLSVFHKYRLKYAVAVLTILLLAAGLHASVYRIFTPENIRSRLQOSIAH	THRKISFD				
m771	MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPENIRSRLQOSIAH	THRKISFD				
	10	20	30	40	50	60
	70	80	90	100	110	120
a771.pep	ADIQRLLPRPTVILKNLTITEPGGDRTAVSVQETKIGLSWKNLWSDQIQIEKVVVSSAE					
m771	ADIQRLLPRPTVILKNLTITEPGGDQTAHSVQETKIGLSWKNLWSDQIQIEKVVVSSAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a771.pep	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQILKEINLNLQSPDSS					
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQILKEINLNLQSPDSS					
	130	140	150	160	170	180
	190	200	210	220	230	240
a771.pep	GQPFESSGILVWGKLSVPWKSRLFLSDGIGTPKISPFHF EASTSLDGHGITISTTGSPS					
m771	GQPFESSGILVWGKLSVPWKSRLFLSNGIGPPEISPFHF EASTSLDGHGITISTTGSPS					
	190	200	210	220	230	240
	250	260	270	280	290	300
a771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPTLALRNNSIKIETVNGAFTAGGEYAQWDG					
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG					
	250	260	270	280	290	300
	310	320	330	340	350	360
a771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD					
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD					
	310	320	330	340	350	360
	370	380	390	400	410	420
a771.pep	TVNRLPQPRFISRLDGSLSV PNLQNWNAELNGTFDRQTVA AKFRYTHEDAPHLEAAVALQ					
m771	TVNRLPQPRFISRLDGSLSV PNLQNWNAELNGTFDRQTVA AKFRYTHEDAPHLEAAVALQ					
	370	380	390	400	410	420
	430	440	450	460	470	480
a771.pep	KLNLTPLYDDVRQONGKIFPDTLAKLSGDI EAHLKIGKVQLPGLQLDDMETYLHADKGHI					
m771	KLNLTPLYDDVRQONGKIFPDTLAKLSGDI EAHLKIGKVQLPGLQLDDMETYLHADKGHI					
	430	440	450	460	470	480

1260

```

          490      500      510      520      530      540
a771.pep  ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI
          |||
m771      ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI
          490      500      510      520      530      540

          550      560      570      580      590      600
a771.pep  DLTAGGETRKEIIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRT
          |||
m771      DLTAGGETRKEIIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRT
          550      560      570      580      590      600

          610      620      630      640      650      660
a771.pep  LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIIRNAVHPKNKPIPLKITG
          |||
m771      LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIIRNAVHPKNKPIPLKITG
          610      620      630      640      650      660

          670      680      690      700
a771.pep  TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX
          |||
m771      TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX
          670      680      690      700

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2657>:

```

g772.seq
1  GTGTTTCGGCA CGGTCTTGCG GACTGATGCC GACTGCCTGC AAATCATCGT
51  CGTCGGCAAG TTCTTTCAGG TTGTTGCGTA TGGTTTTCGG GCGTTGGCGG
101 AAGGCGAGTT TCACCAAGTTT GCGGAAATGA TCGAAATCGT CCGCCTTGCC
151 GATACGGTGT TTCACCGGAA TCATGCGCAC CACTGCGGAA TCGATTTTCG
201 GCGCGGGATC GAACGATTTCG GCGGGCACGT CAATCAGCAG CTCCATATCG
251 AAAAAATATT GCAGCATCAC ACCAAGCGA CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATGCGCTCGA CCACTTCTTT TTGCAACATA AAGTGCATAT
351 CGCGGACATC GTCCGCCACC TCCGCCAGTT TGAACAAAAG CGGCGTGGAG
401 ATGTTATACG GCAGGTTGCC GACGATTTTC TTTTGCCTG AGATGCCGTT
451 GAAATCAAAC TGCAACACGT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTTACAGCGG CATACGATGT CGCGGTCGAT TTCGACAACG
551 TCGAGGCGGT TCAGCTTTT CGCCAAAGGT TCGGTAATTG CCGCCAAACC
601 CGGGCCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCC GATAATCCGC GTGTCCTGCA AAAAATTCTG CCCGAAACGC
701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTC CCTCTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGCAGGATC AGACTCTGTT TGGGCGGGGC GTAACCCCTT
801 CCAAATCAGG ACGACACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2658; ORF 772.ng>:

```

g772.pep
1  VFGTVLRTDA DCIQLIIVVGK FFQVVAYGFA ALAEGEFHQF GEMIEIVRLA
51  DTVFHRNHAH HCGIDFRRGI ERFRHVNQQ LHIEKILQHH TQATVVVAFR
101 RGNHALDHFF LQHKVHIGDI VRHLRQFEQK RRGDVIRQVA DDFLFA*DAV
151 EIKLQHVAFV NHQFIRKRQR FQAYDVAVD FDNVQAVQLF RQRFNGCRQT
201 RADFNHDIIR LRAHGVDNIA DNPRVLQKIL PETLAGFVFF HRVSSSVETP
251 PFRAAGSDSV WAGRNPFQIR TTHRAVLVVS SCVLEHKCVY SIRLMSAL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2659>:

```

m772.seq
1  ATGTTTCGGCG CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51  CGCCTGCAAG CTCTTTCAGA TTGTTGCGTA TGGTTTTCGG GCGTTGGTGG
101 AAGGCGAGTT TCACGAGTTT GGCAAAATGC TCGAAATCGT CCGCCTTGCC
151 GATCGGGTGT TTCACCGGAA TCATACGGAC GACGGCGGAA TCCACTTTCG
201 GCGCAGGGTC GAACGATTTCG GCGGTACGT CAATCAGCAT TTCCATATCG
251 AAAAAATATT GCAGCATCAC GCCAAGCGG CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATACGCTCGA CCACTTCTTT TTGCAGCATA AAGTGCATAT
351 CGACGACATC GTCCGCCACC TCCGCCAGCT TGAACAAAAG CGGTGTGGAA
401 ATGTTGTACG GGAGGTTGCC GACGATTTTC TTTTGCCTG CGATGCCGTT
451 GAAATCAAAC TGCAATACAT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTTACAGCGG CATACGATGT CGCGGTCGAT TTCGACAACG
551 TGCAGGCGGT TCAGCTTTT CGCCAAAGGT TCGGTAATCG CCGCCAAACC
601 CGGGCCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCT GATAATCCGC GTGTCCTGCA AAAAATTCTG CCCGAAACGC

```

1261

```

701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTC CCTTTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ATGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2660; ORF 772>:

m772.pep

```

1 MFGAVLRIDA DCLQIIVACK LFQIVAYGFA ALVEGEFHEF GKMLEIVRLA
51 DAVFHRNHTD DGGIHFRRRV ERFGRYVNQH FHIEKILQHH AQAQVAVFR
101 RGNHTLDHFF LOHKVHIDDI VRHLRQLEQK RCGNVVREVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RADFNHDIIR LRAHGVDNIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR MAHRAVLYVS SCVLKHKCVY SIRLMSAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 772 shows 85.2% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. gonorrhoeae*

m772/g772 85.2% identity in 298 aa overlap

	10	20	30	40	50	60
g772.pep	VFGTVLR	TADCLQI	IVVGKFF	QVVAYG	FAALAE	GFHQFG
	EMIEIVRLADTVFHRNHAH					
m772	MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD					
	10	20	30	40	50	60
g772.pep	HCGIDFRR	GIERFGR	HVNQQL	HIEKIL	QHHTQAT	VVVAFR
	GNHALDHFFLQHKVHIGDI					
m772	DGGIHFRRRV ERFGRYVNQH FHIEKILQHH AQAQVAVFR RGNHTLDHFFLQHKVHIDDI					
	70	80	90	100	110	120
g772.pep	VRHLRQFE	QKRGRD	VIRQVAD	DFLAXDA	VEIKLQH	VAFVNH
	QFIRKRQR FQTAYDVAVD					
m772	VRHLRQLEQK RCGNVVREVA DDFLFACDAVEIKLQYIAFVNHQFIRKRQR FQTAYDVAVD					
	130	140	150	160	170	180
g772.pep	FDNVQAV	QLFRQR	FGNCRQ	TRADFN	HDIIRL	RAHGVD
	NIADNPRVLQKILPETLAGFVFF					
m772	FDNVQAVQLFRQRFGNRRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF					
	190	200	210	220	230	240
g772.pep	HRVSSSV	ETPPFRA	AGSDSV	WAGRNPF	QIRTT	THRAVL
	YVSSCVLEHKCVYSIRLMSALX					
m772	HRVSFSVETPPFRAVESDSI WEGRNSFQIRMAHRAVLYVSSCVLKHKCVYSIRLMSALX					
	250	260	270	280	290	299
g772.pep						
m772						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2661>:

a772.seq

```

1 ATGTTTCGGCG CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51 CGCCTGCAAG CTCTTTCAGA TTGTGCGTA TGGTTTTCGC GCGTTGGTGG
101 AAGGCGAGTT TCACGAGTTT GCGGAAATGC TCGAAATCGT CCGCCTTGCC
151 GATACGGTGT TTCACCGGAA TCATGCGGAC GACGGCCGAA TCCACTTTCG
201 GCGCGGGGTC GAACGATTCG GCGGCGACGT CAATCAGCAT TTCCATATCG
251 AAGAAATATT GCAGCATCAC GCCCAAGCGG CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATACGATCGA CCACTTCTTT TTGCAGCATA AAGTGCATAT
351 CGACGACATC TTCGCCACCC TCCGCCAGCT TGAACAAAAG CGGCGTGGAA
401 ATGTTGTAGG GCAGGTTGCC GACGATTTTC TTTTTCGCTG CGATGCCGTT
451 GAAATCAAAC TGCAATACAT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTTACAGACG CATACGATGT CGCGGTCGAT TTCGACAACG
551 TGCAGGCGGT TCAGCTTTTTC CGCCAAAGGT TCGGTAATCG CCGCCAAACC
601 CGGACCGATT TCAATCAGCA CATCATCCGC CTGCGGGGCG ACGGCGTTGA
651 CAATATCGGT GATAATCCGC GTGTCCTGCA AAAAATTCTG CCGGAAACGC
701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTC CCTTTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ACGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```



This corresponds to the amino acid sequence <SEQ ID 2662; ORF 772.a>:

## a772.pep

```

1  MFGAVLRIDA DCLQIIVACK LFQIVAYGFA ALVEGEFHEF GEMLEIVRLA
51  DTVFHRNHAD DGRIFHRRGV ERFGRHVNQH FHIEEILQHH AQAQVVAFR
101 RGNHTIDHFF LQHKVHIDDI VRHLRQLEQK RRGNVVGQVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RTDFNHDIIR LRAHGVDNIA DNPRVLQKIL PETLAGFVEF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR TAHRVLYVS SCVLKHKCVY SIRLMSAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 772 shows 95.6% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. meningitidis*

m772/a772 95.6% identity in 298 aa overlap

	10	20	30	40	50	60
a772.pep	MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGEMLEIVRLADTVFHRNHAD					
m772	MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD					
	10	20	30	40	50	60
	70	80	90	100	110	120
a772.pep	DGRIFHRRGVVERFGRHVNQHFIHIEEILQHHQAQAVVAFRRGNHTIDHFFLQHKVHIDDI					
m772	DGGIHFRRRVERFGRYVNQHFIHIEKILQHHQAQAVVAFRRGNHTLDHFFLQHKVHIDDI					
	70	80	90	100	110	120
	130	140	150	160	170	180
a772.pep	VRHLRQLEQKRRGNVVGQVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRFQTAYDVAVD					
m772	VRHLRQLEQKRCGNVVREVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRFQTAYDVAVD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a772.pep	FDNVQAVQLFRQRFGNRRQTRTDFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF					
m772	FDNVQAVQLFRQRFGNRRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF					
	190	200	210	220	230	240
	250	260	270	280	290	299
a772.pep	HRVSFSVETPPFRAVESDSIWEGRNSFQIRTAHRVLYVSSCVLKHKCVYSIRLMSALX					
m772	HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRVLYVSSCVLKHKCVYSIRLMSALX					
	250	260	270	280	290	

g773.seq not found yet

g773.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2663>:

## m773.seq

```

1  ATGGGATTGG GTGCAACGAC TTTTGTGCGT TCGGGTGCTA TAGGCGGAGG
51  TCTGTGCAGT ACCGGGATTG GCTGTGCGGC CGGTGGACTT ATTGCAACGG
101 CAGGTATGAC CGGTGGTTAT ACACAGGCC T CAGAAGGAAG CCGGCAATTG
151 TTTGGCACTT ACCAGTCCGA TTTTGGTAAA AAAGTTGTCC TATCTTTGGG
201 TACACCAATA GAATACGAAT CGCCGTTAGT ATCTGATGCG AAAAATCTAG
251 CCGTATGGGG ATTGGAACG CTGATTACGC GCAAATTGGG AAACCTGGCA
301 ACGGGTGTGA AAACCTCCTT GACTCCGAAA ACTGCTGACG TACAGCGAAA
351 TATCCTGTCC CAATCCGAAG TCGGTATCAA GTGGGGCAAG GGGATTGAAG
401 GACAGGGAAT GCCTTGGGAG GATTATGTCG GTAAGGGCTT GTCTGCCAAT
451 GCAAGGTAC CTA AAAAATT TAAAACATT GATTATTTG ATCGTGGTAC
501 AGGCACGGCA ATCAGTGCCA AAACCTCTGA TACGCAAACT ACGGCACGCC
551 TGTCCAAACC CGAACAGCTT TACAGTACCA TGAAAGGGTA CATCGATAAG
601 ACGGCAAAAT TCAAAAGTTA TGAATTATCA GAAGTACCGT TAAGGGCAGA
651 CATGATCAAA CAGCGCGAAA TCCATCTGGC CATACCCGCA CAAACTAATA
701 AGGAGCAAAG ATTGCAGTTG CAACGTGTGG TAGAGTATGG CAAAAGTCAA
751 AACATTACAG TCAAAATTAC GGAGATCGAA TAA

```

1263

This corresponds to the amino acid sequence <SEQ ID 2664; ORF 773>:

```
m773.pep
1  MGLGATTFVG SGAIGGGLCS TGIGCAAGGL IATAGMTGGY TQASEGSRQL
51  FGTYQSDFGK KVVLSLGTPI EYESPLVSDA KNLA VWGLET LITRKLGNLA
101 TGVKTS LTPK TADVQRNLS QSEVGIKWGK GIEGQGPWE DYVGKGLSAN
151 ARLPKNFKTF DYFDRGTGTA ISAKTLDTQT TARLSKPEQL YSTMKG YIDK
201 TANFKSYELS EVPLRADMIK QREIHLAIPA QTNKEQRLQL QRVVEYGKSQ
251 NITVKITEIE *
```

a773.seq not found yet

a773.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2665>:

```
g774.seq
1  ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCTGCCTC
51  CTGTGCTTCC GTTTTACCCG TTCCGGAGGG CAGCCGAACC GAAATGCCGA
101 CACAGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC CACTCTGCAA
151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201 GGAATGTTA AACGGGAAAG TCAAAGCATT GGAGCATACG AAAATACACC
251 CTTCGGGCAG GACATACGTC CAAAAACTCG ACGACCGCAA ATTGAAAGAG
301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CCGTCGAAAC
351 CGCACAAAAA CTCTACAATC AGGCACTCAA ACACTATCAA AACGGCAGGT
401 TTTCTGCCGC AGCCGCCTTG TTGAAGGGGG CGGACGGCGG AGACGGCGGC
451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501 GGGGAACGTG GAATCTGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551 TCAAAGACAG CCCAACCGCG CCCGAAGTCA TATTCAAAAT CGGCGAATGC
601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GGCAGAGCCT
651 GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGCAGCCG
701 TACGCAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2666; ORF 774.ng>:

```
g774.pep
1  MKTKLPLFII WLSVSASCAS VLPVPEGSRT EMPTQENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVEML NGKVKALEHT KIHPSGRTYV QKLDDRKLKE
101 HYLNTEGSA SAHTVETAQN LYNQALKHYQ NGRFSAAAAL LKGADGGDGG
151 SIAQRSMYLL LQSRARMGNC ESVEIGGRY ANRFKDSPTA PEVIFKIGEC
201 QYRLQKQDIA RATWRS LIQT YPGSPA AKRA AA AVRRK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2667>:

```
m774.seq
1  ATGAAGATCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCCGCCTC
51  CTGTGCTTCC GTTTCACCCG TTCCGGCAGG CAGCCAAACC GAAATGTCGA
101 CACGGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC GACCTTGCAA
151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201 GGAAACCTTA AACGGCAAAG TCAAAGCACT GGAACACGCA AAAACACATT
251 CTTCGGGCAG GGCATACGTC CAAAAACTCG ACGACCGCAA GTTGAAGAG
301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CTGTGAAAC
351 CGCACAAAAA CTCTACAATC AGGCACTCAA ACACTATAAA AGCGGCAAGT
401 TTTCTGCCGC TGCCTCCCTG TTGAAGGGCG CGGACGGAGG CGACGGCGGC
451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501 GGGCAACTGC GAATCCGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551 TCAAAGACAG CCCAACCGCG CCTGAAGCCA TGTTCAAAAT CGGCGAATGC
601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GGCAGAGCCT
651 GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGCAGCCG
701 TGCGCAAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2668; ORF 774>:

```
m774.pep
1  MKIKLPLFII WLSVSASCAS VSPVPAGSQT EMSTRENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVETL NGKVKALEHA KTHSSGRAYV QKLDDRKLKE
101 HYLNTEGSA SAHTVETAQN LYNQALKHYK SGKFSAAASL LKGADGGDGG
151 SIAQRSMYLL LQSRARMGNC ESVEIGGRY ANRFKDSPTA PEAMFKIGEC
201 QYRLQKQDIA RATWRS LIQT YPGSPA AKRA AA AVRRK*
```

Computer analysis of this amino acid sequence gave the following results:

1264

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 774 shows 92.8% identity over a 237 aa overlap with a predicted ORF (ORF 774) from *N. gonorrhoeae*

m774/g774 92.8% identity in 237 aa overlap

	10	20	30	40	50	60
g774.pep	MKT <del>K</del> LPLFI <del>I</del> WLSVSAS <del>C</del> SVLPVPEGSRT <del>E</del> MP <del>T</del> QENASDGI <del>P</del> YPVPTLQDRLDYLEGKI					
m774	MKIKLPLFI <del>I</del> WLSVSAS <del>C</del> SVSPV <del>P</del> AGSQTEMSTRENASDGI <del>P</del> YPVPTLQDRLDYLEGKI					
	10	20	30	40	50	60
	70	80	90	100	110	120
g774.pep	VRLSNEVEMLNGKVKALEHTKIHPSGR <del>T</del> YVQKLDD <del>R</del> KLKEHYLNTEGGSASAHTVETAQN					
m774	VRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDD <del>R</del> KLKEHYLNTEGGSASAHTVETAQN					
	70	80	90	100	110	120
	130	140	150	160	170	180
g774.pep	LYNQALKHYQNGRFSAAAALLKGADGGDGSIAQRSMYLLLSRARMGN <del>C</del> ESVIEIGGRY					
m774	LYNQALKHYKSGKFSAAASLLKGADGGDGSIAQRSMYLLLSRARMGN <del>C</del> ESVIEIGGRY					
	130	140	150	160	170	180
	190	200	210	220	230	
g774.pep	ANRFKDSPTAPEVIFKIGECQYRLQ <del>Q</del> KDIARATWRS <del>L</del> IQTYPGSPA <del>A</del> KRAAAAVRKR <del>X</del>					
m774	ANRFKDSPTAPEAMFKIGECQYRLQ <del>Q</del> KDIARATWRS <del>L</del> IQTYPGSPA <del>A</del> KRAAAAVRKR <del>X</del>					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2669>:

a774.seq

```

1  ATGAAGACCA AATTACCGCT TTTATCATT TGGCTGTCCG TATCCGCCGC
51  CTGTTCTTCC CCGTTTCCC GCAATATTCG GGATATGCGG CTCGAACCGC
101 AGGCAGAGGC AGGTAGTTCG GACGCTATTC CCTATCCCGT TCCCACTCTG
151 CAAGACCGTT TGGATTATCT GGAAGGCACA CTCGTCCGCC TGTCGAACGA
201 AGTGGAAACC TTAACGGCA AAGTCAAAGC ACTGGAGCAT GCGAAACAC
251 ACCCTTCCAG CAGGGCATA GTCCTAAAC TCGACGACCG CAAGTTGAAA
301 GAGCATTACC TCAATACCGA AGGCGGCAGC GCATCCGCAC ATACCGTCGA
351 AACCGCACAA AACCTCTACA ATCAGGCACT CAAACACTAT AAAAGCGGCA
401 GGTTTTCTGC CGCTGCCTCC CTGTTGAAAG GCGCGGACGG AGGCGACGGC
451 GGCAGCATCG CGCAACGCAG TATGTACCTG TTGCTGCAAA GCAGGGCGCG
501 TATGGGCAAC TCGCAATCCG TCATCGAAAT CGGAGGGCGT TACGCCAACC
551 GTTTCAAAGA CAGCCCAACC GCGCCTGAAG CCATGTTCAA AATCGGCGAA
601 TGCCAATACA GGCTTCAGCA AAAAGACATT GCAAGGCGCA CTTGGCGCAG
651 CCTGATACAG ACCTATCCCG GCAGCCCGGC GGCAAAACGC GCCGCCGCAG
701 CCGTGCGCAA ACGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2670; ORF 774.a>:

a774.pep

```

1  MKTKLPLFII WLSVSAACSS PVSRNIQDMR LEPQAEAGSS DAIPYPVPTL
51  QDRLDYLEGT LVRLSNEVET LNGKVKALEH AKTHPSSRAY VQKLDDRKLK
101 EHYLNTEGGS ASAHTVETAQ NLYNQALKHY KSGRFSAAAS LLKGADGGDG
151 GSIAQRSMYL LLQSRARMGN CESVIEIGGR YANRFKDSPT APEAMFKIGE
201 CQYRLQQKDI ARATWRSLIQ TYPGSPAAKR AAAAVRKR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 774 shows 89.5% identity over a 238 aa overlap with a predicted ORF (ORF 774) from *N. meningitidis*

m774/a774 89.5% identity in 238 aa overlap

	10	20	30	40	50	60
a774.pep	MKT <del>K</del> LPLFI <del>I</del> WLSVSAACSSPVS <del>R</del> NIQDMRLEPQAEAGSSDAIPYPVPTLQDRLDYLEG <del>T</del>					
m774	MKIKLPLFI <del>I</del> WLSVSAS <del>C</del> SVSPV <del>P</del> AGSQTEMSTRENASDGI <del>P</del> YPVPTLQDRLDYLEG <del>K</del>					
	10	20	30	40	50	

1265

```

          70      80      90      100     110     120
a774.pep   LVRLSNEVELNGKVKALEHAKTHPSSRAYVQKLD DRKLKEHYLNTEGGSASAHTVETAQ
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m774       IVRLSNEVELNGKVKALEHAKTHSSGRAYVQKLD DRKLKEHYLNTEGGSASAHTVETAQ
          60      70      80      90      100     110

          130     140     150     160     170     180
a774.pep   NLYNQALKHYKSGRFSAAASLLKGADGGDGG SIAQRSMYLLQLSRARMGNCSVIEIGGR
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m774       NLYNQALKHYKSGKFSAAASLLKGADGGDGG SIAQRSMYLLQLSRARMGNCSVIEIGGR
          120     130     140     150     160     170

          190     200     210     220     230     239
a774.pep   YANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRS LIQTYPGSPA AKRAAAAVRKRX
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m774       YANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRS LIQTYPGSPA AKRAAAAVRKRX
          180     190     200     210     220     230

```

g790.seq not found yet

g790.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2671>:

```

m790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATAGTC CTTAACGATG TCCAAGGCGA TACGACCATC AACAAACATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ATGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTCG
551 CCCCCTCGCA GTACACGTTT GCCGTTGCCA TGCCCCGACG GTCCATGTCTG
601 CCGGTTATCG AAAAGGGAGA CTTGCTGGTG GTCGAGCCGC GTATGTGCCC
651 TCGGGACGAA GACATCGCGC TGATTGAACT GTCCGACAAG CGGCTGGTCG
701 TCGCGCACCT TGTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG
751 GGCAGGCCGT CTGAAGCCTT TGACCTGCCC GAAGGCAGCA CGATTTTAGG
801 TGTGGTGTCT GAGTCAAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTGAT TCGGATTACC GCCCTGATG TGTGGACGGT TGGTATGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAATCAGC
951 CGTATGCTTT CTTGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2672; ORF 790&gt;:

```

m790.pep
1  MARRSKTFEE AA AEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTC SR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSIV LNDVQGD TTI NNHHTHTHNH SDADGKALSM
151 RLTPRPLLD RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMCPADE DIALIELSDK RLVVAHLVID IAGRMLIYQT
251 GRPSEAFDLP EGSTILGVVL ESKNGLCP PH ROEGVLIRIT APDVWTVGMI
301 SAKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNPN NA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2673>:

```

a790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATAATC CTTAACGATG TCCAAGGCGA TACGACCATC AACAAACATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ACGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTCG
551 CCCCCTCACA ATATACGTTT GCCGTTGCCA TGCCCCGACG GTCCATGTCTG
601 CCGGTTATCG AAAAGGGGGA TTTGCTGGTG GTCGAGCCGC GTATGCGCCC
651 TCGGGACGAA GACATCGTAC TGATTGAACT GTCCGACAAG CGGCTGGTCG
701 TCGCGCACCT TGTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG

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1266

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751 GGCAGGCCGT CTGAAGCCCT CGACCTGCCC GAAGGCAGCG TGATTTTAGG
801 TGTGGTGCTG GAGTCAAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTGTGAT TCGGATTACC GCCCTGATG TGTGGACGGT TGGTACGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAAATCAGC
951 CGTATGCTTT CTTGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGT

```

This corresponds to the amino acid sequence <SEQ ID 2674; ORF 790.a>:

```

a790.pep
  1 MARRSKTFEE AAAEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCRSR
 51 YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSII LNDVQGDTTI NNHHTHTHNN SDADGKALSM
151 RLTPRPLLSL RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVVAHLVID IAGRMLIYQT
251 GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNPEN NAC

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 790 shows 98.2% identity over a 342 aa overlap with a predicted ORF (ORF 790) from *N. meningitidis*

a790/m790 98.2% identity in 342 aa overlap

	10	20	30	40	50	60
a790.pep	MARRSKTFEEAAAEEVEERFGHRGIKLVEFEGTAKPCVINC PKHGNQTCRSRYSNMFIGSSW					
m790	MARRSKTFEEAAAEEVEERFGHRGIKLVEFEGTAKPCVINC PKHGNQTCRSRYSNMFIGSSW					
	10	20	30	40	50	60
	70	80	90	100	110	120
a790.pep	GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSII					
m790	GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSIV					
	70	80	90	100	110	120
	130	140	150	160	170	180
a790.pep	LNDVQGDTTINNHHTHTHNSDADGKALSMRLTPRPLLSDRQAAAFARTGKLTGSFDLFA					
m790	LNDVQGDTTINNHHTHTHNSDADGKALSMRLTPRPLLSDRQAAAFARTGKLTGSFDLFA					
	130	140	150	160	170	180
	190	200	210	220	230	240
a790.pep	SVVAPSQYTF AVAMPDTSMS PVIEKGDLLVVEPRMRPADE DIVLIELSDKRLVVAHLVID					
m790	SVVAPSQYTF AVAMPDTSMS PVIEKGDLLVVEPRMCPAEDIALIELSDKRLVVAHLVID					
	190	200	210	220	230	240
	250	260	270	280	290	300
a790.pep	IAGRMLIYQTRPSEALDLPESVILGVVLESKNGLCPPHRQEGVLIRITAPDVWTVGTI					
m790	IAGRMLIYQTRPSEAFDLPEGSTILGVVLESKNGLCPPHRQEGVLIRITAPDVWTVGMI					
	250	260	270	280	290	300
	310	320	330	340		
a790.pep	SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNPNNAC					
m790	SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNPNNAX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2675>:

```

g791.seq
  1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CTACTTGTTT
 51 TGGTTTGTGT TTTGGTTTTT GTGTATTTGG AGTGGGCTCG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACGCGCGT CTTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GAGAAGTCAT
201 CCGTATGTAT GGGGAGCAGC GGC GCGAATT TACAAAAATC GGC GATTTC
251 CCGAGGTGTT CCGGAATGCG GTTATTGCCG CCGAGGATAA ACGCTTTTAC
301 CCGCATTGGG GGGTGGATGT TTGGGGTGTT GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACACAGCAGG

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1267

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401 TGGCGAAAAA TTTTATTTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCTA TAAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTTGAG TTGTATTTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CGGAGCGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCATTGA ATGAGGAAC TGCATTATGAG CGGTTTGTTT GGAATTCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCGGGAA CTGTATGAGA
851 AATATGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCACCAGTC ATCAGAAGGC GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCGAT CGCGGCAGCA GCTACCGCGG TGCGGAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTTGG ATGTTACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTGCGCTTG
1151 ACAGGCCGCG CTGCGGTTTT GCGGCCGAG CGGTCGATAA TGAGAAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGTTT AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CCGTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTT TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTCCCTGCC GGGGAAAGGG
1501 CCGAACCGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGCTTCGGCT TCCAGCCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACGACGC CGTTGAAAGT GCGCGAGGCA TATAGTGTAT
1751 TTGCGAAGCG CGGATATAGG GTTCTCTCGC ACGTGATCGA TAAGATTAT
1801 GACAGAGACG CAGGTTGCG CGCCAAATG CAACCTTGG TGCGAGGCA
1851 AAATGCCCTT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTCGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAAACGGGT ACGACCAACG ACAATAAAGA
2001 TGCGTGGTTT TCGGTTTGA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG CCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAAGGG ATGAAAATGC CTGAAGGTGT GGTACAGCAG AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAT GCTGGACAAC
2251 AGCGGTATTG CCGCGCAACC TTCCCGACGG GCAAAAAGAG ATGATGAAGC
2301 GGCAGTAGAA AACGAACAGC AGGGAAGGTC TGACGAAACG CGTCAGGACG
2351 TACAGGAAAC GCGGTGCTT CCGAGCAATA CGGATTCCAA ACAGCAGCAG
2401 TTGGATTCCC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2676; ORF 791.ng>:

g791.pep

```

1 MVNYYSAMIK KILTTCFGLF FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEQRREETKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RVRKIDQSA LYVAEMVRRE LYEKYGEDAY TQGFKVYTTV
301 RTDHQKAATE ALRKALRNFD RGSSYRGAEN YIDLKSESDV EETVSQYLSG
351 LYTVDKMVPA VVLDTTKKN VVIQLPGGRR VALDRRALGF AARAVDNEKM
401 GEDRIIRGAV IRVKNNGGRW AVVQEPLLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRPSELP ASLSMALGTG ETTPKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQM QPLVAGQNAP QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRDIAAGKTG TTNDNKDAWF VGFNPDVVT A VYIGFDKPKS MGRAGYGGTI
701 AVPVWVDYMR FALKGKQKKG MKMPEGVVS NGEYMKERM VTDPLMLDN
751 SGIAPQPSRR AKEDDEAAVE NEQGRSDET RQDVQETPVL PSNTDSKQQQ
801 LDSLF*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2677>:

m791.seq

```

1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTC
51 TGGTTTGGTT TTTGGGTTTT GTGTATTTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AACTGCCCGT CTTTGGATTC TTTGCAGCAT
151 TACCAGCCTA AATGCCGTT GACTATTTAT TCGGCGGATG GGGAAAGTCAT
201 CCGTATGTAT GGGAGCAGC GCGCGAATT TACAAAAATC GCGGATTTCC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CCGCATTTGG GGTGGATGT TTTGGGTGTT GCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC

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1268

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451 AATGAGGTGT TGCTTGCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTC AATCAGATTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTC ATAAGAATGT CCGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAACT GCATTACGAG CGGTTTGTTC GGAAATCGA
801 TCAGAGTGCG TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGTTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCAT CGCGGCAGCA GCTACCGCGG TCGGGAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCCCGCC GTTGTGTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGCGG GTTACGCTTG
1151 ACAGGCGCGC CTGGGTTTT GCGGCCCGG CGGTCAATAA TGAATAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGCGGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGG GCTTTGGGTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTT TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CGCGCTCCAC AGTGGTTAAC GATGCGCCGA TTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTGCGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGC ACGTAATCGA TAAGATTTAT
1801 GACAGAGACG CGAGGTTGCG CGCCCAAATG CAACCTTTGG TGCTGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACGGGT ACGACCAATG ACAATAAGGA
2001 TCGGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAATGCG CTGAAGGTGT GGTGAGCAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GCGGACGGC AGGCGGCGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAAAC GCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGGATTCTC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2678; ORF 791>:

```

m791.pep
1 MVNYYSAMIK KILTTTCFLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFKVYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLKSEDEV EETVSQYLSG
351 LYTVDMVPA VLDVTKKKN VVIQLPGGRR VTLDRRALGF AARAVNNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPLLQG ALGSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPKKG
501 PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRLLRAQ QPLVAGQNAP QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGKQKKG MKMPEGVVS NGEYMKERM VTDPLGLTDN
751 SGIAPQPSRR AKEDDGGAEE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*

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g791/m791 97.3% identity in 805 aa overlap

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g791.pep      10      20      30      40      50      60
               MVNYYSAMIKKILTTTCFLFFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
               |||
m791          10      20      30      40      50      60
               MVNYYSAMIKKILTTTCFLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY

g791.pep      70      80      90      100     110     120
               SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGVNVVS
               |||
m791          70      80      90      100     110     120
               SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGVNVVS

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1269

	130	140	150	160	170	180
g791.pep	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
g791.pep	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPVNPRAKLRQKYILNNMLE					
m791	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPVNPRAKLRQKYILNNMLE					
	190	200	210	220	230	240
	250	260	270	280	290	300
g791.pep	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKGEDAYTQGFKVYTTV					
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKGEDAYTQGFKVYTTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
g791.pep	RTDHQKAATEALRKALRNFDGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMPVA					
m791	RADHQKVATEALRKALRNFDGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMPVA					
	310	320	330	340	350	360
	370	380	390	400	410	420
g791.pep	VVLDTVTKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIRGAVIRVKNNGGRW					
m791	VVLDTVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRGAVIRVKNNGGRW					
	370	380	390	400	410	420
	430	440	450	460	470	480
g791.pep	AVVQEPLLQAGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
m791	AVVQEPLLQAGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
	430	440	450	460	470	480
	490	500	510	520	530	540
g791.pep	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
m791	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
	490	500	510	520	530	540
	550	560	570	580	590	600
g791.pep	GVGYAQQYIRRFGRFSELPAFLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
m791	GVGYAQQYIRRFGRFSELPAFLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
	550	560	570	580	590	600
	610	620	630	640	650	660
g791.pep	DRDGRRLRAQMQLVAGQNAFQAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
m791	DRDGRRLRAQMQLVAGQNAFQAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
	610	620	630	640	650	660
	670	680	690	700	710	720
g791.pep	TTNDNKDAWFVGFNPVTVAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGKQKKG					
m791	TTNDNKDAWFVGFNPVTVAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKQKKG					
	670	680	690	700	710	720
	730	740	750	760	770	780
g791.pep	MKMPEGVVSSNGEYYMKERMVTDPLMLDNGSIAPQPSRRAKEDDEAAVENEQQGRSDET					
m791	MKMPEGVVSSNGEYYMKERMVTDPLTLDNGSIAPQPSRRAKEDDGAEEGGRQAADDEV					
	730	740	750	760	770	780
	790	800				
g791.pep	RQDVQETPVLPSNTDSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2679>:



1270

## a791.seq

```

1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51  TGGTTTGGTT TTTGGGTTT GTGTATTTGG AGTGGGTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAAGTCCGTT CTTTGGATTG TTTGAGCAT
151 TACCAGCTA AAATGCCGTT GACTATTAT TCGGCGGATG GGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAAATC GGCGATTTC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGGTGT GCGCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTG GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTTG AGCAGTGA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTC ATCAGATT TAATCGGTG CCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTGA ATGAGGAAC GCATTACGAG CGGTTTGTTC GGAATTCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCAT ACGCAGGTT TTAAGTTTA TACCACGGTC
901 CCGCGCCATC ATCAGAAAGG GCGAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCAT CGCGGCAGCA GCTACCGCGG TCGGAAAAAC TATATCGATT
1001 TAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTGCGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCGCC GTTGTGTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CCGCAGCGCG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTT GCGGCGCGG CCGTCAATAA TGAATAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGTTTC AAGAGCCGTT GCTGCAGGGG GCTTTGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CCGTTATGAT
1351 TTTCACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTT TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTCCCTGCC GGGGAAAGGG
1501 CCGAACCGTT CGGTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGCGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGCA ACGTAATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAATG CAACCTTTGG TGGCCGGGCA
1851 AAATGCCGCT CAGGCAATCG ATCCGCGCAA TGCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAAACGGT ACGACCAATG ACAATAAGGA
2001 TGCGTGGTTT GTCGGTTTAA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CCGTACGATT
2101 GCGGTGCGCG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAAATGC CTGAAGGTGT GGTGAGCAGC AATGGCGAAT
2201 AATTAATGAA GGAACGTATG GTAACCGATC CCGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CCGCGCAGAA GCGCGACGGC AGCGGCGGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAAC GCGGTTGCTT CCGAGTAATA CTGTTTCCAA ACAGCAGCAG
2401 TTGGATTCTC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2680; ORF 791.a>:

## a791.pep

```

1  MVNYYSAMIK KILTTCTFGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51  YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVVDVGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVKVYTTV
301 RADHOKVATE ALRKALRNFD RGSSYRGAEN YIDLSKSEDEV EETVSYQLSG
351 LYTVDKMPVA VVLDVTKKKK VVQLPGGRR VTLDRRALGF AARAVNNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPLLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRV QAMRQPGSTF KPFVYSALS KGMTASTVNV DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQ QPLVAGQNAQ QAIQPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVT VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGKQKKG MKMPEGVSS NGEYMKERM VTDPLTLN
751 SGIAPQPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*

```

a791/m791 99.9% identity in 805 aa overlap

10

20

30

40

50

60

1271

a791.pep	MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
m791	MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
	10 20 30 40 50 60
a791.pep	70 80 90 100 110 120
m791	SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAVGNVVS
	70 80 90 100 110 120
a791.pep	130 140 150 160 170 180
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
	130 140 150 160 170 180
a791.pep	190 200 210 220 230 240
m791	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPIVNERAKLRQKYILNNMLE
	190 200 210 220 230 240
a791.pep	250 260 270 280 290 300
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFKVYTTV
	250 260 270 280 290 300
a791.pep	310 320 330 340 350 360
m791	RADHQQVATEALRKALRNFDRGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA
	310 320 330 340 350 360
a791.pep	370 380 390 400 410 420
m791	VVLDTVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
	370 380 390 400 410 420
a791.pep	430 440 450 460 470 480
m791	AVVQEPPLQGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
	430 440 450 460 470 480
a791.pep	490 500 510 520 530 540
m791	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI
	490 500 510 520 530 540
a791.pep	550 560 570 580 590 600
m791	GVGYAQQYIRRFGRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
	550 560 570 580 590 600
a791.pep	610 620 630 640 650 660
m791	DRDGRRLRAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG
	610 620 630 640 650 660
a791.pep	670 680 690 700 710 720
m791	TTNDNKDAWFGFNPDVVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKQKG
	670 680 690 700 710 720
a791.pep	730 740 750 760 770 780
m791	MKMPEGVVSSNGEYYMKERMVTDPLGLTLNDSGIAPQPSRRAKEDDGGAAEGGRQAADDEV
	730 740 750 760 770 780

1272

	730	740	750	760	770	780
	790	800				
a791.pep	RQDMQETPVLPSNTGSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2681>:

g792.seq

```

1   ATGTTCCGCA TCGTCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATCACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAA
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGGTGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GTCCGTTTGT
251 CCggacacgg gggcttcGat GGGGACGGCa tTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCGAAGT GAAGGCGGGC GGATCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTCTTCC TCAACGAAAG CCGCAACTAT CTGCGCAAAG
401 GGAAGAGGCG GGCCATTACG GCAATGATGG AAGCTGTTAC CGACAAAAAC
451 AGGATTTTCG AACTGTATTT AAACCAATC GAATGGCACT ACGGCgtTTT
501 CGGCGCGGAA GCTGCGTCCC GgtatTttTA TAAAAACCG GCcgcagACC
551 TGACcAAACA GCAGgcggcg aaactgacgg tactcgtccc cgcgccgttt
601 tactactctg accatccaaa aagcaaacgg ctgcgcaaca aaaccaatat
651 cgtgctcaga cgcattgggt cggcaaatTA ccccaagcg aaacggactg
701 attgttcag atatggaaat gccgcctgaa ctgggggttcg aacggcatat
751 gttttctggg acttataa

```

This corresponds to the amino acid sequence <SEQ ID 2682; ORF 792.ng>:

g792.pep

```

1   MFRIVKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WVPYNRISTN LKKALIASD VRFAGHGGFD GDGIQNAIRR
101 NRNSGEVKAG GSTISQQLAK NLFLNESRNY LRKGEEAAIT AMMEAVTDKN
151 RIFELYLNSI EWHYGVFGAE AASRYFYKPP AADLTkQQA KLTVLVPAPF
201 YYSDHPSKR LRNKTNIIVLR RMGSANYPKA KRTDCSRYGN AA*TGVRTAY
251 VFWDL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2683>:

m792.seq

```

1   ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGATGCCCT ACAAAACGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCCTTTCTG
251 CCGGGCAGCG CGGCTTCGAT TGGGGCGGCA TTCAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCAAAGT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
401 GCGAAGAAGC GCGGATTACC GCGATGATGG AAGCCGTTAC CGACAAAGAC
451 AGGATTTTTC AACTGTATTT AAACCAATC GAATGGCACT ACGGCgtTTT
501 CGGCGCGGAA GCCGCGTCCC GGTATTTTTA TCAAATACCC GCCGCCAAGC
551 TGACCAAAACA GCAGGCGGCA AAACGACGG CGCGCGTCCC CGCCCCGCTC
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CTCCGCAACA AAACCAATAT
651 CGTGCTCAAA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701 GA

```

This corresponds to the amino acid sequence <SEQ ID 2684; ORF 792>:

m792.pep

```

1   MFRIIKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WMPYKRISTN LKKALIASD ARFAGHGGFD WGGIQNAIRR
101 NRNSGKVKAG GSTISQQLAK NLFLNESRSY IRKGEEAAIT AMMEAVTDKD
151 RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTkQQA KLTARVPAPL
201 YYADHPSKR LRNKTNIIVLK RMGSAELPES DTD*

```

g792 / m792 90.4% identity in 230 aa overlap

	10	20	30	40	50	60
g792.pep	MFRIVKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR					
m792	MFRIIKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR					
	10	20	30	40	50	60
	70	80	90	100	110	120
g792.pep	WVPYNRISTNLKKALIASDVRFAGHGGFDGDGIQNAIRRNNSGEVKAGGSTISQQLAK					

[illegible]

```
a792.seq
1      ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51     CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101    CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
151    GAAGGTCGCG ATGTCGCATC GGATTAACCG TGGATGCCCT ACAAAACGAT
201    TTCCACCAAC CTGAAAAAAG CCGTGAATTG TTCCGAAGAT CGCGGTTTCG
251    CCGGGCACGG CGGCTTCGAT TGGGGCGGCA TTCAAACGCG CATCAGGCGC
301    AACCAGGAAC GCGGCAAAAT GAAGGCGGGG GGCTCGACCA TCAGCCAGCA
351    GCTTGCCAAA AGCCTGTTTT TAAACGAAGC CCGCAGCTAT ATCCGCAAAAG
401    GCGAAGAAAG CGGATTTACC CGGATGATGG AAGCCGTTAT CGACAAAGAC
451    AGGATTTTTG AACTGTATTT AAACCTCAAT GAATGGCATC ACGGCGTTTT
501    CGGCGCGGAA GCGCGTCTCC GGTATTTTAA TCAATATACC GCCGCCAAGC
551    TGACCAAAAC CACGGCGGCA AATTATACGG CGCGCGTCCC CGCCGCCGTC
601    TACTAGCCCG ACCATCCGAA AAGCAAACGG CTCGCAACA AAACCAATAT
651    CTGCTCAGA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701    GA
```

```
a792.pep
1  MFRIIKWLIA LPVGIFIFFN AYYVYNIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WMPYKRISTN LKKALIASED ARFAGHGGFD WGGIQNAIFR
101 NRNSGKVKAG GSTISQQLAK NLFNLNRSY IRKGEEAAIT AMMEAVTDKD
151 RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTQQQAA KLTARVPAPL
201 YYADHPKSKR LRKNTNIVLR RMGSAAELPS DTD*
```

	10	20	30	40	50	60
a792.pep	MFRIIKWLIALPVGIFIFFNAYVYGNII	TYRAVAPHRTAFMSMRMKQFEQEGRD	VALDYR			
m792	MFRIIKWLIALPVGIFIFFNAYVYGNII	TYRAVAPHRTAFMSMRMKQFEQEGRD	VALDYR			
	10	20	30	40	50	60
a792.pep	70	80	90	100	110	120
	WMPYKRISTNLKKALIA	SEDARFAGHGGFDWGGI	QNAIRNRNRNSGKVKAGGSTISQQLAK			
m792	WMPYKRISTNLKKALIA	SEDARFAGHGGFDWGGI	QNAIRNRNRNSGKVKAGGSTISQQLAK			
	70	80	90	100	110	120
a792.pep	130	140	150	160	170	180
	NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFELYLNSIEWHYGVFGAEAA	SRFYQIP				
m792	NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFELYLNSIEWHYGVFGAEAA	SRFYQIP				
	130	140	150	160	170	180
a792.pep	190	200	210	220	230	
	AAKLTKQQA	AKLTARVPAPLYADHPKSKRLRNKTNIVLRRMGSAELPESD	TDX			
m792	AAKLTKQQA	AKLTARVPAPLYADHPKSKRLRNKTNIVLRRMGSAELPESD	TDX			
	190	200	210	220	230	

q793.seq

1274

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1   ATGTTGATTA AAAGCGAATA TAAGCCCCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATTAGCTTC GTCCTGATGG
101 CAATGGCGGT CTTGTTTGCC TGTCTGATTG CCCGCGGGCT GTATCTGCAG
151 ACGGTAACGT ATAACTTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAGCA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTGGC GTTGAGCGCG CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GATATGAAGG AAATGCCGTC TGCCGCCCAA TTGGAACGCC TGTCAGAGCT
351 TGTCTGATGT CCGGTTCGATG TTTTGAGGAA CAAACTCGAA CAGAAAGGCA
401 AGTCGTTTAT TTGGATCAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGGA AAACTTTGTA TTTGAAAAAG AATTAAAACG
501 CCATTACCCG ATGGGCAACC TGTTCGCACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTCGGAAC TTTCGCTTGA AGACAGCCTG
601 TATGGCGAAG ACGGCGCGGA AGTTGTTTTG CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCACCAGCA AACCGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCAATAA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTGGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGACCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCTGGTTCG GCAATCAAAC CGTTCGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAAAACGGA CCGTCTCCCG TGCAGCATGA TACCCATGTT
1051 TACCCCTCTT TGGATGTGCG CGGCATTATG CAGAAATCGT CCAACGTCGG
1101 CACAAGCAAA CTGTCTGCGC GTTTCGGCGC CGAAGAAATG TATGACTTCT
1151 ATCATGAATT GGGCATCGGT GTGCGTATGC ACTCGGGCTT TCCGGGGGAA
1201 ACTGCAGGTT TGTGAGAAA TTGGCGCAGG TGGCGGCCCA TCGAACAGGC
1251 GACGATGTCT TTCGGTTACG GTCTGCAATT GAGCCTGCTG CAATTGGCGC
1301 GCGCCTATAC CGCACTGACG CACGACGGCG TTTTGCTGCC GCTCAGCTTT
1351 GAGAAGCAGG CGGTTGCGCC GCAAGGCAAA CGCATATTCA AAGAATCGAC
1401 CGCGCGCGAG GTACGCAATC TGATGGTTTC CGTAACCGAG CCGGCGGGA
1451 CCGGTACGGC GGGTGCGGTG GACGGTTTCG ATGTCGGCGC TAAACCGGC
1501 ACGGCGCGCA AGTTCGTCAA CGGGCGTTAT GCCGACAACA AACACGTCGC
1551 TACCTTTATC GGTTTTGCCC CCGCAAAAAA CCCCCTGTG ATTGTGGCGG
1601 TAACCATCGA CGAACCGACT GCCACGGCT ATTACGGCGG CGTAGTGGCA
1651 GGGCCGCCTC TCAAAAAAAT TATGGGCGGC AGCCTGAACA TCTTGGGCAT
1701 TTCCCGGACC AAGCCACTGA CCGCCGACG CGTCAAAACA CCGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2688; ORF 793.ng>:

g793.pep

```

1   MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAMAVLFA CLIARGLYLQ
51  TVTYNFLKEQ GDNRIVRTQA LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 DMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGSFIWIK RQLDPKVAEE
151 VKALGLENFV FEKELKRHPY MGNLFAHVIG FTDIDGKQOE GLELSLEDSL
201 YGEDGAEVVL RDRQGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPQ RADSEQRRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
351 YPSLDVRGIM QKSSNVGTSK LSARFGAEEM YDFYHELGIQ VRMHSGFPGE
401 TAGLLRNWRR WRPIEQATMS FGYGLQLSL QLARAYTALT HDGVLLPLSF
451 EKQAVAPQ GK RIFKESTARE VRNLMVSVTE PGGTGTAGAV DGFVDVGARTG
501 TARKFVNGRY ADNKHVATFI GFAPAKNPRV IVAVTIDEPT AHGYGGVVA
551 GPPFKKIMGG SLNILGISPT KPLTAAAVKT PS*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2689>:

m793.seq

```

1   ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACTTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAAACA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTGGC GTTGAGTGGC CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCAGAGCT
351 TGTCTGATGT CCGGTTCGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGGA AAACTTTGTA TTTGAAAAAG AATTAAAACG
501 CCATTACCCG ATGGGCAACC TGTTCGCACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTCGGAAC TTTCGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTTG CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACCGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCAATAA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTGGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCGCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCCGGTTTC GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA

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1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGC GCGATAC CCATGTTTAC
1051 CCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACGT TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGTCTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGGGCACCG
1451 GTACGGCGGG TCGGTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTGCCCCCG CAAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGGCGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCCGACCAAG CCACTGACCG CCGCAGCCGT CAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2690; ORF 793>:

```

m793.pep
1  MLIKSEYKPR MLPKEEQVK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNFLKEQ GDNRIVRTQT LPATRGTVSD RRGAVLALSA PTESLFAVEPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKFSFIWIK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYPMGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAENVL RDRQGNIVDS LDSPRNKAPK NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPGRADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEEMY DFXHELIGIV RMHSGFPGET
401 AGLLRNWRWR RPIEQATMSF GYGLQLSLLO LARAYTALTH DGVLLPVSE
451 KQAVAPQKKR IFKESTAREV RNLMSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYGGVAVG
551 PPFKKIMGGS LNLGISPTK PLTAAAVKTP S*

```

g793/m793 98.5% identity in 582 aa overlap

```

g793.pep      10      20      30      40      50      60
MLIKSEYKPRMLPKEEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m793          10      20      30      40      50      60
MLIKSEYKPRMLPKEEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ

g793.pep      70      80      90      100     110     120
GDNRIVRTQALPATRGTVSDRNGAVLALSAPTESLFAVPKDMKEMPSAAQLERLSELVDV
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m793          70      80      90      100     110     120
GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV

g793.pep     130     140     150     160     170     180
PVDVLRNKLEQKGKFSFIWIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m793         130     140     150     160     170     180
PVDVLRNKLEQKGKFSFIWIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG

g793.pep     190     200     210     220     230     240
FTDIDGKGQEGLELSLEDSLYGEDGAENVLDRQGNIVDSLDSPRNKAPQNGKDIILSLD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m793         190     200     210     220     230     240
FTDIDGKGQEGLELSLEDSLHGEDGAENVLDRQGNIVDSLDSPRNKAPKNGKDIILSLD

g793.pep     250     260     270     280     290     300
QRIQTLAYEELNKAVEYHQAAGTVVVLDAARTGEILALANTPAYDPNRPGRADSEQRNR
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m793         250     260     270     280     290     300
QRIQTLAYEELNKAVEYHQAAGTVVVLDAARTGEILALANTPAYDPNRPGRADSEQRNR

g793.pep     310     320     330     340     350     360
AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDDTHVYPSLDVRGIM
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m793         310     320     330     340     350
AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRD-THVYPSLDVRGIM

g793.pep     370     380     390     400     410     420
QKSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRWRPIEQATMS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m793         370     380     390     400     410
QKSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRWRPIEQATMS
360      370      380      390      400      410

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1276

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          430      440      450      460      470      480
g793.pep  FGYGLQLSLQLARAYTALTHDGVLLPLSF EKQAVAPQGKRIFKESTAREVRNLMVSVTE
          |||
m793      FGYGLQLSLQLARAYTALTHDGVLLPV SF EKQAVAPQGKRIFKESTAREVRNLMVSVTE
          420      430      440      450      460      470

          490      500      510      520      530      540
g793.pep  PGGTGTAGAVDGFVDGAKTGTARKFVN GR YADNKHVATFIGFAPAKNPRVIVAVTIDEPT
          |||
m793      PGGTGTAGAVDGFVDGAKTGTARKFVN GR YADNKHVATFIGFAPAKNPRVIVAVTIDEPT
          480      490      500      510      520      530

          550      560      570      580
g793.pep  AHGYGGVVAGPPFFKKIMGGS LNILGISPTKPLTAAAVKTPSX
          |||
m793      AHGYGGVVAGPPFFKKIMGGS LNILGISPTKPLTAAAVKTPSX
          540      550      560      570      580

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2691>:

```

a793.seq
1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACTTT T GAAAGAACAG GGCACACACC GGATTGTGCG
201 GACTCAAACA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTGGC GTTGAGTGCG CCGACGGAGT CCTGTTTGC CGTGCCTAAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTCGATGTG CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAG CGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGGA AAACCTTGTA TTTGAAAAAG AATTAACG
501 CCATTACCCG ATGGGCAACC TGTTTGACA CGTCATCGGA TTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTCGGAAC TTTCGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTTC CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CCGTCGAATA CCATCAGGCA AAAGCCGAAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCGGTAACCG ATATGATCGA ACCCGGTTTC GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGCGCGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACCTG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGTCTTTC GGTACGGCC TGCAATTGAG CCGTCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGCGCG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGGCAACCG
1451 CTACGCGCGG TCGGTTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTTGCCCCCG CCAAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGCGGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCCGACCAAG CCACTGACCG CGCAGCCGT CAAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2692; ORF 793.a>:

```

a793.pep
1  MLIKSEYKPR MLPKEEQVK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNFKLEQ GDNRIVRTQT LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 EMKEMPAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHPY MGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEVVL RDRQGNIVDS LDSPRNKAPK NGKDIIISLD QRIQTLYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRP RADSEQRNRN
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEMY DFYHELIGIV RMHSGFPGET
401 AGLLRNWRWR RPTEQATMSF GYGLQLSLQL LARAYTALTH DGVLLPVSF
451 KQAVAPQGR IFEKSTAREV RNLMSVSTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYGGVVAG
551 PFFKKIMGGS LNILGISPTK PLTAAAVKTP S*

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a793/m793 100.0% identity in 581 aa overlap

1277

a793.pep	10	20	30	40	50	60
	MLIKSEYKPRMLPKKEQVKKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
m793	MLIKSEYKPRMLPKKEQVKKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
	10	20	30	40	50	60
a793.pep	70	80	90	100	110	120
	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
	70	80	90	100	110	120
a793.pep	130	140	150	160	170	180
	PVDVLRNKLKQKGSFIWIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
m793	PVDVLRNKLKQKGSFIWIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
	130	140	150	160	170	180
a793.pep	190	200	210	220	230	240
	FTDIDGKGQEGLELSLEDSLHGEGDAEVVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
m793	FTDIDGKGQEGLELSLEDSLHGEGDAEVVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
	190	200	210	220	230	240
a793.pep	250	260	270	280	290	300
	QRIQTLAYEELNKAVEYHQAKAGTVVVLDAARTGEILALANTPAYDPNRPGRADSEQRRNR					
m793	QRIQTLAYEELNKAVEYHQAKAGTVVVLDAARTGEILALANTPAYDPNRPGRADSEQRRNR					
	250	260	270	280	290	300
a793.pep	310	320	330	340	350	360
	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQ					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQ					
	310	320	330	340	350	360
a793.pep	370	380	390	400	410	420
	KSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
m793	KSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
	370	380	390	400	410	420
a793.pep	430	440	450	460	470	480
	GYGLQLSLLQLARAYTALTHDGVLLPVSFEKQAVAPQGKRIFKESTAREVRNLMVSVTEP					
m793	GYGLQLSLLQLARAYTALTHDGVLLPVSFEKQAVAPQGKRIFKESTAREVRNLMVSVTEP					
	430	440	450	460	470	480
a793.pep	490	500	510	520	530	540
	GGTGTAGAVDGFVDGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRIVAVTIDEPTA					
m793	GGTGTAGAVDGFVDGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRIVAVTIDEPTA					
	490	500	510	520	530	540
a793.pep	550	560	570	580		
	HGYYGGVVAGPPFFKKIMGGSNLILGISPTKPLTAAAVKTPSX					
m793	HGYYGGVVAGPPFFKKIMGGSNLILGISPTKPLTAAAVKTPSX					
	550	560	570	580		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2693>:

g794.seq

1	gtgcgtttca	ATCATTTTCAT	AATGGTAACG	ATTATTATAT	ATGTGATTTTC
51	CCCTGCAAAC	AAGCCGGTCC	GCCGCCCCGG	CGTTCCCACT	TATCCGGCTT
101	TGCCTTATAA	TTGCTTTT	TATGTAACAG	ATTACCTAT	GAATTTCCCC
151	AAAACAGCGG	CCTCCCTGCT	GCTGCTTCTC	GCCTCCCTCG	CCGCACACGC
201	GCTCGATACC	GGCCGCATTC	CGCAAAACGA	AATCGCTGTA	TATGTCCAAG
251	AGCTTGACAG	CGGAAAAGTC	ATCATTTGACC	ACCGTGCCGG	CATACCCGTC
301	AATCCC CGCT	CCACGATGAA	GCTCGTTACC	GCGTTTGCCG	CCTTCAAAAC
351	CTTCGGCAGC	AATTACCGCT	GGGCGACCGA	GTTTAAAAGC	AACGGTACGG
401	TAAACGACGG	CACGCTTGAC	GGAAACCTGT	ATTGGGCGGG	CAGCGGCGAC
451	CCCGTTTTCA	ATCAGGAAAA	CCTGCTTGCC	GTCCAACGCC	AGTTGCGCGA
501	CAAAGGCATC	CGCAATATCA	CGGGCGCCT	GATGCTCGAC	CACAGCCTGT



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551 GGGGCGAAGT CGGCAGTCCC GACCATTTTG AAGCCGACAG CGGTTTCGCCG
601 TTTATGACGC CCCCAAATCC GACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTGGCC CAAAACAAC TGAATAATTAC CGCTCCCAA
751 GCTGCCTGCC CTTCCGTCAA AAAACTGATG CGCGCATCTT TTTCCGGCAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA AAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTTCGG CTTGACGAAC TGATCCGCCA AAGTTTTACC
901 AACCGCTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATAGC
951 CGACACACCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTGATTGCG
1051 CGTTCCGTCT TCCTCAAAC TCGCGGCGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGAGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTTC GAAAACGGTT CGGGTCTGTC CAGAAAAGAA
1201 ACGGTAACGG CGAGAATGAT GCGCGAAATG TTGAAACCGG CTTATTTTACG
1251 CCGGTTTTCG CAAGATTTC TCGACACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCAGCG TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA AAAACATCAT CTCCGGCGCG
1501 GACGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2694; ORF 794.ng>:

```

g794.pep
1 VRFNHFMVT IIIYVISPAN KPVRRPGVPT YPALPYNCFF YVTDSPMNEP
51 KTAASLLLLL ASLAHALDT GRIPONEIAV YVQELDSGKV IIDHRAGIPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLG GNLYWAGSGD
151 PVFNQENLLA VQRQLRDKGI RNITGRLMLD HSLWGEVSGP DHEADSGSP
201 FMTPPNPMTL SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSVKKLM RASFSGNTLK LRGNIPESCL GKPVGVRFMA LDELIRQSFT
301 NRWLLGGGRI SDGIGIADTP EGAOTLAVAH SKPMKEILT MNKRSNLI
351 RSVFLKLGDD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMAOM LETAYFSPFA QDFIDTLPIA GTDGLRNRK KQSGGLRLK
451 TGTLLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLDN FVAKNIISGG
501 DGWLDKLMC KERRA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2695>:

```

m794.seq
1 GTGCGTCTCA ATCATTTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51 CCCTGCAAAAC AAGCCGGGCC GCGGCCACAG CGTTCCCACT TATCCGGCTT
101 TGCCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTG CGCAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCGGTC
301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGGCG CCTTCAAAAC
351 CTCTGGCAGC AATTACCGCT GGGCGACCGA GTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAACCTAT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGAT GCTCAAAAAC AGTTGCGCGA
501 ACAAGGCATA CTCAATATCA CGGGACACCT GATGCTCGAG CACAGCCTGT
551 GGGGCGAAGT GCGCAGCCCC GACGATTTCG AAGCCGACAG CGGTTTCGCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATTAC CGCTCCCAA
751 GCTGCCTGCC CTTGATCAA AAAACTGATG CGTGCATCTT TTTCCGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTTCGG CTTGACGAAC TGATCCGGCA AAGTTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGTA TCGGCATAGC
951 CGACACGCCG GAAGGCGCGC AGACACTTGC CGTTGCACAC GCCAAACCGA
1001 TGAAGAAGAA TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCGTCT TCCTCAAAC TCGCGGCGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGCGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTTC GAAAACGGTT CCGGCCCTGT CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCAAAATG TTGAAACGGC CTTATTTTACG
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT ACCCATCGCC GGCACAGACG
1301 GAACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCAGCG TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCGCG GCCGTTTCCC
1451 TGCTGCCAGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCCGGCGGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2696; ORF 794>:

```

m794.pep
1 VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNEP
51 KTAASLLLLL ASLAHALDT GRIPONEIAV YVQELDSGKV IIDHRSDVPV

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1279

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101 NPASTMKLVTAFAAFKTFGS NYRWATEFKS NGTVNDGTLD GNLYWAGSGD
151 PVFNQENLLD AQKQLREQGI LNITGHLMLD HSLWGEVGSP DDFEADSGSP
201 FMTPPNPMTLSAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPECLGKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGIADTP EGAQTLAVAH AKPMKEILTD MNKRSDNLIA
351 RSVFLKLGGD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMMQOM LETAYFSPFA QDFIDTLPIA GTDGTLRNRF KQSGGLRLK
451 TGTNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLDN FVANNIISGG
501 DGWLDKLMC KERRA*

```

g794/m794 95.5% identity in 515 aa overlap

```

              10      20      30      40      50      60
g794.pep      VRFNHFIMVTIIIIYVISPAKPVRRPGVPTYPALPYNCFFYVTDSPMNFPKTAASLLLLL
              ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794          VRLNHFIMIAIIYVISPAKPARRHVSPTYPALPYNCFFYVTDLPMNFPKTAASLLLLL
              10      20      30      40      50      60

              70      80      90      100     110     120
g794.pep      ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRAGIPVNPASTMKLVTAFAAFKTFGS
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794          ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS
              70      80      90      100     110     120

              130     140     150     160     170     180
g794.pep      NYRWATEFKSNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQQRQLRDKGIRNITGRLMLD
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794          NYRWATEFKSNGTVNDGTLDGNLYWAGSGDPVFNQENLLDAQKQLREQGILNITGHLMLD
              130     140     150     160     170     180

              190     200     210     220     230     240
g794.pep      HSLWGEVGSPDHFADSGSPFMTPPNPMTLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794          HSLWGEVGSPDDFEADSGSPFMTPPNPMTLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
              190     200     210     220     230     240

              250     260     270     280     290     300
g794.pep      QNNLKITASQAACPSVKKLMRASFSGNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794          QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT
              250     260     270     280     290     300

              310     320     330     340     350     360
g794.pep      NRWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTMNKRSDNLIAARSVFLKLGGD
              |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794          NHWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTMNKRSDNLIAARSVFLKLGGD
              310     320     330     340     350     360

              370     380     390     400     410     420
g794.pep      GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794          GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
              370     380     390     400     410     420

              430     440     450     460     470     480
g794.pep      QDFIDTLPIAGTDGTLNRNRFKQSGGLRLKLTGTNNVRALAGYWLGDKPM AVVVIINSGR
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794          QDFIDTLPIAGTDGTLNRNRFKQSGGLRLKLTGTNNVRALAGYWLGDKPM AVVVIINSGR
              430     440     450     460     470     480

              490     500     510
g794.pep      AVSLLPDLDNFVAKNIIISGGDGWLDKLMCKERRAX
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794          AVSLLPDLDNFVANNIIISGGDGWLDKLMCKERRAX
              490     500     510

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2697>:

a794.seq

```

1   GTGCGTCTCA ATCATTTTCAT AATGATAGCG ATTATTATAT ATGTGATTTT
51  CCCTGCAAAAC AAGCCGGGCC GCGCCACAG CGTCCCCTACT TATCCGGCTT
101 TGCCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACA GGTGCGATTC CGCAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCCGTC

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1280

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301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAAC
351 CTTTCGGCAGC AATTACCGCT GGGCGACCGA GTTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTGT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 ACAAGGCATA CGCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTTC AAGCCGACAG CGGTTTCGCCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGACAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATTAC CGCCTCCCAA
751 GCTGCTGCC CTTGATCAA AAACTGATG CGTGCATCTT TTTCCGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCG CTTGACGAAC TGATCCGGCA AAGTTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATATC
951 CGACACGCCG GAAGGCGCGC AGACGCTTGC CGTGCACAC TCAAAGCCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCTGCT TCCTCAAACT CGGCGCGGAC GGCAAACTGC CGCCCGTTTC
1101 CGAACAGGCA GCGTCTGCCG TCCGGCGTGA ACTTGCCGTG TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTTG GAAAACGGTT CAGGTCTGTC CAGAAAAGAA
1201 AGGTAACCG CGAATATGAT GCGCAAAATG TTGGAACGG CTTATTTTCA
1251 CCCGTTTGCA CAAGATTTCA TCGATACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTAGC CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCAGCG TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGTGCCCCGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCCGGCGGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2698; ORF 794.a>:

a794.pep

```

1 VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNFP
51 KTAASLLLLL ASLAHALDT GRIPONEIAV YVQELDSGKV IIDHRSQVVP
101 NPASTMKLVTAFAAFKTFGS NYRWATEFKS NGTVNDGTLG GNLWAGSGD
151 PVFNQENLLAVQRLREQGIRNITGHLMLD HSLWGEVGS DDFEADSGSP
201 FMTPPNPTML SAGMVMVRAE RNAADSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSNTLKL RGNIPESCLGKPVGVRMFALDELIRQSFT
301 NHWLLGGGRISDGIGISDTPEGAQTLAVAH SKPMKEILTD MNKRSNLIARS
351 RSVFLKLGGD KLPVAVSEQA ASAVRRELAV SGIDVADLVLENGSGLSRKE
401 RVTARMMAQM LETAYFSPFA QDFIDTLPIA GTDGTLRNRF KQSGGLRLRK
451 TGTLLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLDN FVANNIISGG
501 DGWLDAKLKC KERRA*

```

a794/m794 98.6% identity in 515 aa overlap

a794.pep	10	20	30	40	50	60
	VRLNHFIMIA	IIIIYVISPAN	KPARRHSVPT	YPALPYNCFF	YVTDLPMNFP	KTAASLLLLL
m794	VRLNHFIMIA	IIIIYVISPAN	KPARRHSVPT	YPALPYNCFF	YVTDLPMNFP	KTAASLLLLL
a794.pep	70	80	90	100	110	120
	ASLAHALDT	GRIPONEIAV	YVQELDSGKV	IIDHRSQVVP	NPASTMKLVTAFAAFKTFGS	
m794	ASLAHALDT	GRIPONEIAV	YVQELDSGKV	IIDHRSQVVP	NPASTMKLVTAFAAFKTFGS	
a794.pep	130	140	150	160	170	180
	NYRWATEFKS	NGTVNDGTLG	GNLWAGSGD	PVFNQENLLAV	QRLREQGIRNITGHLMLD	
m794	NYRWATEFKS	NGTVNDGTLG	GNLWAGSGD	PVFNQENLLAV	QRLREQGIRNITGHLMLD	
a794.pep	190	200	210	220	230	240
	HSLWGEVGS	PDDFEADSGSP	FMTPPNPTML	SAGMVMVRAE	RNAADSTDIL	TDPPLPHIFA
m794	HSLWGEVGS	PDDFEADSGSP	FMTPPNPTML	SAGMVMVRAE	RNAAGSTDIL	TDPPLPHIFA
a794.pep	250	260	270	280	290	300
	QNNLKITASQ	AACPSIKKLM	RASFSNTLKL	RGNIPESCLG	KPVGVRMFAL	DELIRQSFT
m794	QNNLKITASQ	AACPSIKKLM	RASFSNTLKL	RGNIPESCLG	KPVGVRMFAL	DELIRQSFT
a794.pep	310	320	330	340	350	360
	NHWLLGGGRIS	DGIGISDTPE	GAQTLAVAH	SKPMKEILTD	MNKRSNLIARS	SVFLKLGGD

1281

```

|||||
m794      NHWLLGGGRISDGIADTPEGAQTLAVAHAKPMKEILTDMNKRSDNLIARSVFLKLGGD
          310      320      330      340      350      360

          370      380      390      400      410      420
a794.pep  GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
          |||||
m794      GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
          370      380      390      400      410      420

          430      440      450      460      470      480
a794.pep  QDFIDTLPIAGTDGTLRNRFKQSGGLRLKTGT LNNVRALAGYWLGDKPMVAVVIINSGR
          |||||
m794      QDFIDTLPIAGTDGTLRNRFKQSGGLRLKTGT LNNVRALAGYWLGDKPMVAVVIINSGR
          430      440      450      460      470      480

          490      500      510
a794.pep  AVSLLPDLDNFVANNIISGGDGWLDAKLMCKERRAX
          |||||
m794      AVSLLPDLDNFVANNIISGGDGWLDAKLMCKERRAX
          490      500      510

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2699>:

```

g900.seq
1   ATGccgTCTG AAATGCCGTC TGAAACGTGG CAGGCGGAGG TTCGGACGGC
51  ATTGGGT TTA TTTCAACGGG CGGATGCCGA CCGCATCGCG TACTTTATCC
101 AACAAATTCGC GCGCTTCTTT GCGCGCTTTT TGC GCGcctg cctGCAAAAT
151 CTCTTCGATT TCGAAGGAT TAGAGGTCAA TCGTTGTAG CGTTCGCGCA
201 GTTCTGCCAA TTCGGCGTTG ATTTTCGCCG CCGAAAGTTT TTTCGCCTCG
251 CCCCAGCCA AGCCGTCGGC AAGCATTTGC GTAAATTCCG CCGTTTCAGA
301 CGGCGTGGAG AAGGCTTTAT AGATTTCAAA CAAAGGGCTT TCGTCGGGCT
351 GTTTCGGCTC GCCCGGCTCT TTCATGTTGG TAATGATTTT GTTGACCGAT
401 TTTTGGGTTT TTTTGTCTGT TTCCCAAAGC GGAATGGTAT TGCCGTAGGA
451 TTTGGACATT TTGCGTCCGT CCAAACCGAC CAAGAGTTCG ACGTTTTCGT
501 CGATTTTCAC TTCGGGCagg GTGaagagt cTTGGAaacc gtgggtgaag
551 cggccggcAa tgtcgcgcgc cATTTCgacg tgttgGATTT GGTCGCGCCC
601 GACGGGGACT TCGTTGGCGT TGAACATCAA AATGTCGGCA GTCATCAGAA
651 TCGGATAACT GAACAAACCC ATTTCCACAC CGAAATCGGG GTCTTCTGTC
701 CCGTTTTCGG CATTGGCTTG AACGGCGGCT TTGTAGGCGT GGGCGCGGTT
751 CATCAAACCC TTGGCGGTGA TGCAGGTCAG AATCCAGTTC AACTCCATCA
801 CTTCCGGGAT GTCGCTTTGG CGGTAGAAGG TGGTGCCTC GGGGTGAGT
851 CCGCAGGCAA GCCAAGTGGC GGCAACGGCt tgGGTGGATT GGTGAATCAT
901 CTCCTGCTCG TGGCATTGTA TGATGCCGTG GTAATCGGCG AGGAAGAGGA
951 AGGATTCCGT ATCGGGGTTT TGCGCCGCGC GGACGGCGGG GCGGATGCGC
1001 CCGACGTAGT TGCCAGATG CGGGGTGCCG GTGGTGGTTA CGCCGTCAG
1051 AACTCGTTTT TTGCTCATAA AAATGTCTT ACGGCAGCAA TGCCGTCTGA
1101 AAGGGAAaA. gatgcgCCGA TTATACCGCA TTTGCCACAT ACATCCAGCC
1151 GacaACagaC TTTTCATAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2700; ORF 900.ng>:

```

g900.pep
1   MPSEMPSETW QAEVRTALGL FQRADADRIA YFIQQFARFF ARFLRACLQN
51  LFDLRRIRGQ CVVAFQAFCQ FGVDfRRRKf FRLAPSQAVG KHLRKfRRfR
101 RRGEgFIDfK QRAfVGLfRL ARLfHVGNdf VDRfLGFfVfV fPKRNGIaVG
151 FGHFASVQTD QEFdVfVdFH FGQGEeFLET VGEAAGNVAR HFDVLDLVAP
201 DGDFVGVEHQ NVGSHQNRIE EQTHfHTEIG VFLPVfRIGL NGGFVGVGAV
251 HQTLLGGDAGQ NPVQLHHfGN VALAVEGGAL GVESAGKPSG GNGLGGLVNH
301 LLLVAFDDAV VIGEEEGFG IGVLRRADGG ADGADVVAQM RGAGGGYAGQ
351 NSFFAHKNVL TAAMPsEREK DAPIIPLPH TSSRQQTfPY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2701>:

```

m900.seq
1   ATGCCGTCTG AAACGCGGCA GCGGAGGTT CGGACGGCAT CGGGTTCATT
51  TCAACGGGCG GATGcCGACC GCATCg TA CTTTGTCCAA TAATTCGCGT
101 GCTTCTTTAC GCGCTTTCGC CGCGCCTGCC TGCAAAATCT CTTCGATTG

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1282

```

151 CGAAGGGTCG GCGGTCAGCT CGTTGTAGCG TTCGCGCGGT TCGGCGAGTT
201 CCGCGTTGAT TTTCGCGGCC AAAAGTTTTT TGGCTTCACC CCACGCCAAG
251 CCGTCGGCAA GCATTTTCGT AAATTCCACC GTTTCAGACG GCGTGGAGAA
301 GGCTTTGTAG ATTTCAAACA ATGGGCTTTC GTCGGGCTGT TTCGGCTCGC
351 CCGGCTCTTT CATATTGGTG ATGATTTTGT TGACCGATT TTGGGTTTTT
401 tTGTCGTTTT CCCAAAGCGG AATGGTGTG CCGTAGGATT TGGACATTTT
451 GCGTCCGTCC AAACCGACCA AGAGTTCGAC GTTTTCATCG ATTTTCACTT
501 CGGGCGAGGT GAAGAGTTCC CGGAAGCGGT GGTGAAGCG GCCGGCGATG
551 TCGCGCGCCA TTTCGACGTG TTGGATTGG TCGCGCCCGA CgGGCaCTTC
601 GTTGGCGTTG AACATCAGAA TATCGGCAGT CATCAGAATC GGATAACTGA
651 ACAAACCCAT TTCCACACCG AAATCAGGGT CTTCTGCCC GTTTTCTGCA
701 TTTGCTGCA CCGCGGCTT GTAGGCATGG GCGCGGTTCA TCAAACCCTT
751 GGCAGTGATG CAGGTCAGAA TCCAGTTCAA TTCCATCACT TCgGGAGTGT
801 CGCTTTGGCG GTAGAAGGTG GTGCGCTCGG GGTGAGTCC GCAGGCAAGC
851 CAAGTGGCGG CAACGGCTTG GGTGGATTGG TGAATCATCT CCGGCTCGTG
901 GCATTTGATG ATACCGTGGT AATCGGCGAG GAAGAGGAAG GATTTCGGTAT
951 CGAGGTTTTG CGCCGCGCGG ACGGCGGGGC GGATGGCGCC GACGTAGTTG
1001 CCCAGATGCG GGATGCCGGT GGTGGTTACG CCGGTCAGAA CTCGTTTTTT
1051 GCTCATAAAA ATGTCCTTGC GGCATCAATG CCGTCTGAAA GGGAAAAAGA
1101 TGTGCCGATT ATACCCGATT TGCCACCTAC ATCCAGCCGA CAACAGACTT
1151 TTCCATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2702; ORF 900>:

```

m900.pep
  1 MPSETRQAEV RTASGSFQRA DADRIXVFQV *FACFFTRFR RACLQNLFDL
 51 RRVGGQLVVA FARFGEFGVD FRRQKFFGFT PRQAVGKHFR KFHRFRRRGE
101 GFVDFKQWAF VGLFRLARLF HIGDDFVDRF LGFFVVFPRK NGVAVGFGHF
151 ASVQTDQEFD VFIDFHFGQG EEFPEAVVEA AGDVARHFDV LDLVAPDGHF
201 VGVEHQNIGS HQNRITEQTH FHTEIRVFLP VFCICLHGGF VGMGAVHQTL
251 GSDAGQNPVQ FHHFGSVALA VEGGALGVES AGKPSGGNGL GGLVNHRLRV
301 AFDDTVVIGE EEEFGGIEVL RRADGGADGA DVVAQMRDAG GGYAGQNSFF
351 AHKNVLAASM PSEREKDVPI IPDLPTSSR QQTFFPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 900 shows 87.0% identity over a 386 aa overlap with a predicted ORF (ORF 900.ng) from *N. gonorrhoeae*:

```

m900/g900

      10      20      30      40      50
m900.pep  MPSETRQAEVRTASGSFQRADADRIXVFQVX*FACFFTRFRRAACLQNLFDLRRVGGQ
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g900      MPSEMPSETWQAEVRTALGLFQRADADRIAYFIQQFARFFARFLRAACLQNLFDLRRIRGQ
          10      20      30      40      50      60

      60      70      80      90     100     110
m900.pep  LVVAFARFGEFGVDFRRQKFFGFTPRQAVGKHFRKFHRFRRRGEGFVDFKQWAFVGLFRL
          ||||| :| :||| ||||| :|| :||| ||||| :||| :||| ||||| |||||
g900      CVVAFQAQFCQFGVDFRRRKFFRLAPSQAVGKHLRKFRFRRRRGEGFIDFKQRAFVGLFRL
          70      80      90      100     110     120

      120     130     140     150     160     170
m900.pep  ARLFHIGDDFVDRFLGFFVVFPRKNGVAVGFGHFASVQTDQEFDFVFIDFHFGQGEEFPEA
          ||||| :| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g900      ARLFHVGNDFVDRFLGFFVVFPRKNGIAGVFGHFASVQTDQEFDFVDFVDFHFGQGEEFLET
          130     140     150     160     170     180

      180     190     200     210     220     230
m900.pep  VVEAAGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTEIRVFLPVFCICL
          ||||| :| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g900      VGEAAGNVARHFDVLDLVAPDGDGDFVGVEHQNVGSHQNRITEQTHFHTEIGVFLPVFRIGL
          190     200     210     220     230     240

```

1283

	240	250	260	270	280	290
m900 . pep	HGGFVGMGAVHQTLGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNH					
	:     :     :     :     :     :					
g900	NGGFVGVGAVHQTLGGDAGQNPVQLHHFGNVALAVEGGALGVESAGKPSGGNGLGGLVNH					
	250	260	270	280	290	300

	300	310	320	330	340	350
m900 . pep	LRLVAFDDTVVIGEEEEFGFIEVLRRADGGADGADVVAQMRDAGGGYAGQNSFFAHKNVL					
	:     :     :     :     :     :					
g900	LLLVAFD DAVVIGEEEEFGFIEVLRRADGGADGADVVAQMRGAGGGYAGQNSFFAHKNVL					
	310	320	330	340	350	360

	360	370	380
m900 . pep	AASMPSEREKDVPIIPDLPTSSRQQTFFPYX		
	:     :     :		
g900	TAAMP SEREKDAPIIPDLPTSSRQQTFFPYX		
	370	380	390

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2703>:

a900 . seq (partial)

```

1   GAGGTTCCGA   CGGCATTGGG   TTTATTTCAA   CGGGCGGATA   CCGACCGCAT
51  CACGTACTTT   GCCCAATAAT   TCGCGTGCTT   CTTTACGCGC   TTTTTCGCGC
101 CCTGCCTGCA   AAATCTCTTC   GATTTCGCGA   GGGTCGGCGG   TCAGCTCGTT
151 GTAGCGTTTC   CGCGGTTTCG   CGAGTTCGGC   GTTGATTTTC   GCCGCCAAAA
201 GTTTTTTTGC   CTCGCCCCAA   GCCAAGCCGT   CGGCAAGCAT   TTTTCGTAAAT
251 TCTGCCGTTT   CAGACGGCGT   GGAGAAAGCT   TTGTAGATTT   CAAACAGAGG
301 GCTTTCGTCG   GGCTTCTTCG   GCTCGCCCGG   CTCTTTCATA   TTGGTGATGA
351 TTTTGTGAC   CGATTTTGG   GTTTTTTGT   CGTTTCCCA   AAGCGGAATG
401 GTGTTGCCGT   AGGATTTGGA   CATTTTGCGT   CCGTCCAAAC   CAACCAAGAG
451 TTCGACGTTT   TCGTCGATTT   TCACTTCGGG   CAGTGTGAAG   AGTTCCCGBA
501 AGCGGTGGTT   GAAGCGGCCG   GCAATATCGC   GTGCCATTTT   AACGTGTTGG
551 ATTTGGTCGC   GACCGACTGG   AACTTCATGG   GCATTGAACA   TGAGAATGTC
601 GGCAGTCATG   AGGATAGGGT   AGCTGTACAA   ACCCATTTCC   ACGCCGAAAT
651 CGGGGTCTTC   CTGCCCGTTT   TCCGCATTTG   CCTGCACGGC   GGCTTTGTAG
701 GCGTGGGCGC   GGTTCATCAA   ACCCTTGGCG   GTGATGCAGG   TCAGAAATCCA
751 GTTCAATTCC   ATCACTTCGG   GAATGTCGCT   TTGACGGTAG   AAGGTGGTGC
801 GCTCGGGGTC   GAGTCCGCAG   GCAAGCCAAG   TGGCGGCAAC   GGCTTGGGTG
851 GATTGGTGAA   TCATCTCCGG   CTCGTGGCAT   TTGATGATAC   CGTGGTAATC
901 GCGGAGGAAG   AGGAAGGATT   CGGTATCAGG   GTTTTTCGCC   GCGCGGACGG
951 CGGGGCGGAT   AGCACCGACG   TAGTTGCCCA   GATGCGGGAT   GCCGGTGGTG
1001 GTTACGCCGG   TCAGAACTCG   TTTTTTGCTC   ATAAAAATGT   CCTTGGGGCA
1051 TCAATGCCGT   CTGAAAGGGA   AAAAGATGCG   CCGATTATAC   CCGATTTGCC
1101 ACCTACATCC   AGCCGACAAC   AGACTTTTCC   ATATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2704; ORF 900.a>:

a900 . pep (partial)

```

1   EVRTALGLFQ   RADTDRITYF   AQ*FACFFTR   FLRACLQNLF   DLRRVGGQLV
51  VAFARFGEFG   VDFRRQKFFC   LAPSQAVGKH   FRKFCRFRRR   GESFVDFKQR
101 AFVGLLRLLAR   LFHIGDDFVD   RFLGFFVVP   KRNGVAVGFG   HFASVQTNQE
151 FDVFVDFHFG   QCEEFPEAVV   EAAGNIACHF   NVLDLVATDW   NFMGIEHENV
201 GSHEDRVAVQ   THFHAIEGVF   LPVFRICLHG   GFVGVGAVHQ   TLGGDAGQNP
251 VQFHHFGNVA   LTVEGGALGV   ESAGKPSGGN   GLGGLVNHRL   LVAFDDTVVI
301 GEEEEFGFIR   VLRRADGGAD   STDVVAQMRD   AGGGYAGQNS   FFAHKNVLA
351 SMPSEREKDA   PIIPDLPTS   SRQQTFFPY*

```

m900/a900 88.4% identity in 378 aa overlap

	10	20	30	40	50	60
m900 . pep	MPSETRQAEVRTASGSFQRADADRIXEFVQXFACFFTRFRRACLQNLFDLRRVGGQLVVA					
	:     :     :     :     :					
a900	EVRTALGLFQRADTDRITYFAQXFACFFTRFRRACLQNLFDLRRVGGQLVVA					
	10	20	30	40	50	
	70	80	90	100	110	120

1284

```

m900.pep  FARFGEFGVDFRRQKFFGFTPRQAVGKHFRKFHRRRRGEGFVDFKQWAFVGLFRLARLF
a900      FARFGEFGVDFRRQKFFCLAPSQAVGKHFRKFCRFRRRGESFVDFKQRAFVGLLRRLARLF
           60      70      80      90      100     110

           130     140     150     160     170     180
m900.pep  HIGDDFVDRFLGFFVVFPRKNGVAVGFGHFASVQTDQEFDFVDFIDFHFGQGEFPEAVVEA
a900      HIGDDFVDRFLGFFVVFPRKNGVAVGFGHFASVQTNQEFDFVDFIDFHFGQCEEFPEAVVEA
           120     130     140     150     160     170

           190     200     210     220     230     240
m900.pep  AGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTAIRVFLPVFCICLHGGF
a900      AGNIACHFNVLDLVATDWNFMGIEHENVGSHEDRVAVQTHFAEIGVFLPVFRICLHGGF
           180     190     200     210     220     230

           250     260     270     280     290     300
m900.pep  VGMGAVHQTLGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNHRLRV
a900      VGVGAVHQTLGGDAGQNPVQFHHFGNVALTVEGGALGVESAGKPSGGNGLGGLVNHRLRV
           240     250     260     270     280     290

           310     320     330     340     350     360
m900.pep  AFDDTVVIGEEEEFGFIEVLRADGGADGADVVAQMRDAGGGYAGQNSFFAHKNVLAASM
a900      AFDDTVVIGEEEEFGFIRVLRADGGADSTDVVAQMRDAGGGYAGQNSFFAHKNVLAASM
           300     310     320     330     340     350

           370     380
m900.pep  PSEREKDVPIIPDLPTSSRQQTFFPYX
a900      PSEREKDAPIIPDLPTSSRQQTFFPYX
           360     370

```

g901.seq not found yet

g901.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2705>:

```

m901.seq
1  ATGCCCGATT TTTGATGTC CAATTTGGCC GTTGCCTTT CCATCACATT
51  GGCTGCCGGT TTGTTACCG TATTAKyAG TGGCTTGGTG ATGTTTTCCT
101 AAACGCCCAA TCCGCGTGTG TTGTCGTTG GTTTGGCGTT TGCCGGCGGT
151 GCGATGGTAT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTGCGGCG GCGACCATGG
251 CATTTTGGC CGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
301 AACCCGCATG AAACTTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA
351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGGCGGTTT GCGATTACTG
401 CGCACAATTT CCCCGAAGGC TTGGCGACGT TTTTGGCCAC ATTGGAATAA
451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTTGCCACC CGCAGCCGTA
551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTTGGGG
601 GCGGCTTTGG GCTATTGTTT TTTGCAGCCG TTTTGTGCGC CTGCCGTGTT
651 TGGTTCGGTA TTCGGCGTGA TAGCCGGTGT GATGGTGTTC TTGGCGTTGG
701 ACGAGCTGnt GCCGGCTGCC AAACGCTATT CAGACGGCCA TGAAACCGTT
751 TACGGCCTGA CAACGGGTAT GCGCGTGATT GCCGTCAGCC TGGTATTGTT
801 CCATTTTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2706; ORF 901&gt;:

```

m901.pep
1  MPDFSMSNLA VAFSITLAAG LFTVLXSGLV MFSKTPNPRV LSFGLAFAGG
51  AMVYVSLTEI FSKSSEAFAE IYDKDHAFAA ATMAFLAGMG GIALIDRLVP

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1285

```

101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWVAC LLSGLAEPLG
201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELXPAA KRYSDGHETV
251 YGLTTGMAVI AVSLVLFHF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2707>:

**a901.seq**

```

1 ATGCCCCGATT TTTTCGATGTC CAATTTGGCC GTTGCCTTTT CCATTACGTT
51 GGCTGCCCGT TTGTTTACCG TATTAGGCAG CGGCTTGGTG ATGTTTTCCA
101 AAACGCCCAA TCCGCGCGTG TTGTCGTTTG GTTTGGCATT TGCCGCGCGT
151 GCGATGGTGT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTGCGGCG GCGACCATGG
251 CATTTTGGC AGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
301 AACCCGCATG AAAC TTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA
351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GGCGGCGTTT GCGATTACTG
401 CGCACAAATTT CCCC GAAGC TTGGCGACGT TTTTGGCCAC ATTGGAAAAT
451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTTGGCACC CGCAGCCGTA
551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTTGGGG
601 GCGGCTTTGG GCTATTGGT TTTGCAGCCG TTTTGTGCGC CTGCCGTGTT
651 TGGTTCGGTA TTCGGCGTGA TAGCCGGTGT GATGGTGT TTGGCGTTGG
701 ACGAGCTGCT GCCGGCTGCC AAACGCTATT CAGACGGCCA TGAAACCGTT
751 TACGGCCTGA CAATGGGCAT GGCGGTGATT GCCGTCAGCC TGGTATTGTT
801 CCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2708; ORF 901.a>:

**a901.pep**

```

1 MPDFSMSNLA VAFSITLAAG LFTVLGSLV MFSKTPNPRV LSFGLAFAGG
51 AMVYVSLTEI FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP
101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWVAC LLSGLAEPLG
201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA KRYSDGHETV
251 YGLTMGMAVI AVSLVLFHF*

```

**m901/a901** 98.9% identity in 269 aa overlap

m901.pep	10	20	30	40	50	60
a901	10	20	30	40	50	60
m901.pep	70	80	90	100	110	120
a901	70	80	90	100	110	120
m901.pep	130	140	150	160	170	180
a901	130	140	150	160	170	180
m901.pep	190	200	210	220	230	240
a901	190	200	210	220	230	240
m901.pep	250	260	270			
a901	250	260	270			



The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2709>:

```
g902.seq
1  ATGCCGTCCG AACCCGAACG GCGGCATGGC AATACTGCCC TACCCCTTCCC
51  GATAGCCGCA CGCCCAACGG TCGGTTTTTC CGGCAAGCCT TTCAAGATAA
101 CCGGCAAGTG TGTCGTATTG CGCCGCCGCA TTGTCCAAGC GGTGATTTC
151 ACGCCGCGCC TGTTCCGCCG GGGCATTTC GCCGATGTAC CAGCCTATGT
201 GTTTCGCTGC GATGCGCACA CCGACGGTCT CACCATAAAA CGCGTGCATG
251 GCGCGGATGT GGTTCAAAAT GCGGCTCTG CATTCTGCCA AACTCAAGGC
301 AGGCGGTAAA ACGCCGTGTT CGGCATAATG CTTCAAATCG CGGAAAAACC
351 ACGGCCTGCC TTGCGCGCCG CGCCCTATCA TGATGCCGTC GCGGCGGTT
401 TGTTTGAGGA cggCGGCGG TTTTgCGGc GAagtGATGT CGCCGTTGac
451 cCaggCCGGG ATGTTcAGAc ggCTTTTGGT CTCGGcGatg agttCGTAAC
501 gcGCCTCGCC TTTGTACATT TGCGTGcGcG CGcgcGcgtg aacggcaaGg
551 gcggcaatgc cgcaatcttc ggcgattttg gcgacggcgG gcaggttttg
601 atcgtcgtcg tgccaacca AacggGTTTT GaggGTAACG GGTAcgcCCG
651 CCGCCTTgac caccgcctcc aAAatggcGg caaccagcgg CTCGTCCTGC
701 ATCagcGCGC TACCGGCTTG GACGTTGCAC ACTTTCttgg cgggGCAGCC
751 CATAttgATG TCGATGACCT GCGCCCCGAG TCCGACGTTg taacgcgcGg
801 catCCGCCAT CtgttcggGG TCGCTGCCGG CAATCTGCAC GGCAACGATG
851 CCGccttcac cggcaAAAtc actgcggtgc aGGGTTTTTC CGGTATTCTT
901 GAGCGTCGGA TCGCTGGCCA GCATTTTCGCA CACCGCCCAA CCTGCGCCAA
951 ACGCCCGACA GAGGCGGCGG AAGGGTTTGT CGGCAATGCC CGCCATCGGC
1001 GCAAGTGCGA TGGGGTTGTC GATAAAATAA CCGCCGATGT GCATAATGGG
1051 CCCGCGTTTC AAAAAAGTGC GCCATTGTAC ATTTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2710; ORF 902.ng>:

```
g902.pep
1  MPSEPERRHG NTALPFPIAA RPTVGFSGKP FKITGKCVVL RRRIVQAVDF
51  TPRLFAVGHF ADVPAYVFAC DAHTDGLTIK RVHGADVQON GGS AFCQTQG
101 RR*NAVFGIM LQIAEKPRFA LRAAPYHDAV GGGLFEDGGG FLRRSDVAVD
151 PGRDVQTAFG LGDEFVTRLA FVHLRARAPV NGKGGNA AIF GDFDGGQVL
201 IVVPTQTGF EGNFYARRLD HRLQNGGNQR LVLHQRATGL DVAHFLGGAA
251 HIDVDLRLPE SDVVTIRIRH LFGVAAGNLH GNDAAFIGKI TAVQGFSGIP
301 ERRIAGQHFA HRPTCAKRPT EAAEGFVGNA RHRRKCDGVV DKITADVHNG
351 PAFQKSAPLY IF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2711>:

```
m902.seq
1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTT GGGCGGTAGG
51  CGCACGCCCC ACTGTCGGTT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA
101 AGCATGTCTG ATTGCGCCGC CGCACTGTCC AAGCGTTGA TTTCACGACG
151 TgTCTgTTCG CCGTcGGGCA TTTCTGTCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG TATGGCGCGG
251 ATGTGGTTCA AAATAGCGGC GCGCATTCT GCCAACTCA AGGCAGGCGG
301 CAAAACACCG TGTTCCGGCAT AATGTTTCAA ATCGCGGAAG AACCACGGCC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCGGCGGC GGTTTGTTTG
401 AGGACGGCTT GGGCTTTTTC CGGCGAAGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGTTTTTCGC GATGAGTTTC TAACGCGCTT
501 CGCCTTTGTA CATTTGCGTA CGCGTGCCTC CGTGGACGGC AAGGGCGGCG
551 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCTGCCGCAC
651 GGACGACGGC TTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCCCT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATTT CGCACACCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTGCGTAA TGCCCGCCAT CGGcGCaAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2712; ORF 902>:

1	LHFQRIIKCS	EGIWAVGARP	TVGFFGKSFK	ITCKHVVLRR	RTVQAVDFTT
51	CLFAVGHFVD	VPAYVFACDA	HTGGVAVKRV	YGADVQNSG	GAFCQTQGRR
101	QNTVFGIMFQ	IAEPRPALR	AAPYHNAVGG	GLFEDGLGFL	RRSNVAVDPD
151	RDVQTAGFGF	DEFVTRFAFV	HLRTRASVDG	KGGDAAIFGD	FGDDGQVLMV
201	VVPTQTGFEG	NGYACRTDDG	FQNGGNQRLV	LHQRATGLDI	ADFFSGTAHV
251	DVDKLRPKAD	VVTRGIRHLL	RIASGNLHGN	NAAFIGKIAA	VQGFSSISER
301	RVAGQHFHAH	PTCAKISAKS	AERFVGNARH	RRKCDGVVDK	IAADVHNGSA
351	FOKSTPLYIF	*			

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 902 shows 80.9% identity over a 345 aa overlap with a predicted ORF (ORF 902.ng) from *N. gonorrhoeae*:

m902/q902

m902.pep LHFQRIIKCSEGIWAVGARPTVGFSGKSFKITCKHVVLRRRTVQAVDFTTCLFAVGHF  
:  
g902 MPSEPERRHGNTALPFPPIAARPTVGFSGKPFKITGKCVCVLLRRRIVQAVDFTPRLFAVGHF

10 20 30 40 50 60

m902.pep 60 70 80 90 100 110  
VDVPAYVFACDAHTGGVAVKRVYGADVQNSSGAFCQTQGRRQNTVFGIMFQIAEEPRPA  
:  
g902 ADVPAYVFACDAHTDGLTIKR VH GADVQNGGS AFCQTQGRRXNAVFGIMLQIAEKPRPA

70 80 90 100 110 120

m902.pep 120 130 140 150 160 170  
LRAAPYHNAVG GGL FED GL FL RRS NV AV DP DR DV QTA FG FGD E FVT RF AF VHL RTR ASV  
:  
g902 LRAAPYHDAVG GGL FED G GGL FL RSD VAV DP GR DV QTA FGL GDE FVT RL AF VHL RAR APV

130 140 150 160 170 180

m902.pep 180 190 200 210 220 230  
DGKG GDAA I FGDFGDDGQVLMVVVPTQTGFEGNGYACRTDDGFQNGGNQRLVLHQ RATGL  
:  
g902 NGKGGNAAI FGDFGDDGQVLI VVVPTQTGFEGNGYARRLDHRLQNGGNQRLVLHQ RATGL

190 200 210 220 230 240

m902.pep 240 250 260 270 280 290  
DIADFFS GSTAHVDVDKL RP KADV TRGIR HLLRIA SGN LH GN NAAF IG KIA A VQG FS SIS  
:  
g902 DVAHFLG GA AHIDVD DL RPESDVVTRRIRHLFGVAAGNLHGNDAAF IG KITAVQGFSGIP

250 260 270 280 290 300

m902.pep 300 310 320 330 340 350  
ERRVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHN GS AFQKSTPLY  
:  
g902 ERRIAGQHFAHRPTCAKRPTEAAEGFVGNARHRRKCDGVVDKITADVHN GP AFQKSAPLY

310 320 330 340 350 360

m902.pep 360  
IFX  
:  
g902 IFX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2713>:

a902.seq

1	TTGCACTTTC	AAAGGATAAT	CAAGTGTTCA	GAAGGCATTT	GGGCGGTAGG
51	CGCACGCCCCA	ACTGTCGGTT	TTTTTCGGCAA	GTCTTTCAAG	ATAACCTGCA

1288

```

101 AACATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TGTCTGTTTCG CCGTCGGGCA TTTCGTCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG CATGGCTCGG
251 ATGTGGTTCA AAATAGTGGC GGTACATTCT GCCAAACTCA AGGCAGGCGG
301 TAAAACACCG TGTTTCGCGT AATGTTTCAA ATCGCGGAAG AACCACGGTC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCTGCGGC GGTGTTGTTT
401 AGGACGGCTT GGGCTTTTTC CCGCGAGGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC AATCAGGTCG TAAGCCGCTT
501 CGCCTTTGTA CATTTCGCTG CGCGTGCCTC CGTGGACGGC AAGGGCGGCA
551 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCCGCCGCTT
651 TGACCACCGC CTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCTT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATTT CGCACACCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCCCAT CCGCGCAAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTCAAAAAA GTACGCCATT GTACATTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2714; ORF 902.a>:

**a902.pep**

```

1 LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVLRR RTVQAVDEFTT
51 CLFAVGHEVD VPAYVFACDA HTGGVAVKRV HGSDVVQNSG GTFCQTQGRR
101 *NTVFGVMFQ IAEEPRALR AAPYHNAVCG GLFEDGLGFL RRGNAVDPD
151 RDVQTAFGFG NQVVSRAFAV HLRARASVDG KGGNAIFGD FGDDGQVLMV
201 VVPTQTGFEG NGYARRFDHR LQNGGNQRLV LHQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFAHR PTCAKISAKS AERFVGNAHR RRCDCGVVDK IAADVHNGSA
351 FQKSTPLYIF *

```

**m902/a902** 94.7% identity in 360 aa overlap

	10	20	30	40	50	60
m902.pep	LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVLRR RTVQAVDEFTT CLFAVGHEVD					
a902	LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVLRR RTVQAVDEFTT CLFAVGHEVD					
	10	20	30	40	50	60
m902.pep	VPAYVFACDA HTGGVAVKRVY GADVVQNSG GAFQCQTQGRR QNTVFGIMFQIAEEPRPALR					
a902	VPAYVFACDA HTGGVAVKRVHGS DVVQNSG GTFQCQTQGRR XNTVFGVMFQIAEEPRALR					
	70	80	90	100	110	120
m902.pep	VPAYVFACDA HTGGVAVKRVY GADVVQNSG GAFQCQTQGRR QNTVFGIMFQIAEEPRPALR					
a902	VPAYVFACDA HTGGVAVKRVHGS DVVQNSG GTFQCQTQGRR XNTVFGVMFQIAEEPRALR					
	70	80	90	100	110	120
m902.pep	AAPYHNAVGGGLFEDGLGFLRRSNVAVDPDRDVQTAFGFGDEFVTRFAFVHLRTRASVDG					
a902	AAPYHNAVCGGLFEDGLGFLRRGNVAVDPDRDVQTAFGFGNQVVSRAFAFVHLRARASVDG					
	130	140	150	160	170	180
m902.pep	AAPYHNAVGGGLFEDGLGFLRRSNVAVDPDRDVQTAFGFGDEFVTRFAFVHLRTRASVDG					
a902	AAPYHNAVCGGLFEDGLGFLRRGNVAVDPDRDVQTAFGFGNQVVSRAFAFVHLRARASVDG					
	130	140	150	160	170	180
m902.pep	KGGDAIFGDFGDDGQVLMVVVPTQTGFEGNGYACRTDDGFQNGGNQRLVLHQRATGLDI					
a902	KGGNAIFGDFGDDGQVLMVVVPTQTGFEGNGYARRFDHRLQNGGNQRLVLHQRATGLDI					
	190	200	210	220	230	240
m902.pep	KGGDAIFGDFGDDGQVLMVVVPTQTGFEGNGYACRTDDGFQNGGNQRLVLHQRATGLDI					
a902	KGGNAIFGDFGDDGQVLMVVVPTQTGFEGNGYARRFDHRLQNGGNQRLVLHQRATGLDI					
	190	200	210	220	230	240
m902.pep	ADFFSGTAHV DVDKLRPKADV VTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSISER					
a902	ADFFSGTAHV DVDKLRPKADV VTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSISER					
	250	260	270	280	290	300
m902.pep	ADFFSGTAHV DVDKLRPKADV VTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSISER					
a902	ADFFSGTAHV DVDKLRPKADV VTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSISER					
	250	260	270	280	290	300
m902.pep	RVAGQHFAHR PTCAKISAKS AERFVGNAHR RRCDCGVVDKIAADVHNGSAFQKSTPLYIF					
	310	320	330	340	350	360

1289

```

a902      |||||
          RVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF
          310      320      330      340      350      360

m902.pep   X
           |
a902       X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2715>:

```

g903.seq
1  ATGGCAACAC AGGTAGGCGG TGCAAattcG gatgaggCAA GCCCCTGCTT
51 TCCTATTTCT GAGGTGGAaT TGGTGGGTGA aGaaacggct aAATTCGgt
101 tTGCGCTcaa ccaTGCCTTG tgccAAACAC ATTTTGtttc cGgcaagtgt
151 CTGcATGcgg gcgacattAA TCAAAtcaTG TCCTTAGCAC AAAATGCTTT
201 GATCGGCAGG GGATATACCA CGACCCGTAT CTGGCTGCG CCACAGGATT
251 TGAATAGTGG caaGCTTCAA TTAAccctga tgccggGCTA TcTgcgtcC
301 ATAcgaATCG atcgggtccaa cgatgatcaa ACCCATgcAG GACGTATTGC
351 AGCATTCCAA AACAAATTTT CCACCCGCTC GAACGATCTG TTGAATCTGC
401 GTGATTTGGA ACAAGGACTG GAAAATCTCA AATGTCTCCC GACTGCGGAA
451 GCCGATCTCC AAATCgttcc cgtaGAGAGA GAACcAAACC AAAGTGATGT
501 CGTGGTGCAA TGGCGGTAAC GTCTGCTGCC CTACTGTGTG AGTGTGGGGA
551 TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG AAATATCACT
601 TTCTCTGCCG ACAATCCTTT TggactgAGT GATATGTTCT ATGTAAATTA
651 TGGACGTTCA ATTGGCGGTA CGcccgATGA GGAAAATTTT GACGCCATC
701 GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC AGCCCCTTTC
751 GGTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT ACCATCAGGC
801 GGTTCGGA TTATCGGAAG TCTATGACTA TAATGGAAA AGTTACAACA
851 CTGATTTCGG CTTCAACCGC CTGTTGTATC GTGATGCCAA ACGCAAACCC
901 TATCTCAGTG TAAAACTGTG GACGAGGGAA AAAAAAGTT ACATTGATGA
951 TGCCGAAC TGCTGTACAAC GCGGTAAAAC CACAGGTTGG TTGGCAGAAC
1001 TTTCCACAA AGGATATATC GGTGCGAGTA CGGCAGATTT TAAGTTGAAA
1051 TATAAACACG GCACCGGCAT GAAAGATGCT CTGCGCGCGC CTGAAGAAGC
1101 CTTTGGCGAA GGCACGTCAC GTATGAAAAT TTGGACGGCA TCGGCTGATG
1151 TAAATACTCC TTTTCAAATC GGTAAACAGC TATTGCGCTA TGACACATCC
1201 GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG ACAAACGGC
1251 TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA ATGAGTTTGC
1301 CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG GCAATTTAAA
1351 CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG TTTCAGGACA
1401 ATCCGCCAAA TGGTTATCGG GCCAAACTCT AGCCGGCACA GCAATTGGGA
1451 TACGCGGCA GATAAAGCTT GCGGCAACC TGCATTACGA TATATTACC
1501 GGCCGTGCAT TGAAAAAGCC cgaatatatt cAGACGAAGA Aatgggtaac
1551 ggggtTTCAG gtgggttatt cgTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2716; ORF 903.ng>:

```

g903.pep
1  MATQVGGANS DEASPCFPIS EVELVGEETA KFRFALNHAL CQTHFVSGKC
51 LHAGDINQIM SLAQNALIGR GYTTTRILAA PQDLNSGKLO LTLMPGYLRS
101 IRIDRSNDDQ THAGRIAAFQ NKFPTRNDL LNLRLDLEQGL ENLKCLPTAE
151 ADLQIVPVER EPNQSDVVVQ WRXRLLPYCV SVGMDNSGSE ATGKYQGNIT
201 FSADNPFGLS DMFYVNYGRS IGGTPDEENF DHRKEGGSN NYAVHYSAPF
251 GKWTWAFNHN GYRYHQA VSG LSEVYDYNK SYNTDFGFNR LLYRDAKRKT
301 YLSVKLWTRE TKS YIDDAEL TVQRRKTTGW LAELSHKGYI GRSTADFKLK
351 YKHGTGMKDA LRAPEEAFGE GTSRMKIWTA SADVNTPFQI GKQLFAYDTS
401 VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE MSLPAERGWE WRNDLSWQFK
451 PGHQLYLGLAD VGHVSGQSAK WLSGQTLAGT AIGIRGQIKL GGNLHYDIFT
501 GRALKKPEYF QTKKWTGTFQ VGYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2717>:

```

m903.seq
1  ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTAACTG ATGCAAATGT
51 CCGTTTTGAG CAACCATTTG AGAAGAACAA TTATGTCTG AGTGAAGATG
101 AAACACCGTG TACTCGGTA AATTACATTA GTTTAGATGA TAAGACGGTG

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1290

```

151 CGCAAATTTT CTTTCTTCC TTCTGTGCTC ATGAAAGAAA CAGCTTTTAA
201 AACTGGGATG TGTTTAGGTT CCAATAATTG GAGCAGGCTA CAAAAAGCCG
251 CGCAACAGAT ACTGATCGTG CGTGGCTACC TCACCTCCCA AGCTATTATC
301 CAaCCACAGA ATATGGATTC GGAATTCTG AAATTACGGG TATCAGCAGG
351 CGAAATAGGG GATATCCGCT ATGAAGAAAA ACGGGATGGG AAGTCTGCCG
401 AGGGCAGTAT TAGTGCATTG AATAACAAAT TTCCCTTATA TAGGAACAAA
451 ATTCTCAATC TTCGCGATGT AGAGCAGGGC TTGGAAAACC TGCGTCGTTT
501 GCCGAGTGTT AAAACAGATA TTCAGATTAT ACCGTCCGAA GAAGAAGGCA
551 AAAGCGATTT ACAGATCAAA TGGCAGCAGA ATAAACCCAT ACGGTTTCAGT
601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTCGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTtTATG
701 TTTCATATGG ACGCGGTTTG GCGCACAAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAA CTGAAAGCGG ATCCAGAAAT TACAGCGTGC ATTATTCGGT
801 GCGCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAAACAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGACTTCA
951 TAAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTACAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGCTTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCTGCACCGG
1151 AAGAAAACGG CGGCGATATT CTTCCAGGTA CATCTCGTAT GAAAAATCATT
1201 ACTGCCAGTT TGGACGAGC CGCCCCATTT AyTTTAGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCGTTGGTTG
1301 CCCAAGATAA ATTGTCATC GGCAGCCGCT ACACCGTTCG CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGCG AGAATACTTT
1401 AACTTGGTAT TTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAAGTG TCGGCTTCAG AGGAGGGCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTGA ATTACAGTTT CTA

```

This corresponds to the amino acid sequence <SEQ ID 2718; ORF 903>:

m903 . pep

```

1  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV
51  RKFSFLPSVL MKETAFKTM CLGSNNLSRL QKAAQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEKRDG KSAEGSISAF NKNKFLYRNL
151 ILNLRDVEQG LENLRLPSV KTDIQIIPSE BEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL AHKTDLTDAT
251 GTETESGSR S YSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNGKQ
301 YQSSLAAERM LWRNRLHKTS VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHAYLN RWQLDGKLSY KRGTMQRQSM PAPEENGDDI LPGTSRMKII
401 TASLDAAAPF XLGKQOFFYA TAIQAQWNKT PLVAQDKLSI GSRVTVRGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 903 shows 48.9% identity over a 519 aa overlap with a predicted ORF (ORF 903.ng) from *N. gonorrhoeae*:

m903/g903

```

          10      20      30      40      50      60
m903 . pep  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL
              |:::|||  :::|  :::|  :::|  :::|
g903        MATQVGGANSDEASPCFPISEVELVGEETAKFRFALNHA
              10      20      30

          70      80      90      100     110     120
m903 . pep  MKETAFKTMCLGSNNLSRLQKAAQILIVRGYLTSAIIQPQNMDSGILKLRVSAGEIG
              : : | | : | | : : : : : | : | | | : : : | : : | | : | : | :
g903        LCQTHFVSGKCLHAGDINQIMSLAQNALIGRGYTTTRILAAPQDLNSGKLQTLMPGYLR
              40      50      60      70      80      90

```

1291

m903.pep	130	140	150	160	170	180
	DIRYEEKRDGKSAEGSISAFNNKFPLYRNKILNLRDVEQGLNLRRLPSVKTDIQIIPSE					
g903	SIRIDRSNDQTHAGRIAAAFQNKFPTRSDLLNLRDLEQGLNLRKCLPTAEADLQIVPVE					
	100	110	120	130	140	150
m903.pep	190	200	210	220	230	
	EE-GKSDLQIKWQONK-PIRFSIGIDDAGGKTTGKYQGNVALSFDNPLGLSDFYVSYGR					
g903	REPNSDQSDVVQWRXRLLPYCVSVGMDNSGSEATGKYQGNITFSADNPFGLSDMFVNYGR					
	160	170	180	190	200	210
m903.pep	240	250	260	270	280	290
	GLAHKTDLTDTGTETESGSRYSVHYSVPVKKWLFNFHNGHRYHEATEGYSVNYDYNG					
g903	SIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAFNHNGYRYHQAVSGLSEVYDYNG					
	220	230	240	250	260	270
m903.pep	300	310	320	330	340	350
	KQYQSSSLAAERMLWRNRLHKTSVGMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAY					
g903	KSYNTDFGFNRLLYRDAKRKTYLSVKLWTRTKSYIDDAELTVQRRKTTGWLAEELSHKGY					
	280	290	300	310	320	330
m903.pep	360	370	380	390	400	410
	LNRWQLDGKLSYKRGTMQRSMPEENGDDILPGTSRMKIITASLDAAAPFXLGKQQFF					
g903	IGRSTADFKLYKHGTGMKDALARPEEAFGE--GTSRMKIWTASADVNTPFQIGKQLFA					
	340	350	360	370	380	390
m903.pep	420	430	440	450	460	470
	YATAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYWQNTLTWYFHPNHQFY					
g903	YDTSVHAQWNKTPLTSQDKLAIGGHHTVIRGFDGEMSLPAERGWYWRNDSWQFKPGHQLY					
	400	410	420	430	440	450
m903.pep	480	490	500	510	520	530
	LGADYGRVSGESAQYVSGKQLMGAVVGFRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTV					
g903	LGADVGHVSGQSAKWLSGQTLAIGIRGQIKLGGNLHYDIFTGRALKKPEYFQTKKWV					
	460	470	480	490	500	510
m903.pep	540					
	YGFNLNYSFX					
g903	TGFQVGYSFX					
	520					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2719>:

a903.seq

1	ATGCAGCGTC	AGCAGCACAT	AGATGCTGAA	TTGTAACTG	ATGCAAATGT
51	CCGTTTCGAG	CAACCATTGG	AGAAGAACAA	TTATGTCCTG	AGTGAAGATG
101	AAACACCGTG	TACTCGGGTA	AATTACATTA	GTTTAGATGA	TAAGACGGCG
151	CGCAAATTTT	CTTTCTTCC	TTCTGTGCTC	ATGAAAGAAA	CAGCTTTTAA
201	AACTGGGATG	TGTTTAGGTT	CCAATAATTT	GAGCAGGCTA	CAAAAAGCCG
251	CGCAACAGAT	ACTGATTGTG	CGTGGCTACC	TCACTTCCCA	AGCTATTATC
301	CAACCACAGA	ATATGGATTG	GGGAATTCTG	AAATTACGGG	TATCAGCAGG
351	CGAAATAGGG	GATATCCGCT	ATGAAGAAAA	ACGGGATGGG	AAGTCTGCCG
401	AGGGCAGTAT	TAGTGCATTC	AATAACAAAT	TTCCCTTATA	TAGGAACAAA
451	ATTCTCAATC	TTCGCGATGT	AGAGCAGGGC	TTGGAAGAAC	TGCGTCGTTT
501	GCCGAGTGTT	AAAACAGATA	TTCAGATTAT	ACCGTCCGAA	GAAGAAGGCA
551	AAAGCGATTT	ACAGATCAAA	TGGCAGCAGA	ATAAACCCAT	ACGGTTTCAGT

a903.pcp

1	MQRQOHIDAE	LLTDANVRFE	QPLEKNNYVL	SEDETPCTRV	NYISLDDKTA
51	RKFSFLPSVL	MKETAFKTGM	CLGSNNLSRL	QKAAQQILIV	RGYLTSQLII
101	QPQNMDSGIL	KLRVSAGEIG	DIRYEKR DG	KSAGSISAF	NNKFPLYRNK
151	ILNLRDVEQG	LENLRRLPSV	KTDIQIIPSE	EEGKSDLQIK	WQONKPIRFS
201	IGIDDAAGKT	TGKYQGNVAL	SFDNPLGLSD	LHYVYSGRGL	VHKTDLT DAT
251	GTETESGSRG	YSVHYSVPVK	KWLFSFNHNG	FRYHEATEGY	SVNYDYNGKQ
301	YQSSLA AERM	LWRNRFHKTS	VGMKLWTRQT	YKYIDDAEIE	VQRRRSAGWE
351	AELRH RAYLN	RWQLDGKLSY	KRGTMGRQSM	PAPENG GGT	IPGTSRMKII
401	TAGLDA AAFP	MLGKQQFFYA	TAIQAQWNKT	PLVAQDKLSI	GSRYTVXGFD
451	GEQSLFGRG	FWYQNTLTWY	FHPNHQFYLG	ADYGRVSGES	AQYVSGKQLM
501	GAVVGFRGGH	KVGGMFAYDL	FAGKPLHKPK	FGOTTNTVYG	FNLYNSF*

	10	20	30	40	50	60
m903.pep	MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDET	PCTRVNYISLDDKTVRKFSFLPSVL				
a903	MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDET	PCTRVNYISLDDKTVRKFSFLPSVL				
	10	20	30	40	50	60
m903.pep	70	80	90	100	110	120
	MKETAFKTGMCLGSNNLSRLQKAAQQILIVRGYLT	SQAI IQPNMDSGILKLRVSAGEIG				
a903	MKETAFKTGMCLGSNNLSRLQKAAQQILIVRGYLT	SQAI IQPNMDSGILKLRVSAGEIG				
	70	80	90	100	110	120
m903.pep	130	140	150	160	170	180
	DIRYEEKRDGKSAEGSISAFNNKFPLYRNKILNLRD	VEQGLENLRLPSVKTDIQIIPSE				
a903	DIRYEEKRDGKSAEGSISAFNNKFPLYRNKILNLRD	VEQGLENLRLPSVKTDIQIIPSE				
	130	140	150	160	170	180
m903.pep	190	200	210	220	230	240
	EEGKSDLQIKWQQNKPIRFSIGIDDAGGKTTGKYQ	GNVALSFDNPLGLSDLFVVSYGRGL				
a903	EEGKSDLQIKWQQNKPIRFSIGIDDAGGKTTGKYQ	GNVALSFDNPLGLSDLFVVSYGRGL				
	190	200	210	220	230	240
m903.pep	250	260	270	280	290	300
	AHKTDLTLDATGTETESGSRSYSVHYSVPVKKWLF	SFNHNGHRYHEATEGYSVNYDYGKQ				
a903	VHKTDLTLDATGTETESGSRSYSVHYSVPVKKWLF	SFNHNGHRYHEATEGYSVNYDYGKQ				

1293

	250	260	270	280	290	300
	310	320	330	340	350	360
m903.pep	YQSSSLAERMLWRNRLHKTSVGMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
a903	YQSSSLAERMLWRNRFHKTSVGMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
	370	380	390	400	410	420
m903.pep	RWQLDGKLSYKRGTMGRQSMPEENGDDILPGTSRMKIITASLDAAAPFXLGKQQFFYA					
a903	RWQLDGKLSYKRGTMGRQSMPEENGDDIPGTSRMKIITAGLDAAAPFMLGKQQFFYA					
	430	440	450	460	470	480
m903.pep	TAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
a903	TAIQAQWNKTPLVAQDKLSIGSRYTVXGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
	490	500	510	520	530	540
m903.pep	ADYGRVSGESAQYVSGKQLMGAVVGFRRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
a903	ADYGRVSGESAQYVSGKQLMGAVVGFRRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
	490	500	510	520	530	540
m903.pep	FNLNYSFX					
a903	FNLNYSFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2721>:

g904.seq

```

1  ATGATGCAGC ACAATCGTTT CTTGCGGGTC GGGGCCGGTg gaGACGATGG
51  CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGCA ATGCGTCGTA GCTTTTCACG CCGACAGTCG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGTTTGCA GGTTCACACC GCATCCGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGC CTGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATGCA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCAAGC GCAGCGGCGC GCGCGGCCGG TTACCGAACC GAATTCGTGT
401 CCGCGCTCCG CCAAACCTGC GCCTACTTCG TCGAACAAAT CGGTCGGGAA
451 CGGGCCCCGA CCGACGCGCG TGGTATAGGC TTTGACGATG CCCAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC CGCGCCGGCG
551 AGACAGTTGG ACGAGGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGCGCGCCTT CAAACAGCAG TTTTTCGCCG TTTTGTGTTT
651 TTTGTTTCAA CACGCggaac acgtcgGCAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGTCCGGC
751 GTTATGCAGG TATTGGAGTT GGACGTTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTACAG CAGTTTTTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 GCGGATTTTG CCTTTGCCGC GCGATGCTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGg gaaacgAcaa cGCCCCAACC gatGAAGCAA TCCAATCCTT
1101 CGTGCAGGAT ACCGCTCGGA ATCAGGCGCA AAATGGTTT TTTGCCGCCG
1151 ACGACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGGAAAG GCACgacGct
1201 gCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTgc gccGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGatata A

```

This corresponds to the amino acid sequence <SEQ ID 2722; ORF 904.ng>:

g904.pep

```

1  MMQHNRFFAV GAGGDDGDRR AADFFNPFQI CFGIGRQCVV AFHADSRFAP

```



1294

```

51  AGHGFVNRFA GFHRIRTARQ DVGFAAAWQF VADADIDGFN AVHYIEFGNA
101 HTGNAVDLDG AFQGGGIKPA AAARAAGYRT EFVSALRQTC AYFVEQFGRE
151 RARTDARGIG FDDAQNI IQH LRTYARACRS RAGETVGRGN EGVSAVVDVQ
201 QRTLRAFKQQ FFAVFVFFVQ HAGHVGNHRR NARRDFFDNR HHVFRFNRSR
251 VMQVLELDVV IGKDG IQFFT QFFRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAAARCF AGLVERDVVR QDQRAGR RDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGNDNART DEAIQSFVQD TARNQAQNGF FAADDQGMAR IVAALEAHDA
401 AGFFRQPVND FTFTLVAPLC ADYINIFSHS HITYRY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2723>:

```

m904.seq
1   ATGATGCAGC ACAATCGTTT CTTCTCGGTC GGGGCCGgTG GAGACGATGG
51  CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCG
101 TTTTCGGGCA ATGCGCCGTA GTCCTTCACG CCGAAAGTGG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGCTTGCA GGTTTCCACC GCATCGGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGT CGGGCAATTC ATAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TAGTAATACA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCAGCC GCAGCGGCGT GCGCGTCCGG TTACCGAACC GAATTCGTGT
401 CCGCGTTCTG CCAAACCTAC GCCTACTTCG TCGAACAATT CCGTCGGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCCAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC TGCGCCCGCC
551 AGACAGTTGG ACGAGGTAAC GAAGGGATAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGC CGCCTT CAAACAGCAG TTTTTCGCCG TTTTGTGTTT
651 TCTCGTTCAA CACGCGGGAC ACGTCGGTAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTAA CCGGCTCGGC
751 ATTGTGCAGA TGTGTCAGTT GGACATTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTTCACG CAGTTTtTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CCGCGTGCCA CTTTGTCCTT GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 GCCGATTTTG CCTTGCCCGC GCG .AtcTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAAACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTT TTTGCCGCCG
1151 ACAACCAAGG TATGCCCCGC ATTGTGCGCG CTTTGAAGC GCACCaCGCC
1201 GCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTAsT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2724; ORF 904>:

```

m904.pep
1   MMQHNRFFSV GAGGDDGDRR AADFFNPFQI CFGVFGQCAV VLHAESGFAP
51  AGHGFVNRLA GFHRIGTARQ DVGFAAVGQF IADADIDGFN AVHYIEFSNT
101 HTGNAVDLDG AFQGGGIKPA AAACASGYRT EFVSAFCQTY AYFVEQFGRE
151 RARTDARGIG FDDAQNI IQH LRTYARACRS CARQTVGRGN EGISAVVDVQ
201 QRTLRAFKQQ FFAVFVFLVQ HAGHVGNHRR NARRDFFDNR HHVFRFNRLG
251 IVQMLQLDIV IGKDG IQFFT QFXRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAXIF AGLVERDVVR QDQRAGR RDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQMAR IVAALEAHHA
401 AGFFRQPVND FTFTLVAPLC ADXYNIFSHS HITYRY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 904 shows 90.4% identity over a 436 aa overlap with a predicted ORF (ORF 904.ng) from *N. gonorrhoeae*:

```

m904/g904
10      20      30      40      50      60
m904.pep MMQHNRFFSVGAGGDDGDRRAADFFNPFQICFGVFGQCAVVLHAESGFAPAGHGFVNRLA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g904      MMQHNRFFAVGAGGDDGDRRAADFFNPFQICFGIGRQCVAHFADSRFAPAGHGFVNRLA
10      20      30      40      50      60
70      80      90      100     110     120

```

## 1295

m904 . pep	GFHRIGTARQDVGFAAVQGFIADADIDGFNAVHYIEFSNTHTGNVAVDLGAFQGGGIKPA
g904	GFHRIRRTARQDVGFAAAWQFVADADIDGFNAVHYIEFGNAHTGNVAVDLGAFQGGGIKPA
	70 80 90 100 110 120
m904 . pep	AAACASGYRTEFVSAFCQTYAYFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
g904	AAARAAGYRTEFVSALRQTCA YFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
	130 140 150 160 170 180
m904 . pep	CARQTVGRGNEGISA VVDVQORTLRAF KQFFAVFVFLVQHAGHVGNHRRNARRDFFDNR
g904	RAGETVGRGNEGVS AVVDVQORTLRAF KQFFAVFVFFVQHAGHVGNHRRNARRDFFDNR
	190 200 210 220 230 240
m904 . pep	HHVFRFNRLGIVQMLQLDIVIGKDG IQFFTQFXRMQ QIGGANGAACHFV FVGRADAAAGR
g904	HHVFRFNRS GVMQVLELDV VIGKDG IQFFTQFFRMQ QIGGANGAACHFV FVGRADAAAGR
	250 260 270 280 290 300
m904 . pep	ADFAFAARIFAGLVERDVVRQDQRAGRRDFQTAFDV FHACRVQLVDF AQQGFGGDDNART
g904	ADFAFAARCFAGLVERDVVRQDQRAGRRDFQTAFDV FHACRVQLVDF AQQGFGGNDNART
	310 320 330 340 350 360
m904 . pep	DEAVQTFMQDAARNQAQNGFFAADNQGMARIVAAL EAHHAAGFFRQPVNDF TFLVAPLC
g904	DEAIQSFVQD TARNQAQNGFFAADDQGMARIVAAL EAHDAAGFFRQPVNDF TFLVAPLC
	370 380 390 400 410 420
m904 . pep	ADXYNIFSHSHITYRYX
g904	ADYYNIFSHSHITYRYX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2725>:

a904 . seq

1	ATGATGCAGC	ACAATCGTTT	CTTCGCGGTC	GGGGCCGGTG	GAGACGATGG
51	CGACCGGCGC	ACCGCAGACT	TCTTCAATCC	GTTTCAAATA	TGCTTTGGCA
101	TTGGCAGGTA	ATGCGTCGTA	GCTTTTCACG	CCGAAAGTGG	ATTTCGCTCCA
151	ACCGGCGCATG	GTTTCGTAAA	TCGGCTTGCA	GGCTTCTACC	GCATCAGAGC
201	CGCAAGGCAG	GATGTCGGTT	TTGCCGCCGT	CGGGCAATTC	GTAGCCGACG
251	CAGATATTGA	TGGTTTCAAC	GCCGTCCATT	ACATCGAGTT	TGGTAATACA
301	CATACCGGAA	ATGCCGTTGA	TTTGGATGGA	GCGTTTCAGG	GCGGCGGCAT
351	CAAACGAGCC	GCAGCGGCGT	GCGCGTCCGG	TTACCGAACC	GAATTCGTGT
401	CCGCGTTCTG	CCAAACCTGC	TCCGACTTCG	TCGAACAATT	CGGTCGGGAA
451	CGGGCCCGAA	CCGACGCGCG	TGGTATAGGC	TTTGACGATG	CCCAAAACAT
501	AATCCAGCAT	TTGAGGGCCT	ACGCCGCGC	CTGCCGAAGC	CGCGCCGGCG
551	AGGCAGTTGG	ACGAAGTAAC	GAAGGGGTAA	GTGCCGTAGT	CGATGTCCAA
601	CAACGCACCT	TGCGCGCCTT	CAAACAGCAG	TTTTTCGCCG	TTTTTGT TTT
651	TTTCGTTCAA	CACGCGGGAC	ACGTCGGTAA	TCATCGGCGT	AATGCGCGGC
701	GCGACTTTTT	CGATAACCGC	CATCACGTCT	TCCGCTTTCA	CCGACTCGGC
751	ATTGTGCAGA	TGTTGCAGTT	GGACGTTGTA	ATAAGCAAAG	ACGGCATCCA
801	GTTTTTCACG	CAGTTTTTCA	GGATGCAGCA	AATCGGCGGC	GCGAATGGCG
851	CGGCGTGCCA	CTTTGTCTTC	GTAGGCAGGG	CCGATGCCGC	GGCCGGTCTG
901	GCCGATTTTG	CCTTTGCCGC	GCGATGCTTC	TCGGGCTTGG	TCGAGCGCGA

1296

```

951 TGTGATAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAGACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACAACCAAGG TATGACCCGC ATTGTGGCCG CCTTGGGAAGC GCACCACGCC
1201 TCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 .TCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2726; ORF 904.a>:

```

a904.pep
1  MMQHNRFFAV GAGGDDGDRR TADFFNPFI CFIGR*CVV AFHAESGFAP
51  TGHGFVNRLA GFYRIRAAARQ DVGFAAVGQF VADADIDGFN AVHYIEFGNT
101 HTGNAVLDLG AFQGGGIKPA AAACASGYRT EFVSAFCQTC SDFVEQFGRE
151 RARTDARGIG FDDAQNIQH LRAYARACRS RAGEAVGRSN EGVSAVVDVQ
201 QRTLRAFQKQ FFAVFVFFVQ HAGHVGNNRR NARRDFFDNR HHVFRFHRLG
251 IVQMLQLDVV ISKDGIIQFF QFFRMQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAARCF SGLVERDVIR QDQRAGRRDF QTAFDVFHAC RVQLVDFQQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQMTR IVAALEAHHA
401 SGFFRQPVND FTFTLVAPLC ADYYNIFSHS HITXRY*

```

m904/a904 91.3% identity in 436 aa overlap

m904.pep	MMQHNRFFSVGAGGDDGDRRAADFFNPFI	CFGVFGQCAVVLHAESGFAPAGHGFVNRLA
a904	MMQHNRFFAVGAGGDDGDRRTADFFNPFI	CFGIGRXCVVAFHAESGFAPTGHGFVNRLA
	10 20 30 40 50 60	
m904.pep	GFHRIGTARQDVGFAAVGQFIADADIDGFNAVHYIEFSNTH	TGNAVLDLDAFGGGGIKPA
a904	GFYRIRAAARQDVGFAAVGQFVADADIDGFNAVHYIEFGNTH	TGNAVLDLDAFGGGGIKPA
	70 80 90 100 110 120	
m904.pep	AAACASGYRTEFVSAFCQTYAYFVEQFGRERARTDARGIGFDDAQNIQH	LRAYARACRS
a904	AAACASGYRTEFVSAFCQTCSDFEQFGRERARTDARGIGFDDAQNIQH	LRAYARACRS
	130 140 150 160 170 180	
m904.pep	CARQTVGRGNEGISA	VVDVQRTLRAFQKQFFAVFVFLVQHAGHVGNNRRNARRDFFDNR
a904	RAGEAVGRSNEGISA	VVDVQRTLRAFQKQFFAVFVFFVQHAGHVGNNRRNARRDFFDNR
	190 200 210 220 230 240	
m904.pep	HHVFRFNRLGIVQMLQLDIVIGKDGIIQFFTFQFXRMQIGGANGAACHFVFVGRADAAAGR	
a904	HHVFRFHRLGIVQMLQLDVVISKDGIIQFFTFQFFRMQIGGANGAACHFVFVGRADAAAGR	
	250 260 270 280 290 300	
m904.pep	ADFAFAAXIFAGLVERDVVRQDQRAGRRDFQTAFDVFHACRVQLVDFQQGFGGDDNART	
a904	ADFAFAARCFSGLVERDVIRQDQRAGRRDFQTAFDVFHACRVQLVDFQQGFGGDDNART	
	310 320 330 340 350 360	
m904.pep	DEAVQTFMQDAARNQAQNGFFAADNQMARI	VAALEAHHAAGFFRQPVNDFFTFTLVAPLC
a904	DEAVQTFMQDAARNQAQNGFFAADNQMTRI	VAALEAHHASGFFRQPVNDFFTFTLVAPLC
	370 380 390 400 410 420	

1297

```

m904.pep    ADXYNIFSHSHITYRYX
             || ||||| |||| |||
a904        ADYYNIFSHSHITXRYX
             430

```

g906.seq not found yet  
g906.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2727>:

```

m906.seq
1  ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
51 GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAACAAA
301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2728; ORF 906>:

```

m906.pep
1  MKYIVSISLA MGLAACSFEG FKNPNWDAAS FWELKNYANP YPGSASAALD
51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDYPENK
101 KYEWPREEGK TK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2729>:

```

g907.seq (partial)
1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTgcaAC GCCGCCGCCT
51 GCTGTGTGCC GCCGGCGCGC TGTGTATCAG CCCGCTGGCG CACGCCGGCG
101 CGCAACGTGA AGAAACGctt gCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTGACA ATCCGAAAGA
201 GGGCGAACGT TGGTTGTCCG CGATGTCGGC ACGTTTGGCA AGATTCTGTC
251 CCGACGAGGG GGAGCGGCGC AGGCTGCTGG TCAATATCCA ATACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGa ttgaagtgga
351 aagcgggtac cgagctcgaa tcatatca..

```

This corresponds to the amino acid sequence <SEQ ID 2730; ORF 907.ng>:

```

g907.pep (partial)
1  MKKPTDTLPV NLQRRRLCA AGALLISPLA HAGAQREETL ADDVASVMRS
51 SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPDEGERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESGY RARIIS...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2731>:

```

m907.seq
1  ATGAGAAAAC CGACCGATAC CCTACCCGTT AATCTGCAAC GCCGCCGCCT
51 GTTGTGTGCC GCCGGTGCGT TGTGTCTCAG TCCTCTGGCG CACGCCGGCG
101 CGCAACGTGA GGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTTGACA ATCCGAAAGA
201 GGGCGAGCGT TGGTTGTCTG CCATGTCGGC ACGTTTGGCA AGGTTCGTCC
251 CCGAGGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGGTTAT GCCGTTkTGG AAAAActACA TCGGCAAAAC GGCGCACAAc
451 CTGTTGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCGCTT GCCCGCTTTA
551 ACGGCAGCTT GGGCAGCAAT AAATATCCGA ACGCCGTTTT GGgCGCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2732; ORF 907>:

```

m907.pep
1  MRKPTDTLPV NLQRRRLCA AGALLLSPLA HAGAQREETL ADDVASVMRS
51 SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPEEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAISGVA RGLMQVMPXW KNYIGKPAHN

```

1298

151 LFDIRTNLRY GCTILRHYRN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW  
201 RNRWQWR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 907 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 907.ng) from *N. gonorrhoeae*:

g907/m907

	10	20	30	40	50	60
g907 . pep	MKKPTDTLPVNLQRRRL	LLCAAGALLISPLAHAGA	QREETLADDVASVMR	SSVGSVNP	PRL	
	:	:	:	:	:	:
m907	MRKPTDTLPVNLQRRRL	LLCAAGALLSPLAHAGA	QREETLADDVASVMR	SSVGSVNP	PRL	
	10	20	30	40	50	60
	70	80	90	100	110	120
g907 . pep	VFDNPKEGERWLSAMS	ARLARFVPEDEGER	RRLLVNIQYESSR	AGLDTQIVLGLIE	ESGY	
m907	VFDNPKEGERWLSAMS	ARLARFVPEEEER	RRLLVNIQYESSR	AGLDTQIVLGLIE	ESAF	
	70	80	90	100	110	120
g907 . pep	RARIIS					
m907	RQYAISGVGARGLMQ	VMPXWKNYIGKPA	HNLFDIRTNLRYG	CTILRHYRNLEK	GNIVRAL	
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2733>:

a907 . seq

1	ATGAAAAAAC	CGACCGATAC	CCTACCCGTC	AATCTGCAAC	GCCGCCGCCT
51	ATTGTGTGCT	GCCGGCGCGC	TGTTGCTCAG	CCCGCTGGCA	CAAGCCGGCG
101	CGCAACGTGA	AGAAACGCTT	GCCGACGATG	TGGCTTCCGT	GATGAGGAGC
151	TCTGTGCGCA	GCATAAATCC	GCCGAGGCTG	GTGTTGACAC	ATCCGAAAGA
201	GGGCGAGCGT	TGGCTGTCCG	CGATGTCTGC	TCGGTTGGCA	AGGTTCGTCC
251	CCGATGAGGA	GGAGCGGCGC	AGGCTGCTGG	TCAATATCCA	GTACGAAAGC
301	AGCCGGGCGG	GTTTGGATAC	GCAGATTGTG	TTGGGGCTGA	TTGAGGTGGA
351	AAGCGCGTTC	CGCCAGTATG	CAATCAGCGG	TGTCGGCGCG	CGCGGCCTGA
401	TGCAGGTTAT	GCCGTTTTGG	AAAACTACA	TCGGCAAACC	GGCGCACAAAC
451	CTGTTGACAC	TCCGCACCAA	CCTGCGTTAC	GGCTGTACCA	TCCTGCGCCA
501	TTACCGGAAT	CTTGAAAAAG	GCAACATCGT	CCGCGCACTC	GCCCCTTTTA
551	ACGGTAGCCT	CGCAGCAAT	AAATATCCGA	ACGCCGTTTT	GGGCGCGTGG
601	CGCAACCGCT	GGCAGTGGCG	TTGA		

This corresponds to the amino acid sequence <SEQ ID 2734; ORF 907.a>:

a907 . pep

1	MKKPTDTLPV	NLQRRRLCA	AGALLSPLA	QAGAQREETL	ADDVASVMRS
51	SVGSINPPRL	VFDNPKEGER	WLSAMSARLA	RFVPDEEERR	RLLVNIQYES
101	SRAGLDTQIV	LGLIEVESAF	RQYAISGVGA	RGLMQVMPFW	KNYIGKPAHN
151	LFDIRTNLRY	GCTILRHYRN	LEKGNIVRAL	ARFNGSLGSN	KYPNAVLGAW
201	RNRWQWR*				

m907/a907 97.6% identity in 207 aa overlap

	10	20	30	40	50	60
m907 . pep	MRKPTDTLPVNLQRRRL	LLCAAGALLSPLAHAGA	QREETLADDVASVMR	SSVGSVNP	PRL	
	:	:	:	:	:	:
a907	MKKPTDTLPVNLQRRRL	LLCAAGALLSPLAQAGA	QREETLADDVASVMR	SSVGSINP	PRL	
	10	20	30	40	50	60
	70	80	90	100	110	120
m907 . pep	VFDNPKEGERWLSAMS	ARLARFVPEEEER	RRLLVNIQYESSR	AGLDTQIVLGLIE	ESAF	
a907	VFDNPKEGERWLSAMS	ARLARFVPEEEER	RRLLVNIQYESSR	AGLDTQIVLGLIE	ESAF	

1299

	70	80	90	100	110	120
	130	140	150	160	170	180
m907.pep	RQYAI	SGVG	ARGLM	QVMP	XWK	NYIGK
a907	RQYAI	SGVG	ARGLM	QVMP	FWKN	YIGK
	130	140	150	160	170	180
	190	200				
m907.pep	ARFNG	SLGS	SNKY	PNAVL	GAWR	NRWQ
a907	ARFNG	SLGS	SNKY	PNAVL	GAWR	NRWQ
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2735>:

```

g908.seq
1  ATGAG.AAAA GCCGTCTAAG CCGGTATAAA CAAAATAAAC TCATTGGGCT
51  ATTTGTCGCA GGTGTAAGT CAAGAACAGC GGCAGAGTTG GTAGGCATTA
101 ATAAAAATAC CGCAGCCTAT GATTTTCATC GTTTACGATG ACTGATTAT
151 CAAAACGGTC CGCATTTAGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCCTACT TTATTCCTA TTATCCGTGA
351 acaagtgaac cctgacagta ttgtttatac ggattgttat CgTAGCTATG
401 ATGTATTAGA Tgtgagcgaa ttagccatT TTagcttcgc tgaaacttcg
451 ttttcgtaTC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2736; ORF 908.ng>:

```

g908.pep
1  MXKSRLSRYK QNKLIGLFVA GVTARTAAEL VGINKNTAAY DFHRLR*LIY
51  QNGPHLEMFD GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTPNTQTAT LFPIIREQVK PDSIVYTDCY RSYDVLDVSE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2737>:

```

m908.seq
1  ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAmTAAAC TCATTGAACT
51  GTTTGTCACA GGTGTAAGT CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTTGGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCCTACT TTATTCCTA TTATCCGTGA
351 ACAAGTGAAC CCTGACAGCA TTTTATATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2738; ORF 908>:

```

m908.pep
1  MRKSRLSRYK QXKLIELFVT GVTARTAAEL VGVNKNTAAY YFHRLRLLIY
51  QNSPHLEMFD GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTPNTQTAT LFPIIREQVK PDSIFYTDCY RSYDVLDVRE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 908 shows 93.4% identity over a 166 aa overlap with a predicted ORF (ORF 908.ng) from *N. gonorrhoeae*:

```

g908/m908
10 20 30 40 50 60
g908.pep MXKSRLSRYKQNKLIGLFVAGVTARTAAELVGINKNTAAYDFHRLRLXLIYQNGPHLEMFD

```

m908	MRKSRLS QYKQXKLI ELFVTGVTARTAAELVGVNKNTAAYYFHLRLLLIYQNSPHLEMF	10	20	30	40	50	60
		70	80	90	100	110	120
g908.pep	GEVEADESYFGGQQRKGKRGGAAGKVAVFGLLKRNGKVYTVTVPNQTATLFP IIREQVK						
m908	GEVEADESYFGGQQRKGKRGGAAGKVAVFGLLKRNGKVYTVTVPNQTATLFP IIREQVK	70	80	90	100	110	120
		130	140	150	160		
g908.pep	PDSIVYTDCYRSYDVLVDVSEFSHF SFAETSFSYQSQHTFCRTTKPYX						
m908	PDSIFYTDCYRSYDVLVDVREFSHF SFAETSFSYQSQHTFCRTTKPYX	130	140	150	160		

```
a908.seq
1  ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAATAAAC TCATTGAGCT
51  ATTTGTGCGA GGTGTAAC TG CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTTGGA ATATGTTTGAT GCGGAAGTAG AAGCAGATGA
201 AAGTTATTTT GCGCGACAAC GCAAAGGCAA ACGCGGTGCG GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACC GCTACT TTATTTCTTA TTATCCGTGA
351 ACAAGTGAAA CCTGACAGCA TTGTTTATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A
```

**a908.pep**

1	<u>MRKSRLSQYK</u>	<u>QNKLIELFVA</u>	<u>GVTARTAAEL</u>	VGVNKNTAAY	YFHLRLLLIY
51	QNSPHLEMF	GEVEADESYF	GGQRKGKGR	GAAGKVAVFG	LLKRNGKVYT
101	VTVPNTQTAT	LFPIIREQVK	PDSIVYTDY	RSYDVLVDRE	FSHFSFAETS
151	FSYQSQHTFC	RTTKPY*			

	10	20	30	40	50	60
m908.pep	MRKSRLSQYKQXKLI	ELFVTGVTARTAAEL	VGVNKNTAAYYFHRL	RLLLIYQNSPHLEM	F	
		:				
a908	MRKSRLSQYKQKLI	ELFVAGVTARTAAEL	VGVNKNTAAYYFHRL	RLLLIYQNSPHLEM	F	
	10	20	30	40	50	60
	70	80	90	100	110	120
m908.pep	GEVEADESYFGGQR	KGKRGRGAAGKVAV	FGLLKRNGKVYTV	TVTPNTQTATLFPI	IREQVK	
a908	GEVEADESYFGGQR	KGKRGRGAAGKVAV	FGLLKRNGKVYTV	TVTPNTQTATLFPI	IREQVK	
	70	80	90	100	110	120
	130	140	150	160		
m908.pep	PDSIFYTDCYRSYD	VLVDVREFSHFSFA	ETSFSYQSQHTFC	RTTKPYX		
a908	PDSIVYTDYRSYD	VLVDVREFSHFSFA	ETSFSYQSQHTFC	RTTKPYX		
	130	140	150	160		

```
g909.seq (partial)
      1  atcggtaaaa ccgtaacttat cCTgaccatc tccgccgcc ttttgtcggg
     51  ctgcacatgG gaaacttatc aagacggcag cggcaaaacc gccgtccgtg
    101  caaaatgttc caccggcacg ccgctgtgtt ggcaagacgg gcgcggctcg
```

1301

```

151 aaaaaggtgg actgcgacga gtacggtggc gaacgccggg ccgtgttgcg
201 caaccaaaag cgggggaagc ccgcgacgag gagagccgca acgctgggga
251 aaccgagttt ccgggcgagg gacggggggg ggcgggtgaa cagggcagaa
301 acggggggagg ggaagcgatc ggcgagg..

```

This corresponds to the amino acid sequence <SEQ ID 2742; ORF 909.ng>:

g909.pep (partial)

```

1 MRKTVLILTI SAALLSGCTW ETYQDGSgKT AVRACSTGT PLCWQDGRGS
51 KKVDCDEYGG ERRAVLNRQK RGKPTRRAA TLGKPSFRAR DGGGRVNRAE
101 TGEKRSAR..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2743>:

m909.seq

```

1 ATGCGTAAAA CCTTCCTCTT CCTGACCGCT GCCGCCGCC TTTTGTGCGG
51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
101 AAAAATATCC CGCCGGCACG CCCGTTTATT ACCAAGACGG CAGCTACTCG
151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC
201 CAATCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
251 AACCAAAGTT TCAAACCGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2744; ORF 909>:

m909.pep

```

1 MRKTFILFLTA AAALLSGCAW ETYQDGNgKT AVRQKYPAGT PVYYQDGSYS
51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 909 shows 53.3% identity over a 90 aa overlap with a predicted ORF (ORF 909.ng) from *N. gonorrhoeae*:

m909/g909

	10	20	30	40	50	60
m909.pep	MRKTFILFLTA <del>AAA</del> ALLSGCAWETYQDGNgKTAVRQKYPAGTPVYYQDGSYSKNMNYNQYRP					
		:	:	:	:	:::
g909	MRKTVLILTI <del>SA</del> ALLSGCTWETYQDGSgKTAVRAKSTGTPLCWQDGRGSKKVDCEYGG					
	10	20	30	40	50	60
	70	80	90			
m909.pep	ERHAVLPNQTGNNADEEHRQH <del>WQKPKFQNR</del> X					
	:		::	::	: :	
g909	ERRAVLRNQKRGKPTRRAATLGKPSFRARDGGGRVNR <del>AE</del> TGEGKRSAR					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2745>:

a909.seq

```

1 ATGCGTAAAA CCTTCCTTAT CCTGATGACT GCCGCCGCC TTTTGTGCGG
51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
101 AAAAATATCC CGCCGGCACG CCCGTTTATT ACCAAGACGG CAGCTACTCG
151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC
201 CAACCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
251 AGCCCAAATT TCAAACCGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2746; ORF 909.a>:

a909.pep

```

1 MRKTFILILMT AAALLSGCAW ETYQDGNgKT AVRQKYPAGT PVYYQDGSYS
51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

```

**m909/a909 96.7% identity in 90 aa overlap**

	10	20	30	40	50	60
m909.pep	MRKTFILFLTA <del>AAA</del> ALLSGCAWETYQDGNgKTAVRQKYPAGTPVYYQDGSYSKNMNYNQYRP					
	:	:	:	:	:	:
a909	MRKTFILILMTAAALLSGCAWETYQDGNgKTAVRQKYPAGTPVYYQDGSYSKNMNYNQYRP					
	10	20	30	40	50	60



1302

	70	80	90
m909.pep	ERHAVLPNQ	TGNNADEE	HRQHWQKPKFQNRX
a909	ERHAVLPNQ	TGNNADEE	HRQHWQKPKFQNRX
	70	80	90

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2747>:

```

g910.seq
1  ATGAAAAAAC TGTTATTGGC CGCCGTTGTT TCCCTAAATG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGAACAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACTACTGG GGCAAACCTG TTTTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2748; ORF 910.ng>:

```

g910.pep
1  MKKLLLAADV SLNAATAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDYW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2749>:

```

m910.seq
1  ATGAAAAAAC TGTTATTGGC TGCCGTTGTT TCTCTGAGTG CCGCTGCCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCT GTGAAAATGT TGGAGCAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACCATTGG GGTAAGCCTG TGCTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2750; ORF 910>:

```

m910.pep
1  MKKLLLAADV SLSAAAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 910 shows 96.8% identity over a 94 aa overlap with a predicted ORF (ORF 910.ng) from *N. gonorrhoeae*:

```

g910/m910
10      20      30      40      50      60
g910.pep MKKLLLAADVSLNAATAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDYW
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m910      MKKLLLAADVSLSAAAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDDHW
          10      20      30      40      50      60

70      80      90
g910.pep GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m910      GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
          70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2751>:

```

a910.seq
1  ATGAAAAAAC TGTTATTGGT CGCCGTTGTT TCCTTGAGTG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCTATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGAACAGCG CGGTTATCAG
151 GTTCACGATG TCGATGCCGA CGACCATTGG GGCAAACCTG TTTTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATTGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2752; ORF 910.a>:

```

a910.pep

```

1303

1 MKKLLLVAVV SLSAATAFAG DSAERQIYGD PYFEQNRTKA VKMLEQRGYQ  
 51 VHDVDADDDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR\*

m910/a910 95.7% identity in 94 aa overlap

	10	20	30	40	50	60
m910.pep	MKKLLLA	AVVSLS	AAAAFAG	DSAERQI	YGD	PHFEQNRTKAVKMLEQRGYQVYD
a910	MKKLLLV	AVVSLS	AATAFAG	DSAERQI	YGD	PYFEQNRTKAVKMLEQRGYQVHDVDADDDHW
	10	20	30	40	50	60

	70	80	90
m910.pep	GKPVLEVEAYK	DGREYDIVL	SYPDLKIIKEQLDRX
a910	GKPVLEVEAYK	DGREYDIVL	SYPDLKIIKEQLDRX
	70	80	90

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2753>:

g911.seq  
 1 ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCTTGATCGG  
 51 CGCGGCGGCG GTTGCCCTTC TCGCTTTCCG CGTGGCGGGC GGCGGCGCGT  
 101 TCGGCGGTTT GGACAAACT TACGCCGTTT ATGCCGATT CGGCGACATC  
 151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGGCG TATTGGTCGG  
 201 GCGCGTCGGC GCTATCGGGC TTGACCCGAA ATCCTATCAG GCGAGGGTGC  
 251 GCCTTGATTT GGACGGCAAG TATCAGTTCA GCAGTGACGT TTCCGCGCAA  
 301 ATCCTGACTT CGGGACTTTT GGGCGAACAG TACATCGGGC TGCAGCAGGG  
 351 CGGCGATACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAGTT  
 401 CTGCAATGGT TCTGGAAAAC CTGATCGGTA AATTCATGAC CAGCTTCGCC  
 451 GAGAAAAACG CTGAGGCGCG CAATGCGGAA AAAGCCGcag aAtaa

This corresponds to the amino acid sequence <SEQ ID 2754; ORF 911.ng>:

g911.pep  
 1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI  
 51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSAQ  
 101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA  
 151 EKNAEGGNAE KAAE\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2755>:

m911.seq  
 1 ATGAAGAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCCTGATTGG  
 51 CGCGGCGGCG GTTGCCCTTC TCGCTTTCCG CGTGGCGGGC GGTGCGGCGT  
 101 TCGGCGGTTT GGACAAACT TACGCCGTTT ATGCCGATT CGGCGACATC  
 151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGGCG TATTGGTCGG  
 201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC  
 251 GCCTCGATTT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA  
 301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG  
 351 CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAGTT  
 401 CTGCAATGGT TCTGGAAAAC CTTATCGGCA AATTCATGAC GAGTTTGGC  
 451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

This corresponds to the amino acid sequence <SEQ ID 2756; ORF 911>:

m911.pep  
 1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI  
 51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSAQ  
 101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA  
 151 EKNADGGNAE KAAE\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 911 shows 99.4% identity over a 164 aa overlap with a predicted ORF (ORF 911.ng) from *N. gonorrhoeae*:

g911/m911

10 20 30 40 50 60

1304

```

g911.pep  MKKNILEFWVGLFVLIGAAAVAFVLAFLRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          |||
m911      MKKNILEFWVGLFVLIGAAAVAFVLAFLRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          10      20      30      40      50      60

          70      80      90      100     110     120
g911.pep  SAGVLVGRVGAIGLDPKSYQARVRDLDDGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          |||
m911      SAGVLVGRVGAIGLDPKSYQARVRDLDDGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          70      80      90      100     110     120

          130     140     150     160
g911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAAX
          |||
m911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAAX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2757>:

```

a911.seq
1  ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGAAGTGTTCG TCCTGATTGG
51  CGCGGCGGCG GTTGCCCTTC TCGCTTTCCG CGTGGCCGGC GGTGCGGCGT
101 TCGGCGGTTC GGACAAACTT TACGCCGTTT ATGCCGATTG CGGCGACATC
151 GCGCGTTTGA AGGTCAATGC CCCCCTCAAA TCCGCAGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATTT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
351 CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCATG
401 CTGCAATGGT TCTGAAAAAC CTTATCGGCA AATTCATGAC GAGTTTGGC
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2758; ORF 911.a>:

```

a911.pep
1  MKKNILEFWV GLFVLIGAAA VAFVLAFLRVAG GAFFGGSDKT YAVYADFGDI
51  GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRDLDDGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

```

**m911/a911** 100.0% identity in 164 aa overlap

```

m911.pep  MKKNILEFWVGLFVLIGAAAVAFVLAFLRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          |||
a911      MKKNILEFWVGLFVLIGAAAVAFVLAFLRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          10      20      30      40      50      60

          70      80      90      100     110     120
m911.pep  SAGVLVGRVGAIGLDPKSYQARVRDLDDGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          |||
a911      SAGVLVGRVGAIGLDPKSYQARVRDLDDGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          70      80      90      100     110     120

          130     140     150     160
m911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAAX
          |||
a911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAAX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2759>:

```

g912.seq
1  gtgAAAAaat cctcctTcat cagcGCATTG GGCATCGgtA TTTTGAGCAT
51  CGGCATGGCA TTTGCCTCCC CGGCCGACGC AGTGGGACAA ATCCGCCAAA
101 ACGCCACACA GGTTTTGACC ATCCTCAAAA GCGGCGACGC GGCTTCTGCA

```

1305

```

151 CGCCCAAAAG CCGAAGCCTA TGCGGTCCCC TATTTTCGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG TACCGCGTCC GACGCGCAAA
251 AACAAAGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTCAA AAACGCGACC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAGGGCGGCA AGGAAATCGT CGTCCGTGCC GAAGTCGGCA
401 TCCCCGGTCA GAAGCCCGTC AATATGGAAT TTACCACCTA CCAAAGCGGC
451 GGCAAATACC GTACCTACAA CGTCGCCATC GAAGGCACGA GCCTGGTTAC
501 CGTGTACCGC AACCAATTCG GCGAAATCAT CAAAGCCAAA GGCATCGACG
551 GGCTGATTGC CGAGTTGAAA GCCAAAAACG GCGGCAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2760; ORF 912.ng>:

```

g912.pep
  1 VKKSSFISAL GIGILSIGMA FASPADAVGQ IRQNATQVLT ILKSGDAASA
 51 RPKAEAYAVP YFDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRTYTYS
101 GTMLKFKNAT VNVKDNPIVN KGGKEIVVRA EVGIPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGTSLVTVYR NQFGEI IKAK GIDGLIAELK AKNGGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2761>:

```

m912.seq
  1 ATGAAAAAAT CCTCCCTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT
 51 CCGCATGGCA TTTGCCGCC CTGCCGACGC GGTAAGCCAA ATCCGTCAAA
101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA ACGCGCATGC CAACACCGCT
151 CGCCAAAAAG CCGAAGCCTA TGCATTTCCC TATTTTCGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAAA
251 AACAAAGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTAAA AAACGCCAAC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAAGGCGGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG
401 TACCCGGGCA AAAACCCGTC AACATGGAAT TCACCACCTA CCAAAGCGGC
451 GGTAAATACC GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC
501 CGTGTACCGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GCGGTGGACG
551 GACTGATTGC CGAGTTGAAA GCCAAAAACG GCGGCAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2762; ORF 912>:

```

m912.pep
  1 MKKSSLISAL GIGILSIGMA FAAPADAVSQ IRQNATQVLS ILKNGDANTA
 51 RQKAEAYAIP YFDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRTYTYS
101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTVYR NQFGEI IKAK GVDGLIAELK AKNGGK*

```

Computer analysis of this amino acid sequence gave the following results:

#### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 912 shows 91.8% identity over a 196 aa overlap with a predicted ORF (ORF 912.ng) from *N. gonorrhoeae*:

```

g912/m912

      10      20      30      40      50      60
g912.pep VKKSSFISALGIGILSIGMAFASPADAVGQIRQNATQVLTILKSGDAASARPKAEAYAVP
          :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m912      MKKSSLISALGIGILSIGMAFAAPADAVSQIRQNATQVLSILKNGDANTARQKAEAYAIP
          10      20      30      40      50      60

      70      80      90      100     110     120
g912.pep YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKFKNATVNVKDNPIVN
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m912      YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKFKNATVNVKDNPIVN
          70      80      90      100     110     120

      130     140     150     160     170     180
g912.pep KGGKEIIVRAEVGIPGQKPVNMDFTTYQSGGKYRTYNVAIEGTSLVTVYRNQFGEI IKAK
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m912      KGGKEIIVRAEVGVPQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTVYRNQFGEI IKAK
          130     140     150     160     170     180

      190
g912.pep GIDGLIAELKAKNGGKX

```

1306

```

      |:|||||
m912  GVDGLIAELKAKNGGKX
      190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2763>:

```

a912.seq
1   ATGAAAAAAT CCTCCTTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT
51  CGGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAACCAA ATCCGTCAAA
101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA GCGGTGATGC CAACACCGCC
151 CGCCAAAAAG CCGAAGCCTA TGCGATTCCC TATTTTCGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGCGC CACCGCGTCC GACGCGCAAA
251 AACAAGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTAAA AAACGCCAAC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAAGGCGGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG
401 TACCCGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC
451 GGTAATACC GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC
501 CGTGTACCGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GGCGTGGACG
551 GACTGATTGC CGAGTTGAAG GCTAAAAACG GCAGCAAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2764; ORF 912.a>:

```

a912.pep
1   MKKSSFISAL GIGILSIGMA FAAPADAVNQ IRQNATQVLS ILKSGDANTA
51  RQKAEAYAIP YFDFQRM TAL AVGNPWRTAS DAQKQALAKE FOTLLIRTY S
101 GTMLKLK NAN VNVKDNPIVN KGGKEIIVRA EVGVPGQKPV NMDFTTYQS G
151 GKYRTYNVAI EGASLVTYR NQFGEI IKAK GVDGLIAELK AKNGSK*

```

m912/a912 98.0% identity in 196 aa overlap

```

      10      20      30      40      50      60
m912.pep MKKSSLISALGIGILSIGMAFAAPADAVSQIRQNATQVLSILKNGDANTARQKAEAYAIP
      |||||:|||||:|||||:|||||:|||||:|||||
a912      MKKSSFISALGIGILSIGMAFAAPADAVNQIRQNATQVLSILKSGDANTARQKAEAYAIP
      10      20      30      40      50      60

      70      80      90      100     110     120
m912.pep YFDFQRM TALAVGNPWRTASDAQKQALAKEFOTLLIRTYSGTMLKLKNANVNVKDNPIVN
      |||||:|||||:|||||:|||||:|||||:|||||
a912      YFDFQRM TALAVGNPWRTASDAQKQALAKEFOTLLIRTYSGTMLKLKNANVNVKDNPIVN
      70      80      90      100     110     120

      130     140     150     160     170     180
m912.pep KGGKEIIVRAEVLGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNQFGEI IKAK
      |||||:|||||:|||||:|||||:|||||:|||||
a912      KGGKEIIVRAEVLGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNQFGEI IKAK
      130     140     150     160     170     180

      190
m912.pep GVDGLIAELKAKNGGKX
      |||||:||||
a912      GVDGLIAELKAKNGSKX
      190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2765>:

```

g913.seq
1   atGAAAAAAA CCGCCTACGC CATCCTCCTG CTGATCGGGT TCGCTTCCGC
51  CCCTGCATTT GCAGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTC CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCCCT
151 GCGCGCGCGC GCTACCGCAA AGTTACGCCG AAACCCGTCC GCGCCGGCGT
201 GTCCAATTTT TTAAACAACC TGCGCGACGT GGTCAGTTTC GGCAGCAATA
251 TCTTGC GTT GGAcatCAAA cgcgcAAGcg aAGACCTcgT CCGcgtcggc
301 atCAATACCA CCTTCGGTTT GGgcgGGCTC ATTGATATTG CCGGcgcgGGg
351 cggcgttccc gacaataaaa AcacTttgGg cgacacgttt gcctcgtGGG
401 GctgGAAAaa cagcaATTAT TTCGTgttgc CCGtcttagg cccgtccacc

```

1307

```

451 gtccgcgacg cgctcggcac gggcattacc tCTGTTTATC CGCccaagaa
501 tatcgttttc catacccttg ccggacgctg GGgcacgact gCCGCTGCCG
551 CCGTcagtac gcgcgaaggg ctccctcgatt tgaccgacag Tctggacgaa
601 gccgccatCG ACAAATACAG CTACACGCGc gacctctata tgAAAGTCCG
651 CGcacgGCag AccgGTGCAA CACCTGCCGA AGgtacggaa gataacatcg
701 acatcgacat cgACGAATTG GTCGAAAGTG CCGAAACCGG CGCGGCAGAG
751 CCCGCCGTTC ACGAAGATTG CGTATCCGAA ACACAGGCAG AAGCAGCAGG
801 GGAAGCCGAA ACGCAACCTG GAACACAACC CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2766; ORF 913.ng>:

```

g913.pep
  1 MKKTAYAILL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
 51 AARGYRKVTP KPVRAVSNF FNNLRDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGVP DNKNLGDTF ASGWKNSNY FVLPVLGPST
151 VRDALGTGIT SVYPPKNIVF HTPAGRWTG AAAAVSTREG LLDLTDLSDE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDIDEL VESAETGAAE
251 PAVHEDSVSE TQAEAAGEAE TQPQTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2767>:

```

m913.seq
  1 ATGAAAAAAA CCGCCTATGC CTTCCTCCTG CTGATCGGGT TCGCTTCCGC
 51 CCCTGCATTT GCCGAAACCC GCGCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTT CAAATTCAAC GACCAAGCCG ACCGTACAT TTTCGCCCCT
151 GCCGCGCGCG GCTACCGCAA AGTTGCGCCG AAACCCGTCC GCGCCGGCGT
201 TGCCAATTTT TTTAACAACC TGTGCGACGT GGTGAGCTTC GGCAGCAATA
251 TCTTGCGCTT GGACATCAAA CGCGCAAGCG AAGACCTTGT CCGCGTCGGC
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
351 CGGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCCTCGTGGG
401 GATGGAAGAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCTGCTTC CGCACCCCTG TCGGACGCTG GGGCAGGACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTgCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TCGCGGCGAG ACCGGTGCAA CACCTGCCGA AGgtACGGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2768; ORF 913>:

```

m913.pep
  1 MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
 51 AARGYRKVAP KPVRAVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNLGDTF ASGWKNSNY FVLPVLGPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWTG AVSAVSTREG LLDLTDLSDE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 913 shows 94.9% identity over a 277 aa overlap with a predicted ORF (ORF 913.ng) from *N. gonorrhoeae*:

```

g913/m913
      10      20      30      40      50      60
g913.pep  MKKTAYAILLLIGFASAPAF AETRPADPYE GYNRAVSKFNDQADRYIFAPAARGYRKVTP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
m913      MKKTAYAFLLLLIGFASAPAF AETRPADPYE GYNRAVSKFNDQADRYIFAPAARGYRKVAP
          10      20      30      40      50      60

      70      80      90     100     110     120
g913.pep  KPVRAVSNFFNNLRDVVSF GSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGVP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
m913      KPVRAVSNFFNNLCDVVSF GSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP
          70      80      90     100     110     120

```

1308

	130	140	150	160	170	180
g913.pep	DNKNTLGDTFASWGWKNSNYFVLPVLGPSTVRDALGTGITSVYPPKNIVFHTPAGRWGTT					
m913	DNKNTLGDTFASWGWKNSNYFVLPVLGPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					
	130	140	150	160	170	180
	190	200	210	220	230	240
g913.pep	AAAAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDIDEL					
m913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDI--DEL					
	190	200	210	220	230	
	250	260	270			
g913.pep	VESAETGAAEPAVHEDSVSETQAEAAGEAETQPGTQPX					
m913	VESAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
	240	250	260	270		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2769>:

a913.seq

1	ATGAAAAAA	CCGCCTATGC	CTTCCTCCTG	CTGATCGGGT	TCGCTTCCGC
51	CCCTGCATTT	GCCGAAACCC	GCCCCGCCGA	CCCTTATGAA	GGCTACAACC
101	GCGCCGTTT	CAAATTCAAC	GACCAAGCCG	ACCGCTACAT	TTTCGCCCCCT
151	GCCGCGCGCG	GCTACCGCAA	AGTTGCGCCG	AAACCCGTCC	GCGCCGGCGT
201	GTCCAATTT	TTTAACAACC	TGTGCGACGT	GGTCAGCTTC	GGCAGCAATA
251	TCTTGCGCTT	AGACATCAA	CGCGCAAGCG	AAGACCTTGT	CCGCGTCGGT
301	ATCAACACCA	CTTTCGGTTT	GGGCGGGCTT	ATCGACATCG	CCGGCGCGGG
351	CGGCATTCCC	GACAATAAAA	ACACCTTGGG	CGACACGTTT	GCTTCGTGGG
401	GATGGAAAA	CAGCAATTAT	TTCGTGTTC	CCGTCTTAGG	GCCGTCCACC
451	GTCCGCGACG	CGCTCGGCAC	GGGTATTACC	TCCGTTTATT	CGCCCAAGAA
501	TATCGTCTTC	CGCACCCCTG	TCGGACGCTG	GGGCACGACT	GCCGTATCCG
551	CCGTCACTAC	GCGCGAAGGC	CTGCTCGATT	TGACCGACAG	TCTGGACGAA
601	GCCGCCATCG	ACAAATACAG	CTACACGCGC	GACCTCTATA	TGAAAGTCCG
651	TGCGCGGCAG	ACCGGTGCAA	CACCTGCCGA	AGGTACGGAA	GATAACATCG
701	ACATCGACGA	ATTGGTCGAA	AGTGCCGAAA	CCGGCGCGGC	GGAAACTGCC
751	GTTCAAGAAG	ATTCCGTATC	CGAAACACAG	GCAGAAGCAG	CAGGGGAAGC
801	CGAAACGCAA	CCTGGAACAC	AACCTGGAAC	ACAACCTTAA	

This corresponds to the amino acid sequence <SEQ ID 2770; ORF 913.a>:

a913.pep

1	MKKTAYAFLL	LIGFASAPAF	AETRPADPYE	GYNRAVFKFN	DQADRYIFAP
51	AARGYRKVAP	KPVVAGVSNF	FNNLCDVVSF	GSNILRLDIK	RASEDLVRVG
101	INTTFGLGGL	IDIAGAGGIP	DNKNTLGDTF	ASWGWKNSNY	FVLPVLGPST
151	VRDALGTGIT	SVYSPKNIVF	RTPVGRWGTT	AVSAVSTREG	LLDLTDSLDE
201	AAIDKYSYTR	DLYMKVRARQ	TGATPAEGTE	DNIDIDELVE	SAETGAETA
251	VQEDSVSETQ	AEAAGEAETQ	PGTQPGTQP*		

m913/a913 100.0% identity in 275 aa overlap

	10	20	30	40	50	60
m913.pep	MKKTAYAFLLLLIGFASAPAF AETRPADPYEGYNRAVFKFNDQADRYIFAPAARGYRKVAP					
a913	MKKTAYAFLLLLIGFASAPAF AETRPADPYEGYNRAVFKFNDQADRYIFAPAARGYRKVAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m913.pep	KPVVAGVSNFFNNLCDVVSF GSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP					
a913	KPVVAGVSNFFNNLCDVVSF GSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m913.pep	DNKNTLGDTFASWGWKNSNYFVLPVLGPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					
a913	DNKNTLGDTFASWGWKNSNYFVLPVLGPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					

1309

	130	140	150	160	170	180
	190	200	210	220	230	240
m913.pep	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
a913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
	190	200	210	220	230	240
	250	260	270			
m913.pep	SAETGAAETAVQEDSVSETQAEAAAGEAETQPGTQPX					
a913	SAETGAAETAVQEDSVSETQAEAAAGEAETQPGTQPX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2771>:

g914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTGTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCGC CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GacggtttGag gCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTGTTGCGG AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGACGCG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTCTCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAGTGTC AGTCGTGTTT TGCCGATTCTG
451 taggctTCGA CGATTTTTTG CACCAGAGGA TGCCGGACAA CGTCTTCGCC
501 GGTGAAGGTA TGGAAATACA GTCCTGCCAC GCCGTGCAGT TTCTCACGTG
551 CGTCTTTCAA TCCCGATTG ATGTTTTTGG GCAGGTcgaT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCgcccgaag ccGATGCGGG TCAGGAACAT
651 TTTCATTTGT TCGGGCGTGg tgTtttGcgC TTCGTCGAGG ATGATGTATG
701 CGCCGTTGag cgTCCTGCCG CGCATATAG

```

This corresponds to the amino acid sequence <SEQ ID 2772; ORF 914.ng>:

g914.pep

```

1  MKKCILGILT ACAAMPADF RISDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCGDEA
101 IRCRKFD*CI GWTDKETDTE LGFRLCFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTRG CRTTSSPVKV WKYSPATPCS FSRASFNPDL MFLGRSIWLV
201 SPVMTAFAPK PMRVRNIFIC SGVVFCASSR MMYAPLSVLP RI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2773>:

m914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTGTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCGC CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGTG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTGTTGCGA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGACGCG ATAAAGAAAC
351 GGATACGGAT ACGGAGCTTG GCTTCCGTAT CTGTTTTTCT CTGCCTGATT
401 TTCCATGCAT CGGGTTTTCAG ACGGCATTGG AATGTCAGTC GTGTTCTGCC
451 GATTCGTAGG CTTTCGACGAT TTTTTCGACC AAAGGATGCC GGACAACGTC
501 TTCGCCGGTA AAGGTGTGGA AATACAGCCC TTCCACGTTG TGCAGTTTCT
551 CACGCGCATC TTTTAATCCC GATTTGATGT TTTTGGGCAG GTCGATTGCG
601 CTGTTGTGCG CGGTAATGAC GGCTTTCGCG CCGAAGCCGA TCGGGTTCAG
651 GAACATTTTC ATTTGTTTCGG GCGTGGTGTT TTGCGCTTCG TCGAGGATGA
701 TGTATGCGCC GTTGAGCGTC CTGCCGCGCA TATAG

```

This corresponds to the amino acid sequence <SEQ ID 2774; ORF 914>:

m914.pep

```

1  MKKCILGILT ACAAMPADF RIGDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEA
101 IRCRKFDXCI GWTDKETDTE TELGFRICFS LPDFPCIGFQ TALECQSCSA

```



1310

151 DSXASTIFCT KGCRTTSSPV KVKYSPSTL CSFSRASFPN DLMFLGRSIW  
 201 LVSPVMTAFA PKPMVRNIF ICSGVVFCAS SRMMYAPLSV LPRI\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 914 shows 96.7% identity over a 244 aa overlap with a predicted ORF (ORF 914.ng) from *N. gonorrhoeae*:

g914/m914

	10	20	30	40	50	60
g914 . pep	MKKCILGILTACAAMP	AFADRISDL	EARLAQLEHR	VAVLESGGNT	TVKIDLF	SGSNSTMYVC
	:					
m914	MKKCILGILTACAAMP	AFADRIGDLE	ARLAQLEHR	VAVLESGGNT	TVKIDLF	SGSNSTMYVC
	10	20	30	40	50	60
g914 . pep	SVTPFQKTFEASDR	NEGVARQKVR	QACNRETSAM	FCGDEAIR	CRKFDXCIG	WTDKETDT-
m914	SVTPFQKTFEASDR	NEGVARQKVR	QACNRETSAM	FCDEAIR	CRKFDXCIG	WTDKETDTD
	70	80	90	100	110	119
g914 . pep	-ELGFRLCFS	LPDFPCIG	FQTALE	CQSCSADS	XASTIFCT	RGCRRTTSSPVKVKYSPATP
	:					
m914	TELGFRICF	SLPDPFPC	IGFQTALE	CQSCSADS	XASTIFCT	KGCRTTSSPVKVKYSPSTL
	130	140	150	160	170	180
g914 . pep	CSFSRASFPN	DLMFLGRSI	WLVSPVMT	AFAFKPMR	VRNIFIC	SGVVFCASSRMMYAPLSV
m914	CSFSRASFPN	DLMFLGRSI	WLVSPVMT	AFAFKPMR	VRNIFIC	SGVVFCASSRMMYAPLSV
	190	200	210	220	230	240
g914 . pep	LPRI	X				
m914	LPRI	X				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2775>:

a914 . seq

1	ATGAAAAAAT	GTATTTTGGG	CATTTTGACC	GCGTGTGCCG	CCATGCCTGC
51	ATTTGCCGAC	AGAATCGGCG	ATTTGGAAGC	ACGTCTGGCG	CAGTTGGAAC
101	ACCGTGTCGC	CGTATTGGAA	AGCGGCAGCA	ATACCGTCAA	AATCGACCTT
151	TTCGGTTCAA	ATTCCACCAT	GTATGTATGC	AGCGTTACGC	CTTTTCAGAA
201	GACGTTTGAG	GCAAGCGATC	GGAATGAAGG	CGTGGCGCGG	CAGAAAGTGC
251	GTCAGGCGTG	CAACCGCGAA	ACTTCGGCAA	TGTTTTGCGA	AGATGAGGCA
301	ATCCGATGCA	GAAAATTCGA	TTGATGTATC	GGTTGGACGG	ATAAAGAAAC
351	GGATACGGAG	CTTGGCTTCC	GTATCTGTTT	TTCTCTGCCC	GATTTTCCAT
401	GCATCGGGTT	TCAGACGGCA	TTGGAATGTC	AGTCGTGTTC	TGCCGATTCG
451	TAGGCTTCGA	CGATTTTTTG	CACCAAAGGA	TGCCGGACAA	CGTCTTCGCC
501	GGTAAAGGTG	TGGAAATACA	GCCCTTCCAC	GCCGTGCAGT	TTCTCACGCG
551	CATCTTTTAA	TCCCGATTG	ATGTTTTTGG	GCAGGTCGAT	TTGGCTGGTG
601	TCGCGGTAA	TGACGGCTTT	CGCGCCGAAG	CCGATCGGGG	TCAGGAACAT
651	TTTCATTTGT	TCGGGCGTGG	TGTTTTGCGC	TTCGTCGAGG	ATGATGTATG
701	CGCCGTTGAG	CGTCTGCCG	CGCATATAG		

This corresponds to the amino acid sequence <SEQ ID 2776; ORF 914.a>:

a914 . pep

1	MKKCILGILT	ACAAMP	AFAD	RIGDLE	ARLA	QLEHR	VAVLE	SGSNT	TVKIDL
51	FGSNSTMYVC	SVTPFQKT	FE	ASDR	NEGVAR	QKVR	QACNRE	TSAM	FCDEA
101	IRCRKFD*CI	WTDKETDTE	LGFRICF	SLP	DFPCIG	FQTA	LECQ	SCSADS	
151	*ASTIFCTKG	CRTTSSPVKV	WKYSPSTPCS	FSRASFPN	DL	MFLGR	SIWLV		
201	SPVMTAFAPK	PMVRNIFIC	SGVVFCASSR	MMYAPLSVLP	RI*				

1311

m914/a914 98.4% identity in 244 aa overlap

	10	20	30	40	50	60
m914.pep	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC					
a914	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLESGSNTVKIDLFGSNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD					
a914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD--					
	70	80	90	100	110	
	130	140	150	160	170	180
m914.pep	TELGFRICFSLPDFPCIGFQTALECCSCSADXSASTIFCTKGCRTTSSPVKWKYSPSTL					
a914	TELGFRICFSLPDFPCIGFQTALECCSCSADXSASTIFCTKGCRTTSSPVKWKYSPSTP					
	120	130	140	150	160	170
	190	200	210	220	230	240
m914.pep	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
a914	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
	180	190	200	210	220	230
m914.pep	LPRIX					
a914	LPRIX					
	240					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2777>:

g915.seq

1	ATGAAGAAAA	CCCTGTTGGc	AATTGTTGCC	gtTTTCGCCT	TAAGTGCCTG
51	CCGGCaggcg	gaAGaggcac	cgccgCCTTT	ACCCCGGCAG	AtTAGCGacc
101	gttcggtcgg	aCACTAttgC	Agtatgaacc	tgaccgaaca	caacggcccc
151	aaagcccaga	tttttttgaa	cGGCAAACCC	GATCAGCCCG	TTTGGTTCTC
201	CACCGTcaag	cagatgttcg	GCTATACCAA	GCTGCCCGAA	GAGCCCAAAG
251	GCATCCGCGT	GATTTACGTT	ACCGATATGG	GCAATGTTAC	CGATTGGACG
301	AATCCTAATG	CCGACACGGA	GTGGATAGAT	GCGAAAAAAG	CCTTTTACGT
351	CATCGACAGC	GGCTTTATCG	GCGGTATGGG	CGCGGAAGAC	GCGCTGCCGT
401	TCGGCAACAA	GGAGCAGGCT	GAAAAATTTG	CAAAGGATAA	AGGCGGCAAG
451	GTCGTCGGTT	TTGACGATAT	GCCCGATGCT	TACATTTTCA	AGTAA

This corresponds to the amino acid sequence &lt;SEQ ID 2778; ORF 915.ng&gt;:

g915.pep

1	MKKTLLAIVA	VFALSACRQA	EEAPPPLPRQ	ISDRSVGHYC	SMNLTEHNGP
51	KAQIFLNGKP	DQPVWFSTVK	QMFGYTKLPE	EPKGIRVIYV	TDMGNVTDWT
101	NPNADTEWID	AKKAFYVIDS	GFIGGMGAED	ALPFGNKEQA	EKFADKGGK
151	VVGFDMPDA	YIFK*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2779>:

m915.seq

1	ATGAAAAAAA	CCCTGTTGGC	AATTGTTGCC	GTTTCCGCCT	TAAGTGC.tG
51	CCGGCAGGCG	GAAGAGGGAC	CGCCGCCTTT	ACCcCGGCAG	ATTAGCGACC
101	GTTCCGTCGG	ACACTATTGC	AGTATGAACC	TGACCGAACA	CAACGGCCCC
151	AAAGCCCAGA	TTTTCTTGAA	CGGCAAACCC	GATCAGCCCG	TtTGTTCTC
201	CACCATCAAG	CAGATGTTTCG	GCTATACCAA	GCTGCCCGAA	GAGCCTAAAG
251	GCATCCGCGT	GATTTACGTT	ACCGATATGG	GCAATGTTAC	CGATTGGACG
301	AATCCCAATG	CCGACACGGA	GTGGATGGAT	GCGAAAAAAG	CCTTTTACGT
351	CATCGACAGC	GGCTTTATCG	GCGGTATGGG	TGCGGAAGAC	GCGCTGCCGT
401	TCGGCAACAA	AGAGCAGGCT	GAGAAATTTG	CAAAGGATAA	AGGCGGTAAG

1312

451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence &lt;SEQ ID 2780; ORF 915&gt;:

```

m915.pep
  1 MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMGAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 915 shows 97.0% identity over a 164 aa overlap with a predicted ORF (ORF 915.ng) from *N. gonorrhoeae*:

```

m915/g915
      10      20      30      40      50      60
m915.pep MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g915      MKKTLLAIVAVFALSACRQAEEAPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          10      20      30      40      50      60

      70      80      90      100     110     120
m915.pep DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g915      DQPVWFSTIVKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWIDAKKAFYVIDS
          70      80      90      100     110     120

      130     140     150     160
m915.pep GFIGGMGAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDTYIFKX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g915      GFIGGMGAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDAYIFKX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2781>:

```

a915.seq
  1 ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
 51 CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTTC GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2782; ORF 915.a&gt;:

```

a915.pep
  1 MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMGAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*

```

m915/a915 99.4% identity in 164 aa overlap

```

      10      20      30      40      50      60
m915.pep MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a915      MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          10      20      30      40      50      60

      70      80      90      100     110     120
m915.pep DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a915      DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS

```

1313

	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
a915	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2783>:

g917.seq

```

1  ATGGTCAAac atctgccacT cgcCGTCctg actgctTtgc tgcttgCagc
51  gtgcGGCGGT Tcggacaaac cgcctgccga Aaaaccggca ccggcgGaAA
101 accaaAacgt atTgaAAATT TataACTGGT CGGAATACGT CGATCCGGAA
151 ACCGTGCGCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGT GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAATCCG
251 GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAAT CGATAAGTCG ATGATTCCCA ATTATAAACA
351 TCTCAACCCCT GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGACCACG
401 AATACGCCGT GCCGTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACAGTG
501 GGATTGGTG TTCAACCCCG AATACACGTT CAAACTCAA CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATTT ATCCCATGGT GTTGAACTAT
601 TTGGGCAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTGCTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
751 GCGGAGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAAATC CGCGTGATGA TGCCGAAAGA GGGCGTGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA TCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 cgttacCTAC GCGCCTTCGA GCAAGCCGGC GCGGATTG ATGGAGGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCGA GCGGGGAAGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCTTAT CCGGCCGCG GCATTGAAGT TTATGGTGCG
1101 CCACTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2784; ORF 917.ng>:

g917.pep

```

1  MVKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51  TVADFEKKNQ IKVTYDVYDS DETLESKVLV GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS MIPNYKHLNP EMMRLMDGVD PDHEYAVPFY WGTNTFAINT
151 ERVKALGTD KLPDNQWDLV FNPEYTFKLK QCGISYLDLSA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDLNIAKRR AEEAGGKEKI RVMPKKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVY APSSKPARDL MEDEFKNDNT IFPSGEDLKN
351 SFIMVPIRPA ALKFMVRQWQ DVKAGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2785>:

m917.seq

```

1  ATGACCAAAC ATCTGCCCCT GGCCGTCCTG ACTGCTTTGC TGCTTGACG
51  GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCA CCGGCGGAAA
101 ACCAAACGT ATTGAAAATT TACAACTGGT CGGAATATGT CGATCCGGAA
151 ACCGTGCGCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACA GGCAAGTCCG
251 GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGCCACG
401 AATACGCCGT GCCGTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACAGTG
501 GGATTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACTAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC

```

1314

```

751  GCGGCGGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801  GGAAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
851  ATTCTTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901  TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951  CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
1051 AGCTTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2786; ORF 917>:

m917.pep

```

1  MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51  TVADFEKKNG IKVTYDVYDS DETLESKVLT GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FDPEYTSKLG QCGISYLD SA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGD LNI AKRR AEEAGGKEKI RVMPK EGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 917 shows 97.6% identity over a 376 aa overlap with a predicted ORF (ORF 917.ng) from *N. gonorrhoeae*:

m917/g917

m917.pep	10	20	30	40	50	60
	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKKNG					
g917	MVKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKKNG					
	10	20	30	40	50	60
m917.pep	70	80	90	100	110	120
	IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
g917	IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNFVGRQIKAGAYQKIDKSMIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	130	140	150	160	170	180
	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG					
g917	EMMRLMDGVDPDHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFNPEYTFKLG					
	130	140	150	160	170	180
m917.pep	190	200	210	220	230	240
	QCGISYLD SAAEIYPMVLN YLGKNPNSSNT EDIREATALL KKNRPNIKRFTSSGFIDDLA					
g917	QCGISYLD SAAEIYPMVLN YLGKNPNSSNT EDIREATALL KKNRPNIKRFTSSGFIDDLA					
	190	200	210	220	230	240
m917.pep	250	260	270	280	290	300
	RGDTCVTIGFGGDLNIAKRR AEEAGGKEKIRVMMPKEGVGIWVDSFVIPKDAKNVANAHK					
g917	RGDTCVTIGFGGDLNIAKRR AEEAGGKEKIRVMMPKEGVGIWVDSFVIPKDAKNVANAHK					
	250	260	270	280	290	300
m917.pep	310	320	330	340	350	360
	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA					
g917	YINDFLDPEVSAKNGNFVTYAPSSKPARDLMEDEFKNDNTIFPSGEDLKNSFIMVPIRPA					
	310	320	330	340	350	360

1315

```

m917.pep      ALKFMVRQWQDVKAGKX
               |||||
g917          ALKFMVRQWQDVKAGKX
               370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2787>:

```

a917.seq
1   ATGACCAAAC ATCTGCCCCCT GGCCGTCTCTG ACTGCTTTGC TGCTTGCAGC
51  GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCG CCGGCGGAAA
101 ACCGAAACGT ATTGAAAATT TACAACTGGT CGGAATACGT CGATCCGGA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAACTGT
251 GTTACGACAT TGTCCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGCCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGTACGGAC AAGTGCCGG ACAACCAAGT
501 GGATTTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAATAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTTGGCG CGCGCGGATA CCTGCGTAAC AATCGGTTTC
751 GGCGGCGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATCTTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CAGTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2788; ORF 917.a>:

```

a917.pep
1   MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENRNVLKI YNWSEYVDPE
51  TVADFEKKNG IKVTYDVYDS DETLESKVLT GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FDPEYTSKLG QCGISYLDSA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDNLIAKRR AEEAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

```

m917/a917 99.7% identity in 376 aa overlap

```

               10      20      30      40      50      60
m917.pep      MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKKNG
               |||||
a917          MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENRNVLKIYNWSEYVDPETVADFEKKNG
               10      20      30      40      50      60

               70      80      90      100     110     120
m917.pep      IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP
               |||||
a917          IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP
               70      80      90      100     110     120

               130     140     150     160     170     180
m917.pep      EMMRLMDGVDPGHEYAVPFYWGTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG
               |||||
a917          EMMRLMDGVDPGHEYAVPFYWGTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG
               130     140     150     160     170     180

               190     200     210     220     230     240
m917.pep      QCGISYLDSSAEIYPMVLNLYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA
               |||||

```

1316

```

a917      QCGISYLDAAEIYPMVLNLYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA
           190      200      210      220      230      240

           250      260      270      280      290      300
m917.pep  RGDTCVTIGFGGDLNIAKRRAEAEAGGKEKIRVMMMPKEGVGIWVDSFVIPKDAKNVANAHK
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a917      RGDTCVTIGFGGDLNIAKRRAEAEAGGKEKIRVMMMPKEGVGIWVDSFVIPKDAKNVANAHK
           250      260      270      280      290      300

           310      320      330      340      350      360
m917.pep  YINDFLDPEVSAKNGNFVITYAPSSKPAELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a917      YINDFLDPEVSAKNGNFVITYAPSSKPAELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           310      320      330      340      350      360

           370
m917.pep  ALKFMVRQWQDVKAGKX
           ||||||||||||||
a917      ALKFMVRQWQDVKAGKX
           370

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2789>:

g919.seq

```

1  ATGAAAAAAC ACCTGCTCCG CTCCGCCCTG TACGGcatCG CCGCCgccAT
51  CctcgCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCCG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGCGCG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATT TGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCCTGCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTACGCG cgtGGCaggt tgcaggcaAC GGAAGcCTTG
401 Caggtacggt TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCG CTGCCTGCCG GTTTGCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGac ggGGA AAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACCGCCG ACCTCTCCCG ATTCCCATC ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCgcgcTT GACGGCAAag cccCCATCCT CggttacgcC
751 GAagaccCcG tcgaacttTT TTTCATGCAC AtccaaggCT CGGGCCGCCT
801 GAAAAACCCg tcgggcaaat acatCCGCAt cggaTacgcc gacAAAAACG
851 AACAtccgTa tgtttccatc ggACGctata TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcac aaagcCTATA TCGGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCGGTCGG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GCGCAGGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2790; ORF 919.ng>:

g919.pep

```

1  MKKHLRLSAL YGIAAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
51  GTTVAGGGAV YTVVPHLSMP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTERARFPPIY GIPDDFISVP LPAGLRGGKN LVRIRQTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIKGR FEGRSRLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELPFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAYS GNEGFPVGALG
351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

This corresponds to the amino acid sequence <SEQ ID 2792; ORF 919>:

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N.gonorrhoeae*  
ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF  
919.ng) from *N. gonorrhoeae*:  
**m919/g919**

	10	20	30	40	50	60
m919.pep	MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV					
	:   :   :					
g919	MKKHLLRSALYGIAAAILAACQSRSIQTFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m919.pep	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWDVCAQAFQTPVHSFQAKQFFER					
	:					
g919	YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWDVCAQAFQTPVHSFQAKRFFER					
	70	80	90	100	110	120



1318

	130	140	150	160	170	180
m919.pep	YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA					
g919	YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGIPDDFISVPLPAGLRGGKN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m919.pep	LVRI RQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
g919	LVRI RQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m919.pep	DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL					
g919	DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m919.pep	KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA					
g919	KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSGNEGPVGALGTPLMGEYAGA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m919.pep	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVVDYFWGYGDEAGELAGK					
g919	IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVVDYFWGYGDEAGELAGK					
	370	380	390	400	410	420
	430	440				
m919.pep	QKTTGYVWQLLPNGMKPEYRPX					
g919	QKTTGYVWQLLPNGMKPEYRPX					
	430	440				

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2793>:

```

a919.seq
1  ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TGCGGCATCG CCGCCGCCAT
51  CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCCG TCGGCATCCC CGACCCCGCC
151 GGAACGACGG TCGGCGGCGG CGGGGCCGTT TATACCGTTG TGCCGCACCT
201 GTCCCTGCCC CACTGGGCGG CGCAGGATT CGCCAAAAGC CTGCAATCCT
251 TCCGCCCTCG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCCTCCAT TCCGTTTCAG CAAAACAGTT
351 TTTTGAACGC TATTTACGCG CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCCGATTTC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCCG ACCTCTCCCA ATTCCCATC ACTGCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCGATACT CGGTTACGCC
751 GAAGACCCCG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCGAAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCGG CGCACTGGGC
1051 ACGCCGCTGA TGGGCGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG

```

1319

```

1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GGCGACGAAG CCGGCGAACT
1251 TGCCCGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCCCAACG
1301 GTATGAAGCC CGAATACCGC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2794; ORF 919.a>:

a919.pep

```

      1 MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
    51 GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
   101 CAQAFQTPVH SVQAKQFFER YFTPQVAGN GSLAGTVTGY YEPVLKGDDR
   151 RTAQAQRFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
   201 HTADLSQFPI TARTTAIKGR FEGRSFLPYH TRNQINGGAL DGKAPILGYA
   251 EDPVELFFMH IQGSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
   301 KLGQTSMQGI KAYMQQNPQR LAEVLGQNPS YIFFRELTS SNDGPVGALG
   351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
   401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

m919/a919 98.6% identity in 441 aa overlap
      10      20      30      40      50      60
m919.pep MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
      10      20      30      40      50      60

      70      80      90     100     110     120
m919.pep YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER
      70      80      90     100     110     120

      130     140     150     160     170     180
m919.pep YFTPQVAGNGSLAGTVTGYIEPVLKGDDRRRTAQAQRFPIYGIPDDFISVPLPAGLRSGKA
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      YFTPQVAGNGSLAGTVTGYIEPVLKGDDRRRTAQAQRFPIYGIPDDFISVPLPAGLRSGKA
      130     140     150     160     170     180

      190     200     210     220     230     240
m919.pep LVRIRQTGKNSGTIDNTGGTHTADLSRFITARTTAIKGRFEGRSFLPYHTRNQINGGAL
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      LVRIRQTGKNSGTIDNTGGTHTADLSQFPIARTTAIKGRFEGRSFLPYHTRNQINGGAL
      190     200     210     220     230     240

      250     260     270     280     290     300
m919.pep DGKAPILGYAEDPVELFFMHIIQGSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      DGKAPILGYAEDPVELFFMHIIQGSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
      250     260     270     280     290     300

      310     320     330     340     350     360
m919.pep KLGQTSMQGIKAYMQQNPQR LAEVLGQNPSYIFFRELTS SNDGPVGALGTPLMGEYAGA
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      KLGQTSMQGIKAYMQQNPQR LAEVLGQNPSYIFFRELTS SNDGPVGALGTPLMGEYAGA
      310     320     330     340     350     360

      370     380     390     400     410     420
m919.pep VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
      370     380     390     400     410     420

      430     440
m919.pep QKTTGYVWQLLPNGMKPEYRPX
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      QKTTGYVWQLLPNGMKPEYRPX
      430     440

```

Expression of ORF 919

The primer described in Example 1 for ORF 919 was used to locate and clone ORF 919. This sequence was purified and expressed in *E. coli* as provided in Figure 1 #. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 919 is provided in Figure 5 #. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 is provided in Exhibit C #.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2795>:

```
g920.seq (partial)
1  ..ccgatgcagc tggttaccga aaaAGGTAAG GAAAACATGA TTCAACGCGG
51  CACATACAAC TACCAATACC GCAGCAACCG TCCCGTCAAA GACGGCAGCT
101 ACCTCGTTAC CGCCGAATAT CAGCCTACTT TCCGGTCAAA AAACAAAGCA
151 GGCTGGAAAC AGGCTGGCAT CAAAGAAATG CCTGACGCAA GCTATTGCGA
201 ACAAACCCGT ATGTTTCGGTA AAAACATTGT CAACGTGGGA CACGAAAGCG
251 CGGACACCGC CATCATCACC AAACCGGTCG GACAAAACCT GGAAATCGTC
301 CCGCTGGACA ATCccgccga caTTCACgtg ggctaacgCt tcaaaGTccg
351 cgTtCtggttc cgtGGCgaac cgCTGcccaa tgccACCgtt accgCtacAT
401 TTGacggctt cGAcaccagc gaccgcagca aaacgcacaa Aaccgaagcc
451 caagcctTCT ccgacaccac cgacggcgaa ggcgaagtgg acatcatCCC
501 CTTGcgccaa GGCTTttgga aAgcGAGTGT CGAATAcaaa gccgAtttec
551 CCGATcaaAG CCTGTGccga AAACAggcgA ACTACaCaac TTtaaccttc
601 caaatcgccc attctCacca tTAa
```

This corresponds to the amino acid sequence <SEQ ID 2796; ORF 920.ng>:

```
g920.pep (partial)
1  ..PMQLVTEKGK ENMIQRGTYN YQYRSNRPVK DGSYLVTAey QPTFRSKNKA
51  GWKQAGIKEM PDASYCEQTR MFGKNIVNVG HESADTAII T KPVGQNLEIV
101 PLDNPADIHV GXRFKVRVLF RGEPLPNATV TATFDGFDTS DRSKTHKTEA
151 QAFSDTTDGE GEVDIIPLRQ GFWKASVEYK ADFPDQSLCR KQANYTTTLTF
201 QIAHSHH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2797>:

```
m920.seq
1  ATGAAGAAAA CATTGACACT GCTCTCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCCACGCC CACCGmGTCT GGGTCGAAAC CGCCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
251 ACCGAAGCAA CCGTCCCCTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAwACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAArCCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCCTG TTCCGTGGCG
551 AACCCTGACC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAwmCCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CmCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCAAATCG GTCATTGCGA
801 CCATTAA
```

This corresponds to the amino acid sequence <SEQ ID 2798; ORF 920>:

```
m920.pep
1  MKKTLTLLSV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKXK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
```

1321

201 SDRSKTHXXE AQAFSDSTDD KGEVDIIXLR QGFWKANVEH KTDFPDQSVK  
 251 QKQANYSTLT FQIGHSHH\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 920 shows 91.3% identity over a 207 aa overlap with a predicted ORF (ORF 920.ng) from *N. gonorrhoeae*:

g920/m920

				10	20	30
g920.pep				PMQLVTEKGKENMIQRGT	NYQYRSNRPVK	
m920	GGEY	LKAD	LGYG	FPELE	PIAK	DRLHIFSKPMQLVTEKGKENMIQRGT
	40	50	60	70	80	90
g920.pep						
m920	DGSYL	VTA	EYQPT	FRSK	KNKAG	WKQAGIKEMPDASYCEQTRMFGKNIVNVGHESADTAIIT
	100	110	120	130	140	150
g920.pep						
m920	KPVG	QNL	EIVPL	DNPA	DIHV	GXRFKVRVLF
	160	170	180	190	200	210
g920.pep						
m920	QAFSD	TTD	GEGE	VDI	IPLR	QGFWKASVEYKADFPDQSLCRKQANYTTTLFQIAHSHHX
	220	230	240	250	260	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2799>:

a920.seq

1	TGAAAGAAAA	CATTGACACT	GCTCGCCGTT	TCCGCCCTAT	TTGCCGCATC
51	CGCCACAGCC	CACCGCGTCT	GGGTCGAAAC	CGCCACACG	CACGGCGGCG
101	AATACCTTAA	AGCCGACTTG	GGCTACGGCG	AATTTCCCGA	ACTCGAACCC
151	ATCGCCAAAG	ACCGCCTGCA	CATCTTCAGC	AAACCGATGC	AGCTGGTTAC
201	CGAAAAAGGC	AAGGAAAACA	TGATTCAACG	CGGCACATAC	AACTACCAGT
251	ACCGAAGCAA	CCGTCCCGTT	AAGGACGGCA	GTTACCTCGT	CATCGCCGAA
301	TATCAGCCTA	CTTCTGGTTC	AAAAACAAA	GCAGGCTGGA	AACAGGCGGG
351	CATCAAACAA	ATGCCTGACG	CAAGCTATTG	CGAACAAACC	CGAATGTTCG
401	GCAAAAACAT	CGTCAACGTC	GGACACGAAA	GCGCGGACAC	CGCCATCATC
451	ACCAAACCGG	TCGGACAAAA	CTTGGAATC	GTCCCGCTGG	ACAATCCCGC
501	CAACATTCAC	GTAGGCGAAC	GCTTCAAAGT	CCGCGTCTG	TTCCGTGGCG
551	AACCGCTGCC	CAATGCCACC	GTTACCGCCA	CCTTTGACGG	CTTCGACACC
601	AGCGACCGCA	GCAAAACGCA	CAAAACCGAA	GCACAGGCTT	TCTCCGACAG
651	CACAGACGAC	AAAGGCGAAG	TGGACATCAT	CCCCTTGC	CAAGGCTTCT
701	GGAAAGCCAA	TGTGGAACAC	AAAGCCGACT	TCCCCGATCA	AAGCGTGTGC
751	CAAAAACAGG	CGAACTACTC	GACTTTAACC	TTCCAAATCG	GCCATTTCGCA
801	CCATTAA				

This corresponds to the amino acid sequence <SEQ ID 2800; ORF 920.a>:

a920.pep

1	*KKTLLTLLAV	SALFAASAHA	HRVWVETAHT	HGGEY	LKADL	GYGEFPELEP
51	IAKDR	LHIFS	KPMQLVTEKG	KENMI	QRGT	NYQYRSNRPV
101	YQPTF	WSKNK	AGWKQAGIKQ	MPDAS	YCEQ	RMFGKNIVNV
151	TKPVG	QNL	EIVPLDN	PANIH	VGERF	KVRVLF
201	SDRSK	THKTE	AQAFSDSTDD	KGEVD	I	IPLR
251	QKQAN	YSTLT	FQIGHSHH*			

m920/a920 97.0% identity in 267 aa overlap

1322

	10	20	30	40	50	60
m920.pep	MKKTLLTLLSVS	ALFATS	SAHAHRVWVETA	HTHGGEYLKADL	GYGEFFPELEPIA	KDRLHIFS
a920	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX
	10	20	30	40	50	60
	70	80	90	100	110	120
m920.pep	KPMQLVTEKG	KENMIQRGT	YNYQYRSNR	VPVKDGSYL	VIAEYQPTF	WSKXKAGWKQAGIKE
a920	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX
	70	80	90	100	110	120
	130	140	150	160	170	180
m920.pep	MPDASYCEQ	TRMFGKN	IVNVGHESAD	TAIITKPV	QGNLEIVPL	DNPNANHVG
a920	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX
	130	140	150	160	170	180
	190	200	210	220	230	240
m920.pep	FRGEPLPN	ATVTATF	DGFDTS	SDRSKTHX	XAQAFSD	STDDKGEVDII
a920	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX
	190	200	210	220	230	240
	250	260	269			
m920.pep	KTDFPDQ	SVCQKQ	ANYSTLT	FTQIGH	SHHX	
a920	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2801>:

g920-1.seq

```

1  ATGAAGAAAA CATTGACACT GCTCGCcggt TcCGCACTAT TTGCCACATc
51  cgCaCACCCC CACCgCGTCT GGGTCGAAAC CgcccCACACg cAcgGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTCCCCGA ACTCGAACCC
151 ATCGccAAAG ACCgcccTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGT AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAAT
251 ACCGCAGCAA CCGTCCCCTG CAAAGACGGCA GCTACCTCGT TACCGCCGAA
301 TATCAGCCTA CTTTCCGGTC AAAAAACAAA GCAGGCTGGA AACAGGCTGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAACCC CGTATGTTTCG
401 GTAAAAACAT TGTCACCGTG GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTGGGAAATC GTCCCCTGCG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTCTCG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCTA CATTTGACGG CTTTCGACAC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCCCAAGCCT TCTCCGACAC
651 CACCGACGGC AAAGGCGAAG TGGACATCAT CCCCTTGGCG CAAGGCTTTT
701 GGAAAGCGAG TGTCGAATAC AAAGCCGATT TCCCGATCA AAGCCTGTGC
751 CAAAAACAGG CGAACTACAC AACTTTAACC TTCAAATCG GCCATTCTCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2802; ORF 920-1.ng>:

g920-1.pep

```

1  MKKTLLTLLAV SALFATS AHP HRVWVETAHT HGGEYLKADL GYGEFFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGT YNYQYRSNRPV KDGSYLVTAE
101 YQPTFRSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNL EI VPLDNPANH VGERFKVRVL FRGEPLPNAT VTATFDGFD
201 SDRSKTHKTE AQAFSDT TDG KGEVDIIPLR QGFWKASVEY KADFPDQSLC
251 KQQANYTTLT FQIGHSHH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2803>:

m920-1.seq

```

1  ATGAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCCGCGCC CACCgCGTCT GGGTCGAAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTCCCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAAT
251 ACCGAAGCAA CCGTCCCCTG AAGGACGGCA GTTACCTCGT CATCGCCGAA

```

1323

```

301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTCTCT TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCGGATCA AAGCGTGTGC
751 CAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GTCATTGCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2804; ORF 920-1>:

m920-1.pep

```

1 MKKTLTLLAV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51 IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLIVAE
101 YQPTFWSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNL EI VPLDNPANI H VGERFKVRVL FRGEPLPNAT VTATFDGFD T
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KTDFFPDQSV C
251 KQQANYSTLT FQIGHSHH*

```

m920-1/g920-1 96.3% identity in 268 aa overlap

	10	20	30	40	50	60
m920-1.pep	MKKTLTLLAVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
g920-1	MKKTLTLLAVSALFATSAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m920-1.pep	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLIVAEYQPTFWSKNKAGWKQAGIKE					
g920-1	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLIVAEYQPTFRSKNKAGWKQAGIKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m920-1.pep	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNL EIVPLDNPANI H VGERFKVRVL					
g920-1	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNL EIVPLDNPANI H VGERFKVRVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m920-1.pep	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH					
g920-1	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDTTDGKGEVDIIPLRQGFWKASVEY					
	190	200	210	220	230	240
	250	260	269			
m920-1.pep	KTDFFPDQSVCKQKQANYSTLTTFQIGHSHHX					
g920-1	KADFFPDQSLCQKQANYTTLTFQIGHSHHX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2805>:

a920.seq

```

1 TGAAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCGCATC
51 CGCCACGCGC CACCGCGTCT GGTCTGAAAC CGCCACACAG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCACT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAACAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTCTCT TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAGCCGACT TCCCGGATCA AAGCGTGTGC
751 CAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GCCATTGCA
801 CCATTAA

```

1324

This corresponds to the amino acid sequence <SEQ ID 2806; ORF 920-1.a>:

a920.pep

```

1  *KKTLTLLAV SALFAASAHA HRVWVETAHT HGGEYLLKADL GYGEFFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKNK AGWKQAGIKO MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KADFPDQSVK
251 QKQANYSTLT FQIGHSHH*
```

m920-1/a920 98.9% identity in 267 aa overlap

```

              10      20      30      40      50      60
m920-1.pep  MKKTLTLLAVSALFATSAAHHRVWVETAHTHGGEYLLKADLGYGEFFPELEPIAKDRLHIFS
              |||||
a920        XKKTLTLLAVSALFAASAHAHRVWVETAHTHGGEYLLKADLGYGEFFPELEPIAKDRLHIFS
              10      20      30      40      50      60

              70      80      90      100     110     120
m920-1.pep  KPMQLVTEKGKENMIQRGTYNYQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKE
              |||||
a920        KPMQLVTEKGKENMIQRGTYNYQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKQ
              70      80      90      100     110     120

              130     140     150     160     170     180
m920-1.pep  MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL
              |||||
a920        MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL
              130     140     150     160     170     180

              190     200     210     220     230     240
m920-1.pep  FRGEPLPNATVTATFDGFDTSRDKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
              |||||
a920        FRGEPLPNATVTATFDGFDTSRDKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
              190     200     210     220     230     240

              250     260     269
m920-1.pep  KTDFFPDQSVKQKQANYSTLTFFQIGHSHHX
              |::|
a920        KADFPDQSVKQKQANYSTLTFFQIGHSHHX
              250     260
```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2807>:

g921.seq

```

1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTCC TTTCCGggtG
51  Ccagtctatt tatGtgccca cattgacgga aatccccgTg aatcccatca
101 ataCCgtcaa aacggaagCA CCTGCAAAAG GTTTTCGCCT CGCCCCCTCG
151 CATTGGGCGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGcgGCG CAATATCTGA
251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
301 TATGAAATCT ACCTGCGTTC GCGCGTAGAC AGCCAGCGCG GCGAAATCAA
351 TACGGAACAG TCCAAGCTGT ATATCGAGAA TGCCTTGCGC GGCTGGCAGC
401 AGCGTtggaA AAATATGGAT GCCAAACCCG ATAATCCCGC ATTTACCAAC
451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA
```

This corresponds to the amino acid sequence <SEQ ID 2808; ORF 921.ng>:

g921.pep

```

1  MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLAPS
51  HWADVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
101 YEIYLRSAVD SQRGENTEQ SKLYIENALR GWQQRWKNMD AKPDNPAFTN
151 FLMEVMMQMP LK*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2809>:

m921.seq

```

1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTTC TTTCCGGCTG
51  CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA
101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTTCCGCCT TGCCTCTTCG
151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
```

1325

251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG  
 301 TATGAAATCT ACCTGCGTTC GGCGATAGAC AGCCAGCGGG GCGCAATCAA  
 351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC  
 401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC  
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2810; ORF 921>:

m921.pep

1 MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS  
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNNFRKRL VGRNAVDDSM  
 101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN  
 151 FLMEVMKMQP LK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 921 shows 95.7% identity over a 162 aa overlap with a predicted ORF (ORF 921.ng) from *N. gonorrhoeae*:

m921/g921

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	:					
g921	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLAPSHWADVAKISD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	:					
g921	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAVDSQRGEINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
	:     :					
g921	SKLYIENALRGWQQRWKNMDAKPDNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2811>:

a921.seq

1 ATGAAAAAAT ACCTTATCCC TCTTTCCATT GTGGCAGTTC TTTCCGGCTG  
 51 CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCGGTG AATCCTATCA  
 101 ATACCGTCAA AACGGAAGCA CCTGCAAAAAG GTTTCGCCT TGCCTCTTCG  
 151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA  
 201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA  
 251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG  
 301 TATGAAATCT ACCTGCGTTC GGCGATAGAC AGCCAGCGGG GCGCAATCAA  
 351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC  
 401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC  
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2812; ORF 921.a>:

a921.pep

1 MKKYLIPLSI VAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS  
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNNFRKRL VGRNAVDDSM  
 101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN  
 151 FLMEVMKMQP LK\*

m921/a921 99.4% identity in 162 aa overlap

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	:					
a921	MKKYLIPLSIVAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	10	20	30	40	50	60



1326

	70	80	90	100	110	120
m921 . pep	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
a921	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921 . pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQLKX					
a921	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2813>:

g922 . seq

```

1  ATGGAAGA GAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCTGTACG GCGATGGAGG CCCGCACACC CCGGGCAAAT GAAGCCCAAG
101  CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151  GCAGCCGTAC CGGTATCCGA CAGCGGTTT GCCGCCAATG CAAATGTCCG
201  CCGTTTGTG GACGATGAAG TCGGGAAGG GGATTTTCC CAGGCGGAAT
251  GGCAGGATTT TTTGACAAA GCGGCTTACA AGGCGGACAT CGTCAAGATt
301  ATGCACCGAC CCTCCACATC GCGtCCGTGG TATGtgttcc gCacggGAa
351  ttcGGgcagg gcgaaAtttc ACggcgCGCG Caggttttat GcggaaAacc
401  gcgcggttat cgatgatgtg gcgCAAAaT acggcgtGCC TGCCGAGCTT
451  ATCGTGGCGA TTATCGGGAT TGAACGAAT TACGGCAAAA ATACGGGCAG
501  TTTCCGTGTG GCGGACGCAT TGGCGACTTT AGGCTTTGAT TATCCCCGCC
551  GCGCCGGGTT TTTCAAAAA GAATTGGTCG AGCTTTTAAA GCTGGCAAAA
601  GAAGAAGGCG GTGATGTTTT CGCCTTTAAG GGCagcTATG CGGGTGCAAT
651  GGGTATGCCG CAATTATATG CTTTCGAGTA CCGGAAATGG GCGGTGGATT
701  ATGAcgggga cggacatCGG GATATAtggg GCAACGTcgg tgatgtcgcg
751  gcatcggTTG CCAATTAtat gaagCAGCAC GGTGGCGCA CgggcggtAA
801  AATGTTGGTG TCGGCGAcgt tggcgccggg tgccgATGTT CaggcAATCA
851  TTGGCGAAAA AACCGCCCTG ACGCGGACGG TGGCGGATTT GAaggCGTAc
901  ggcacatccc ccggggaaac GCTCGCAGAT GATGAAAAGg cgGTTTTGTT
951  CAAACTGGAA ACCGCACCCG GCGTGTTTGA ATATTATTG GGCTTGAACA
1001  ATTTTATAC GGTATGGCAG TACAACCACA GCCGGATGTA TGTAACGgcg
1051  gtcaggGACA TTGCCAATTC GCTCGGCGGC CCGGATTGT Aa

```

This corresponds to the amino acid sequence <SEQ ID 2814; ORF 922.ng>:

g922 . pep

```

1  MEKRKILPLA ICLAALSACT AMEARTPRAN EAQAPRADEM KESRPAFDA
51  AAVPVSDSGF AANANVRRFV DDEVGKGFDF QAEWQDFFDK AAYKADIVKI
101  MHRPSTSRPW YVFRGNSGR AKFHGARRFY AENRAVIDDV AQKYGVPAEL
151  IVAIIGIETN YGKNTGSFRV ADALATLGFY YPRRAGFFQK ELVELLKLAK
201  EEGGDVFAFK GSYAGAMGMP QFMPSSYRKW AVDYDGDGHR DIWGNVGDVA
251  ASVANVMKQH GWRTGGKMLV SATLAPGADV QAIIGETAL TRTVADLKAY
301  GIIPGETLAD DEKAVLFLKE TAPGVFEYYL GLNNFYTVWQ YNHSRMYVTA
351  VRDIANSLGG PGL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2815>:

m922 . seq

```

1  ATGAAAAAGA GAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCTGTACG GCGATGGAGG CACGCCCACC CCGGGCAAAT GAAGCCCAAG
101  CCCCCCGCGC GGTGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151  GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA CCGGGTTTGC
201  CGCCAATGCA AATGTCCGCC GTTTTGTGGA CGATGAAGTC GGGAAAGGGG
251  ATTTTCCCG GCGGAATGG CAGGATTTT TTAGCAAAGC GGCTTACAAG
301  GCGGACATCG TCAAGATTAT GCACCGCCCC TCCACATCGC GTCCGTGGTA
351  TGTGTTCCGC ACGGGAAAT TCGGCAAGGC GAAATTTTCG GCGCGCGGCC
401  GGTTTTATGC GGAACCCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC
451  GCGGTGCCTG CCGAACTTAT CGTGGCGGTT ATCGGATTG AAACGAATTA
501  CCGCAAAAAT ACGGGCAGTT TCCGTGTGGC GGACGATTG GCGACCTTAG
551  GCTTTGATTA CCCCCGCCGC GCCGGGTTTT TCAAAAAGA ATTGGTCGAG

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1327

```

601 CTTTAAAGC TGGCAAAAGA AGAAGGCGGC GATGTTTTCG CCTTTAAAGG
651 CAGCTATGCG GGC GCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAAATGGGC GGTGGATTAT GACGGGGACG GACATCGGGA CATATGGGGC
751 AACGTCGGCG ATGTCGCGGC ATCGGTTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GCGGGGAAAA TGCTGGTGTC TGCAACATG GCGCCGGGTG
851 CGGATGTTCA GGCAATCATT GGC GAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTTGA AGGCGTACGG CATCATCCCC GCGGAAGAGC TTGCAGATGA
951 TGAAAAGGCG GTTTTGTTCA AACTGGAAAC CGCACC GGC GTGTTTGAAT
1001 ATTATTTGGG CTGAAACAAT TTTTATACGG TATGGCAGTA CAACCACAGC
1051 CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTCGC TTGGCGGCCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2816; ORF 922>:

m922.pep

```

1 MKKRKILPLA ICLAALSACT AMEARPPRAN EAQAPRAVEM KESRPAFDA
51 AAVFDAAAVP VSDSGFAANA NVRRFVDDEV GKGDFSRAEW QDFD KAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVP AELIVAV IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKEEGG DVFAFKGSYA GAMGMPQFMP SSKRWAVDY DGDGHRDIWG
251 NVGDVAASVA NYMKQHGWR TGGKMLVSATL APGADVQAI IGEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYYLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 922 shows 95.9% identity over a 369 aa overlap with a predicted ORF (ORF 922.ng) from *N. gonorrhoeae*:

m922/g922

m922.pep	10	20	30	40	50	60
	MKKRKILPLAICLAALSACTAMEARPPRANEAQAPRAVEMKKESRPAFDAAAVFDAAAVP					
g922	MEKRKILPLAICLAALSACTAMEARTPRANEAQAPRADEMKKESRPAFDAA-----AVP					
	10	20	30	40	50	
m922.pep	70	80	90	100	110	120
	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFD KAAYKADIVKIMHRPSTSRPWYVFR					
g922	VSDSGFAANANVRRFVDDEVGKGDFSQA EWQDFD KAAYKADIVKIMHRPSTSRPWYVFR					
	60	70	80	90	100	110
m922.pep	130	140	150	160	170	180
	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVP AELIVAVIGIETNYGKNTGSFRVADAL					
g922	TGNSGRAKFHGARRFYAENRAVIDDVAQKYGVP AELIVAIIGIETNYGKNTGSFRVADAL					
	120	130	140	150	160	170
m922.pep	190	200	210	220	230	240
	ATLGFDYPRRAGFFQKELVELLKLAKKEEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
g922	ATLGFDYPRRAGFFQKELVELLKLAKKEEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
	180	190	200	210	220	230
m922.pep	250	260	270	280	290	300
	DGDGHRDIWGNVDVAASVAN YMKQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV					
g922	DGDGHRDIWGNVDVAASVAN YMKQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV					
	240	250	260	270	280	290
m922.pep	310	320	330	340	350	360
	ADLKAYGIIPGEELADDEKAVL FKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI					
g922	ADLKAYGIIPGETLADDEKAVL FKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI					

1328

	300	310	320	330	340	350
	370					
m922.pep	ANSLGGPGLX					
g922	ANSLGGPGLX					
	360					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2817>:

```

a922.seq
1   ATGAAAAACA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCCGCC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTTCCTG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACCGCCCC TCCACATCGC GTCCGTGGTA
351 TGTGTTCCGC ACGGAAATT CGGGCAAGGC GAAATTTCGC GGCGCGCGCC
401 GGTTTTATGC GGAAACCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC
451 GGCGTGCCTG CCGAACTTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501 CGGCAAAAAT ACGGCGAGTT TCCGTGTGGC GGACGCATTG GCGACCTTAG
551 GCTTTGATTA CCCCCGCCG GCGGGTTTT TCCAAAAGA ATTGGTCGAG
601 CTTTAAAGC TGGCAAGA AGAAGCGGC GATGTTTTCG CCTTTAAAGG
651 CAGCTATGCG GCGCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAAATGGGC GGTGATTAT GACGGGACG GACATCGGGA CATATGGGCG
751 AATGTTGGCG ATGTCGCGC ATCGATTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GCGGGGAAA TACTGGTGTC TGCAACATTG GCGCCGGGTG
851 CGGATGTTCA GGCAATCATT GGCGAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTTGA AGGCGTACG CATCATCCCC GGCGAAGAGC TTGCCGATGA
951 TGAAGAGGCG GTTTTGTTC AACTGGAAAC CGCACCGGCG GTGTTTGAAT
1001 ATTATTTGGG CTTGAACAAT TTTTATACGG TATGGCAGTA CAATCACAGT
1051 CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTCGC TTGGCGGCCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2818; ORF 922.a>:

```

a922.pep
1   MKNRKILPLA ICLAALSACT AMEARPPRAN EAQAPRADEM KESRPAFDA
51  AAVFDAAAVP VDSGFAANA NVRRFVDDEV GKGDFSRAEW QDFDKAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPaelivav IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKKEEG DVFAFKGSYA GAMGMPQFMP SSYRKWAVDY DGDGHRDIWG
251 NVGDVAASIA NYMKQHGWRT GGKILVSATL APGADVQAI GEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYYLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

m922/a922 98.9% identity in 369 aa overlap

	10	20	30	40	50	60
m922.pep	MKKRKILPLAICLAALSACTAMEARPPRANEQAAPRAVEMKKESRPAFDAAAVFDAAAVP					
	:					
a922	MKNRKILPLAICLAALSACTAMEARPPRANEQAAPRADEMKKESRPAFDAAAVFDAAAVP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m922.pep	VDSGFAANANVRRFVDDEVGKGDFSRAEWQDFDKAAYKADIVKIMHRPSTSRPWYVFR					
a922	VDSGFAANANVRRFVDDEVGKGDFSRAEWQDFDKAAYKADIVKIMHRPSTSRPWYVFR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m922.pep	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
a922	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
	130	140	150	160	170	180
	190	200	210	220	230	240

1329

```

m922.pep  ATLGFDYPRRAGFFQKELVELLKLAKEEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          |||||||
a922      ATLGFDYPRRAGFFQKELVELLKLAKEEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          190      200      210      220      230      240

          250      260      270      280      290      300
m922.pep  DGDGHRDIWGNVGDVAASVANYMKQHGWRGKMLVSATLAPGADVQAIIGEKALTRTV
          |||||||
a922      DGDGHRDIWGNVGDVAASIANYMKQHGWRGKILVSATLAPGADVQAIIGEKALTRTV
          250      260      270      280      290      300

          310      320      330      340      350      360
m922.pep  ADLKAYGIIIPGEEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          |||||||
a922      ADLKAYGIIIPGEEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          310      320      330      340      350      360

          370
m922.pep  ANSLGGPGLX
          |||||||
a922      ANSLGGPGLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2819>:

```

g923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACCGATG GCGTGTGCGG CATTTCTGTC
51  CGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGCG TGCCGTGCGG
151 GGAAACGCC GCATTCCCGA ACACCGCCTG CTCCTGCCTG CCTTGTTCCG
201 CGGTTGGACG GGCGCATACT TGGGTAGTAG GATGTTTCAGG CATAAACCGG
251 CGAAAAAGCG TTTTGTGTG CTGTTCCGTC TGACTGTTTC GGGCAATGTC
301 CTGGCGACCT GCATCCTGAT TGATTATTTC GTTCCGCCCG AACTTTTTGT
351 AAAACTCGGG CAACATCTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2820; ORF 923.ng>:

```

g923.pep
1  MKRQAFFKPM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRRRAVR
51  GKRRIPRHRL LLPALFGGWT GAYLGSRMFR HKTAKKRFV LFRLLTVSGNV
101 LATCILIDYF VPPELFFVLG OHL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2821>:

```

m923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTTCTGTC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGTG CGCCATACGG
151 GGGCAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CATTGCTCGG
201 CGGCTGGGTG GGCAGCATAT TCGGCAGCAT GACATTCAAA CATAAGACAG
251 CGAAAAAGCG TTTTGTGTG CTGTTCCGTC TGACTGTTTC AGGTAATGTC
301 TTGGCGACCC TCATCCTGAT TTATAGTGA TTAAATTTAA ACCAGTACGG
351 CGTTGCCTCG CTTGCGGTA CTATTGTAC TGTCTGCGGC TTCGTGCGCT
401 TGTCTGATT TTTGTTAATC CACTATAT.T ATTTTGTCCC GCCTGAATTT
451 TTCGTAAAC TCGGCAGAA TACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2822; ORF 923>:

```

m923.pep
1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRCRIR
51  GQRRIPRHRL LLPALLGGWV GAYFGSMTFK HKTAKKRFV LFRLLTVSGNV
101 LATLILYSG LNLNQYGVAS PCRTICTVCG FVALS*FLLI HYXYFVPPEF
151 FVKLGQNT*

```

Computer analysis of this amino acid sequence gave the following results:

1330

Homology with a predicted ORF from *N. gonorrhoeae*ORF 923 shows 68.8% identity over a 157 aa overlap with a predicted ORF (ORF 923.ng) from *N. gonorrhoeae*:

g923/m923

	10	20	30	40	50	60
g923.pep	MKRQAFFKPMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRIPEHRL					
m923	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCRAIRGQRRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100		
g923.pep	LLPALFGGWTGAYLGSRMFRHKTAKKRFVVLFRFTVSGNVLATCILID-----					
m923	LLPALGGSWVGAYFGSMTFKHKTAKKRFVVLFRFTVSGNVLATLILIIYSGNLNLYQYGVAS					
	70	80	90	100	110	120
			110	120		
g923.pep	-----YFVPPELFFVKLGQHLX					
m923	PCRTICTVCGFVALSXFLLIHYIYFVPPEFFVKLGQNTX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2823>:

a923.seq

1	ATGAAGCGGC	AGGCTTTCTT	CAAACGTATG	GCGTGTGCGG	CATTTCTGTC
51	TGCCGTTTCG	CTGCGCCTCC	CCGTATTGGG	CGCGTGTAC	GCAATATTGT
101	CCCTCTATGC	GTTTGCACCT	TACGGCATCG	ACAAACGGCG	TGCCGTGCGG
151	GGAAAACGCC	GCATCCCCGA	ACACCGCCTG	CTGCTGCCTG	CCTTGTTCGG
201	CGTTTGGGCG	GGCGCATACT	TGGGCAGCAG	GATATTCAGG	CATAAAACGG
251	CGAAAAAGCG	TTTTGTTGTG	CTGTTCCGTC	TGACTGTTTC	GGGCAATGTC
301	CTGGCGACCC	TCATCCTGAT	TTATAGTGGA	TTAAATTAA	ACCAGTACGG
351	CGTTGCCTCG	CCTTA.GCTC	AAAGAGAACG	ATTCTCTAAG	GTGCTGAAGC
401	ACCAAGTGAA	TCGGTTCGGT	ACTATTGTGA	CTGTCTGCGG	CTTCGTCGCC
451	TTGTCCTGAT	TTTTGTAAAT	CCACTAT.AT	TATTTTGTCC	CGCCTGAATT
501	TTTCGTAAAA	CTCGGCGAGA	ATACCTGA		

This corresponds to the amino acid sequence &lt;SEQ ID 2824; ORF 923.a&gt;:

a923.pep

1	MKRQAFFKLM	ACAAFLSAVS	LRLPVLGACY	AILSLEYAFAL	YGIDKRRRAVR
51	GKRRIPEHRL	LLPALFGGWA	GAYLGSRIFR	HKTAKKRFVV	LFRLTVSGNV
101	LATLILIIYS	GNLNQYGVAS	PXAQRERFSK	VLKHQVNRFR	TICTVCGFVA
151	LS*FLLIHYX	YFVPPEFFVK	LGQNT*		

m923/a923 84.6% identity in 175 aa overlap

	10	20	30	40	50	60
m923.pep	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCRAIRGQRRRIPEHRL					
a923	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m923.pep	LLPALGGSWVGAYFGSMTFKHKTAKKRFVVLFRFTVSGNVLATLILIIYSGNLNLYQYGVAS					
a923	LLPALFGGWAGAYLGSRIFRHKTAKKRFVVLFRFTVSGNVLATLILIIYSGNLNLYQYGVAS					
	70	80	90	100	110	120
			130	140	150	159
m923.pep	PC-----RTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX					
a923	PXAQRERFSKVLKHQVNRFRRTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2825>:

g925.seq

```

1  ATGAAACAAA TGCTTTTGGC cgtcggcggtg ggcGCGGTGT TGGCGGGCTG
51  CGGCAaggat gcCGGCGGtt acgagggtTA TTGGCGCGAA AAGTCGGACA
101 AAAAagaggG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTTCTTAAT
151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGC GG
351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2826; ORF 925.ng>:

g925.pep

```

1  MKQMLLAVGV GAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNYP LN
51  KINVFTGKEE SLLLSEKDGA LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKCGQT QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2827>:

m925.seq (partial)

```

1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTA CTTCCTT

```

This corresponds to the amino acid sequence <SEQ ID 2828; ORF 925>:

m925.pep (partial)

```

1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNYP LN

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 925 shows 94.0% identity over a 50 aa overlap with a predicted ORF (ORF 925.ng) from *N. gonorrhoeae*:

m925/g925

	10	20	30	40	50
m925.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNYP LN				
g925	MKQMLLAVGVGAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNYP LN KINVFTGKE				
	10	20	30	40	50
g925	ESLLLSEKD GAL SINTGIGE IPIKLSDDG KELYVERRRYVK TDAAMKDKII AHQKKCGQT				
	60	70	80	90	100
	110				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2829>:

g925-1.seq

```

1  ATGAAACAAA TGCTTTTGGC CGTCGGCGTG GCGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTTCTTAAT
151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGC GG
351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2830; ORF 925-1.ng>:

g925-1.pep

1332

```

1  MKQMLLAVGV AAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNYFLN
51 KINVFTGKEE SLLLSEKDG LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKCGQT QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNGKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2831>:

## m925-1.seq

```

1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGCGGTTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTACTTCCTT
151 AATAAAATCC ACGTGGTTAC AGGCAAGGAA GAGTCCTTGC TTTTGTCTGA
201 AAAAGACGGC GCGCTTTCGA TAAACACAGG GATAGGGGAA ATCCCGATCA
251 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGTAG GCAGTATGTC
301 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
351 CGGACAAACA GCACAGGCAT ACCGCGACGC GCGAAATGCG TTGCCGTCAA
401 ACCAGACGTA TCAGCAGCAT CTGGCGGCGA TCGAGCAATT GAAACGGCGG
451 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAG
501 AAGCCCGGCA TTGTTGCTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 2832; ORF 925-1>:

## m925-1.pep..

```

1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL
51 NKIHVVTGKE ESLLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
101 KTDAAAMKDKI IAHQKKCGQT AQAYRDARNA LPSNQTYQQH LAAIEQLKRR
151 FEAEFDELEK EIKCNGRSPA LLL*

```

m925/g925 92.5% identity in 173 aa overlap

	10	20	30	40	50	60
m925-1.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKIHVVTGKE					
g925-1	MKQMLLAVGVAAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKINVFTGKE					
	10	20	30	40	50	
	70	80	90	100	110	120
m925-1.pep	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKCGQT					
g925-1	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKKCGQT					
	60	70	80	90	100	110
	130	140	150	160	170	
m925-1.pep	AQAYRDARNALPSNQTYQQHLAAIEQLKRRFEAEFDELEKEIKCNGRSPALLLX					
g925-1	AQAYLDARNALPSNQTYQQRQAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2833>:

## a925-1.seq

```

1  AATAAAATCA ACGTGTTCAC AGGTAAGGAA GAATCTATGC TTTTGTCTGA
51  AAAAGACGGC GCGCTTTCGA TAAACACGGG GATAGGGGAA ATCCCGATCA
101 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGCAG GCAGTATGTC
151 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
201 CGGACAAACG GCACAGGCAT ATCTCGACGC GCGAAATGCG TTGCCGTCAA
251 ACCAGACGTA TCAGCAGCAT CAGGCGGCGA TCGAGCAGTT GAAACGGCGG
301 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAA
351 ACCGACATTG TTGTTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2834; ORF 925-1.a>:

## a925-1.pep

```

1  NKINVFTGKE ESMLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
51 KTDAAAMKDKI IAHQKKCGQT AQAYLDARNA LPSNQTYQQH QAAIEQLKRR
101 FEAEFDELEK EIKCNGKPTL LF*

```

a925-1/m925-1 92.7% identity in 123 aa overlap

		10	20	30
a925-1.pep		NKINVFTGKEESMLLSEKDGALSINTGIGE		
m925-1	AGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKIHVVTGKEESLLLSEKDGALSINTGIGE			
	30	40	50	60
	40	50	60	70
				80
				90

1333

```

a925-1.pep  IPIKLSDDGKELYVERROYVKTDAAMKDIIAHQKKCGQTAQAYLDARNALPSNQTYQQH
|||||
m925-1      IPIKLSDDGKELYVERROYVKTDAAMKDIIAHQKKCGQTAQAYRDARNALPSNQTYQQH
          90      100      110      120      130      140

          100      110      120
a925-1.pep  QAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX
|||||
m925-1      LAAIEQLKRRFEAEFDELEKEIKCNGRSPALLX
          150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2835>:

```

g926.seq (partial)
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCGGAAGGG CGGTTGGCAG TCAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG ACAGTTGTGT CAAGAcAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAGGGT
301 ACGgaagact tGAGCAGGCA GCTGGTCGGT TTCAAACGTC CAATCCAATA
351 TCTGCATATC TGGGCGGAAG GCAGGCGTGT GGCGGGCGCG CCTtaccGCA
401 TCCGTTTACA CGGCATATTG GAACAATAcg GttggACAAT cgggCagaac
451 tgcCGACAGT GGGGGGCaag tccgaacgtt gcaactGAa...

```

This corresponds to the amino acid sequence <SEQ ID 2836; ORF 926.ng>:

```

g926.pep (partial)
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 TEDLSRQLVG FKLPIQYLHI WAEGRRVAGA PYRIRSDGIL EQYGTIGQN
151 CRQWGASPNV ATE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2837>:

```

m926.seq
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCAGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAATACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACGTC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCGTGT GGCGGGCGCG CCTTACCGCA
401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CGGCAGAACC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTCA CCGAAATCGG TATGCCGTCT GAAACCGAAA
551 CCCCGGAACG CTGTGCGGCG CGCACGAGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2838; ORF 926>:

```

m926.pep
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAES
101 AEELSRQLVG FKLPIQYLHI WADGRRVAGA PYRILPDGIL EQYGTIVGRT
151 ADSGGQVRTL QLNNGNLNIR LVFTEIGMPS ETETPERCAA RTR*

```

g926/m926 91.6% identity in 155 aa overlap

```

          10      20      30      40      50      60
g926.pep  MKHTVSASVILLLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
|||||
m926      MKHTVSASVILLLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
          10      20      30      40      50      60

          70      80      90      100     110     120
g926.pep  PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEGETEDLSRQLVGFKLPIQYLHI
|||||
m926      PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAEEELSRQLVGFKLPIQYLHI
          70      80      90      100     110     120

          130     140     150     160
g926.pep  WAEGRRVAGAPYRIRSDGILEQYGTIGQNCRQWGASPNVATE

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1334

|||||:|||||:|:|:|  
 m926 WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS  
 130 140 150 160 170 180

a926.seq

1 ATGAAACACA CTGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC  
 51 GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACACCC  
 101 GCAGTTTCAC GCGGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT  
 151 TCGTATGCAA ATTTGATTG GACATACCAA CCGCCCGTGG AAACCATCAA  
 201 TATCAACACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG  
 251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GCGCGAAAGT  
 301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACCTGC CAATCCAATA  
 351 TCTGCATATC TGGGCAGATG GCAGGCCTGT GCGCGGCGCG CCTTACCGCA  
 401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CCGCAGAACC  
 451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT  
 501 GAACATCAGG CTGGTTTTCA CCGAGATTGG TATGCCGTCT GAAACCGAAA  
 551 CCCAAGAACA ATGCGCGGCA CGCATACAGT AA

a926.pep

1 MKHTVSASVI LLLTACAQLP QNNENLWQPS EHTRSFTAEG RLAVKAEGKG  
 51 SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAES  
 101 AEELSRQLVG FKLPIQYLHI WADGRPVAGA PYRILPDGIL EQYGWTVGRT  
 151 ADSGGQVRTL QLNNGNLNIR LVFTEIGMPS ETETQECCAA RIQ\*

m926/a926 96.9% identity in 191 aa overlap

	10	20	30	40	50	60
m926.pep	MKHTVSASVILLTACAQLPQNNENLWQPS	EHSSFAAEGRLAVKAEGKGS	SYANFDWTYQ			
a926	MKHTVSASVILLTACAQLPQNNENLWQPS	EHTRSFTAEGRLAVKAEGKGS	SYANFDWTYQ			
	10	20	30	40	50	60
m926.pep	PPVETININTPLGSTLGQLCQDRDGALAVD	GKGNVYQAESAEELSRQLVG	FKLPIQYLHI			
a926	PPVETININTPLGSTLGQLCQDRDGALAVD	GKGNVYQAESAEELSRQLVG	FKLPIQYLHI			
	70	80	90	100	110	120
m926.pep	PPVETININTPLGSTLGQLCQDRDGALAVD	GKGNVYQAESAEELSRQLVG	FKLPIQYLHI			
a926	PPVETININTPLGSTLGQLCQDRDGALAVD	GKGNVYQAESAEELSRQLVG	FKLPIQYLHI			
	70	80	90	100	110	120
m926.pep	WADGRRVAGAPYRILPDGILEQYGWTVGRT	ADSGGQVRTLQLNNGNLNIR	LVFTEIGMPS			
a926	WADGRPVAGAPYRILPDGILEQYGWTVGRT	ADSGGQVRTLQLNNGNLNIR	LVFTEIGMPS			
	130	140	150	160	170	180
m926.pep	WADGRRVAGAPYRILPDGILEQYGWTVGRT	ADSGGQVRTLQLNNGNLNIR	LVFTEIGMPS			
a926	WADGRPVAGAPYRILPDGILEQYGWTVGRT	ADSGGQVRTLQLNNGNLNIR	LVFTEIGMPS			
	130	140	150	160	170	180
m926.pep	ETETPERCAARTRX					
a926	ETETQECCAAARIQX					
	190					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2839>:

g927.seq

1 atgaaaacct acGCACAggc ACTCTATacc GCAGCCCTGC TCACCGCCTG  
 51 CAGCCCcgca GCcgatTcaa accaTCCGTC CCGAcAaAAT GCCCCGGCCA  
 101 ATACCGAATC cgacGgaaAA AACATtaccC TGctcaatgc cTcgtagcat  
 151 gtGACACGGT ATTTttacaa agaatacgac cacTtgtttg tcggaaCATA  
 201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAA TCCCACGGCG  
 251 GCTTCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC  
 301 GTAACCATGA ACCAATCTTC CGACATCGAC CTGCTCGAAA AAAA.GGACT  
 351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGATCACGCC GCACCCTACA

1335

401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCcaa ACAGAtccgC  
 451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAAGAC  
 501 CTCGGGCAAC GGACGCTACG CCTTCCTCGG CGCATACGGT TACGGTCTGA  
 551 AAGCCAACAA CGGcaacGAG CAGGAAGCCC AAAAaCTCGT CGCATCCATC  
 601 CTCAAAAACA CACCCGTTTT TGAAAACGGC GGACGCGc.C CGCCGCCACC  
 651 ACCTTCACAC AACGCAACAT CGGCGACGTA CTCATCACTT TTGAAAACga  
 701 agCcaactac gtCAGCAAAA AACTGA

This corresponds to the amino acid sequence <SEQ ID 2840; ORF 927.ng>:

g927.pep

1 MKTYAQALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD  
 51 VTRYFYKEYD HLFVGTYSQSE HPGTSVSIQQ SHGGFSKQAL SVANGLQADV  
 101 VTMNQSSDID LLEKXGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR  
 151 DWNDLAKDGV NIVIAKTSNG GRYAFLGAYG YGLKANNGNE QEAQKLVASI  
 201 LKNTVPVFENG GRXPPPPPSH NATSATYSSL LKTKPTTSAK N\*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2841>:

m927.seq

1 ATGAAACCTT ACGCACCGGC ACTCTATACC GCAGCCCTGC TCACCGCCTG  
 51 CAGCCCCGCA GCCGATTCAA ACCATCCGTC CGGACAAAAT GCCCCGGCCA  
 101 ATACCGAATC CGACGGAAAA AACATTACCC TGCTCAACGC CTCATACGAT  
 151 GTGGCACGGG ATTTTACAA AGAATACAAC CCCTTATTTA TCAAAACATA  
 201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAG TCCCACGGCG  
 251 GCTCCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC  
 301 GTAACCATGA ACCAATCCTC CGACATCGAC CTGCTCGAAA AAAAAGGACT  
 351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGACCACGCC GCGCCCTACA  
 401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCCAA ACAGATCCGC  
 451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAATCC  
 501 CAAACCTCG GGCAACGGAC GCTACGCCTT CCTCGGCGCA TACGGTTACG  
 551 GTCTGAAAC CACCAACGGC AACGAACAGG AAGCCCAAAA ACTCGTCGCA  
 601 TCCATCCTCA AAAACACCCC CGTTTTTGAA AACGGCGGAC GCKCgCCACC  
 651 ACCACCTTCA CACAACGCAA CATCGGCGAC GTACTCATCA CTTTTGAAAA  
 701 CGAAGCCAAC TACGTCAGCr AAAAActGA

This corresponds to the amino acid sequence <SEQ ID 2842; ORF 927>:

m927.pep

1 MKTYAPALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD  
 51 VARDFYKEYN PLFIKTYQSE HPGTSVSIQQ SHGGSSKQAL SVANGLQADV  
 101 VTMNQSSDID LLEKKGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR  
 151 DWNDLAKDGV NIVIANPKTS NGRYAFLGA YGYGLKTTNG NEQEAQKLVA  
 201 SILKNTPVFE NGGRXPPPPS HNATSATYSS LLKTKPTTSA KN\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 927 shows 94.2% identity over a 243 aa overlap with a predicted ORF (ORF 927.ng) from *N. gonorrhoeae*:

g927/m927

	10	20	30	40	50	60
g927.pep	MKTYAQALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVTRYFYKEYD					
m927	MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVTRYFYKEYN					
	10	20	30	40	50	60
	70 80 90 100 110 120					
g927.pep	HLFVGTYSQSEHPGTSVSIQQSHGGFSKQALSVANGLQADVVTMNQSSDIDLLEKXGLVEK					
	:					
m927	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKXGLVEK					
	70	80	90	100	110	120
	130 140 150 160 170					
g927.pep	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIA--KTSNGNGRYAFLGA					
m927	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSNGNGRYAFLGA					
	130	140	150	160	170	180

1336

```

      180      190      200      210      220      230
g927.pep  YGYGLKANNGNEQEAQKLVASILKNTVPVFENGGRXPPPPSHNATSATYSSLLKTKPTTS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m927      YGYGLKTTNGNEQEAQKLVASILKNTVPVFENGGRXPPPP-SHNATSATYSSLLKTKPTTS
          190      200      210      220      230

      240
g927.pep  AKNX
          ||||
m927      AKNX
          240

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2843>:

```

a927.seq
1  ATGAAACCT  ACGCACCGGC  ACTCTATACC  GCAGCCCTGC  TCAGCGCCTG
51  CAGCCCCGCA  GCCGATTCAA  ACCATCCGTC  CGGACAAAAT  GCCCCGGCCA
101 ATACCGAATC  CGACGGAAAA  AACATTACCC  TGCTCAACGC  CTCATACGAT
151 GTGGCACGGG  ATTTTTACAA  AGAATACAAC  CCCTTATTTA  TCAAAACATA
201 CCAATCCGAA  CACCCCGGCA  CATCCGTCAG  CATCCAACAG  TCCCACGGCG
251 GCTCCAGCAA  ACAGGCATTA  TCCGTAGCCA  ACGGCCTTCA  AGCCGATGTC
301 GTAACCATGA  ACCAATCCTC  CGACATCGAC  CTGCTCGAAA  AAAAAGGACT
351 GGTAGAAAAA  GGCTGGCAAC  AAGCCCTCCC  CGACCAGGCC  GCGCCCTACA
401 CCAGCACTAT  GGTTTTCTT  GTCCGAAAAA  ACAACCCCAA  ACAGATCCGC
451 GATTGGAACG  ACCTTGCCAA  AGACGGCGTT  AACATCGTCA  TCGCCAATCC
501 CAAAACCTCG  GGCAACGGAC  GCTACGCCTT  CCTCGGCGCA  TACGGTTACG
551 GTCTGAAAC  CACCAACGGC  AACGAACAGG  AAGCCCCAAA  ACTCGTCGCA
601 TCCATCTCA  AAAACACCCC  CGTTTTTGAA  AACGGCGGAC  GCGCGCCACC
651 ACCACCTCA  CACAACGCAA  CATCGGCGAC  GTACTCATCA  CTTTGA AAAA
701 CGAAGCCAAC  TACGTCAGCA  AAAA ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2844; ORF 927.a>:

```

a927.pep
1  MKTYAPALYT  AALLSACSPA  ADSNHPSGQN  APANTESDGK  NITLLNASYD
51  VARDFYKEYN  PLFIKTYQSE  HPGTSVSIQQ  SHGGSSKQAL  SVANGLQADV
101 VTMNQSSDID  LLEKKGLVEK  GWQALPDHA  APYTSTMVFL  VRKNNPKQIR
151 DWNDLAKDGV  NIVIANPKTS  GNGRYAFLGA  YGYGLKTTNG  NEQEAQKLVA
201 SILKNTPVFE  NGGRAPPPPS  HNATSATYSS  LLKTKPTTSA  KN*

```

m927/a927 99.2% identity in 242 aa overlap

```

      10      20      30      40      50      60
m927.pep  MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a927      MKTYAPALYTAALLSACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          10      20      30      40      50      60

      70      80      90      100     110     120
m927.pep  PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a927      PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
          70      80      90      100     110     120

      130     140     150     160     170     180
m927.pep  GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a927      GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
          130     140     150     160     170     180

      190     200     210     220     230     240
m927.pep  YGYGLKTTNGNEQEAQKLVASILKNTVPVFENGGRXPPPPSHNATSATYSSLLKTKPTTSA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a927      YGYGLKTTNGNEQEAQKLVASILKNTVPVFENGGRAPPPPSHNATSATYSSLLKTKPTTSA
          190     200     210     220     230     240

```

1337

m927.pep      KNX  
                  |||  
 a927            KNX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2845>:

g929.seq

```

1  ATGAAATTGG  GTTTCAAACC  GATACCCCTC  GCCATTGCCG  CAGTATTGTG
51  CGCCCTGGTT  TTGGCACTGC  CCGTACccga  CGGGGTCAAG  CCTCAGGCTT
101  GGACGCTGCT  GGCTATGTTT  GTCGGTGTGA  TTGCCGCCAT  TATCGGCAAG
151  GTTATGCCGT  TGGGCGCGCT  GTCGATTATT  GCCGTCGGGT  TGGTCGCAGT
201  AACC CGCGTA  ACCGCCGACA  AACC GGGCGC  GGCGATGAGC  GATGCGTTGA
251  GTGCGTTCGC  CAATCCGTTG  ATTTGGCTGA  TTGCCATCGC  AGTTATGATT
301  TCGCGCGGTT  TGCTCAAAAC  AGGGCTGGGG  ATGCGTATCG  GATATTTGTT
351  TATCGCCGTT  TTTGGAAGAA  AAacgctggG  CATCGGTTAC  AGTCTCGCTC
401  TTTCCGAAC  TCTGCTGGCT  CCCGTTACCC  CTTCCAATAC  CGCGCGCGGC
451  GGCGGCATTA  TACATCcgAT  TATGCagtcg  attgCgggCA  GttacggctC
501  caatCCCGCA  AAATGtcgG  aaggcaagat  gggtaAATAT  TtggcTTtgg
551  tcaattaTCA  TTCaaTCCC  atttcgctcg  ctAtggctat  taCTGcaact
601  gCCCCaaCC  CTTTAATcgt  caacttgatt  gccGaaaaTt  taggcagtag
651  tttccgtCTT  TcTtgggggg  cgTGGGcgTg  ggcaaTGGCT  Gttcccggcg
701  ttatcgccct  TttcgTTATG  CCTTTGATT  TATATTTTTT  GTATCCGCCT
751  GAAATTAAAG  AAACGCCCAA  TGCTGttcAA  TTTGCCAAAG  ACCGTCTGAG
801  CGAGATGGGT  AAAATGtcgG  CAGACGAAAT  CATTATGGCG  GTCATTTTCG
851  GTATCTTGCT  GCTGTTGTGG  GCAGATGTTT  CCGCCCTTAT  TACCGGCAAT
901  CACGCTTTTA  GTATCAacgc  caccGCCACC  GCATTTATCG  GATTAAGCCT
951  GCTTTTGCTT  TCCGGTGTAT  TGA CT TGGGA  CGATGTTTTG  AAAGAAAAAA
1001  GCGCGTGGGA  TACGATTATT  TGGTTTGGCG  CATTGATTAT  GATGGCCGCA
1051  TTTT TaAATA  AActcggact  gattaaatGG  TTCTCCGGAG  TGTTGGCGGA
1101  AagtgtcggC  GGT TTGGCG  TTAGCGGCAC  GGCTGCGGGC  GTAATCCTCG
1151  TGCTTGCTta  TATGTATGCG  CATTATATGT  TTGCCAGTAC  TACTGCACAT
1201  ATTACCGCTA  TGTTCCGCGC  ATTTCTCGCT  GCTGCCGTTT  CACTGAATGC
1251  CCCGCGATG  CCGACTGCGC  TGATGATGGC  GGCCGCATCC  AACATTATGA
1301  TGACCCTCAC  TCATTATGCG  ACCGGTACTT  CACCTGTGAT  TTTCGGCTCG
1351  GGCTACACCA  CAATGGGAGA  ATGGTGGAAG  GCGGGTTTTA  TCATGAGCGT
1401  AGTCAATTTT  CTGATTTTTT  CCGTTATCGG  CAGCATTTGG  TGGAAAGTTC
1451  TGGGATATTG  GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2846; ORF 929.ng>:

g929.pep

```

1  MKLGFKPIPL  AIAAVLCALV  LALFVPDGVK  PQAWTLLAME  VGVIAAIIGK
51  VMPLGALSII  AVGLVAVTGV  TADKPGAAMS  DALSAFANPL  IWLIAIAVMI
101  SRGLLKTGLG  MRIGYLFIAV  FGRKTLGIGY  SLALSELLLA  PVTPSNTARG
151  GGIHPIMQS  IAGSYGSNPA  KGTEGKMCKY  LALVNYHNSP  ISSAMAITAT
201  APNPLIVNLI  AENLGSSFRL  SWGAWAWAMA  VPGVIAFFVM  PLILYFLYPP
251  EIKETPNAVQ  FAKDRLSEMG  KMSADEIIMA  VIFGILLLLW  ADVPALITGN
301  HAFSINATAT  AFIGLSLLLL  SGVLTWDDVL  KEKSAWDTII  WFGALIMMAA
351  FLNKLGLIKW  FSGVLAESVG  GLGVSGTAAG  VILVLAYMYA  HYMFASHTAH
401  ITAMFGAFLA  AAVSLNAPAM  PTALMMAAAS  NIMMTLTHYA  TGTSPVIFGS
451  GYTTMGEWWK  AGFIMSVVNF  LIFSVIGSIW  WKVLGYW*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2847>:

m929.seq

```

1  ATGAAATTGG  GTTTCAAACC  GATACCCCTC  GCCATTGCCG  CAGTATTGTG
51  CGCCCTGGTT  TTGGCACTGC  CCGTACCCGA  CGGGGTCAAG  CCTCAGGCTT
101  GGACGCTGCT  GGCTATGTTT  GTCGGTGTGA  TTGCCGCCAT  TATCGGCAAG
151  GCCATGCCGT  TGGGCGCGCT  GTCGATTATT  GCCGTCGGGT  TGGTCGCAGT
201  AACC CGCGTA  ACCGCCGACA  AACC GGGCGC  GGCGATGAGC  GATGCGTTGA
251  GTGCGTTCGC  CAATCCGTTG  ATTTGGCTGA  TTGCCATCGC  AGTTATGATT
301  TCGCGCGGTT  TGCTCAAAAC  AGGGCTGGGG  ATGCGTATCG  GATATTTGTT
351  TATCGCCGTT  TTTGGAAGAA  AAACGCTGGG  CATCGGTTAC  AGTCTCGCTC
401  TTTCCGAAC  TCTGCTGGCT  CCCGTTACCC  CTTCCAATAC  CGCGCGCGGC

```

1338

```

451 GGC GGC ATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501 CAATCCC GCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTTCGTCGG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCCGTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701 TTATCGCCTT TTTTCGTTATG CCTTTGATTT TATATTTwyT GTATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAAGCTT
951 GCTTTTGCTT TCCGTGTAT TGACTTGGGA CGATGTTTG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTGGCGGA
1101 AAGTGTCGGC GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCGGCGC ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGCGGATG CCGACCGCGC TGATGATGGC GgCCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCCGGTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGGAA GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTGG TGGAAAGTTC
1451 TGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2848; ORF 929>:

```

m929.pep
1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK POAWTLLAMF VGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLA PVTPSNTARG
151 GGIHPIMQS IAGSYGSNPA KGTEGKMKGK LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYXLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTMTGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 929 shows 98.8% identity over a 487 aa overlap with a predicted ORF (ORF 929.ng) from *N. gonorrhoeae*:

g929/m929

	10	20	30	40	50	60
g929.pep	MKLGFKPIPLAIAAVLCALVLALPVPDGVKPOAWTLLAMFVGVIAAIIGKVMPGLALSII					
m929	MKLGFKPIPLAIAAVLCALVLALPVPDGVKPOAWTLLAMFVGVIAAIIGKAMPLGALSII					
	10	20	30	40	50	60
g929.pep	70	80	90	100	110	120
	AVGLVAVTGVTADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIYLFIAV					
m929	AVGLVAVTGVTADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIYLFIAV					
	70	80	90	100	110	120
g929.pep	130	140	150	160	170	180
	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMKGK					
m929	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMKGK					
	130	140	150	160	170	180
g929.pep	190	200	210	220	230	240
	LALVNYHNSPISSAMAITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
m929	LALVNYHNSPISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					

1339

	190	200	210	220	230	240
	250	260	270	280	290	300
g929 . pep	PLILYFLYPPEIKETPNVQFAKDRLSEMGKMSADEIIMAVIFGILLLLWADV PALITGN					
m929	PLILYXLYPPEIKETPNVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
	250	260	270	280	290	300
	310	320	330	340	350	360
g929 . pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKGLIKW					
m929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKGLIKW					
	310	320	330	340	350	360
	370	380	390	400	410	420
g929 . pep	FSGVLAESVGGGLGVSGTAAGVILVLAHYMAHYMFASTTAHI TAMFGAFLAAVSLNAPAM					
m929	FSGVLAESVGGGLGVSGTAAGVILVLAHYMAHYMFASTTAHI TAMFGAFFAAVSLNAPAM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g929 . pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFSVIGSIW					
m929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
g929 . pep	WKVLGYWX					
m929	WKVLGYWX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2849>:

```

a929 . seq
1  ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCTTGTTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCCATGTTT ATCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GCCATGCCGT TGGGTGCGCT GTCGATTATT GCGTCGGGT TGGTCGCAGT
201 AACCGCGCTA ACCGCCGACA AACCGGGTGC GGCGATGAGC GATGCGTTGA
251 TCGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TC CGCGCGTT TGCTCAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
451 GGCGGCATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTGCTCGG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCCGCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701 TTATCGCCTT TTTCGTTATG CCTTTGATTT TATATTTTTT GTATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAG ACCGCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGTT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTTG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTGCGGGA
1101 AAGTGTGCGC GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCCGGCG ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GGCCGCATCT AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCGGTTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTTGG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

1340

This corresponds to the amino acid sequence &lt;SEQ ID 2850; ORF 929.a&gt;:

```

a929.pep
1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF IGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTSPNTARG
151 GGIHHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAHA
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

m929/a929 99.6% identity in 487 aa overlap

```

              10      20      30      40      50      60
m929.pep      MKLGFKPIPLAIAAVLCALVLALPVPDGVK PQAWTLLAMFVGVIAAIIGKAMPLGALSII
              |
a929           MKLGFKPIPLAIAAVLCALVLALPVPDGVK PQAWTLLAMFIGVIAAIIGKAMPLGALSII
              10      20      30      40      50      60

              70      80      90      100     110     120
m929.pep      AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMISRGLLKTGLGMRI
              |
a929           AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMISRGLLKTGLGMRI
              70      80      90      100     110     120

              130     140     150     160     170     180
m929.pep      FGRKTLGIGYSLALSELLAPVTSPNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY
              |
a929           FGRKTLGIGYSLALSELLAPVTSPNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY
              130     140     150     160     170     180

              190     200     210     220     230     240
m929.pep      LALVNYHNSPISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM
              |
a929           LALVNYHNSPISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM
              190     200     210     220     230     240

              250     260     270     280     290     300
m929.pep      PLILYXLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADVPA
              |
a929           PLILYFLYPP EIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADVPA
              250     260     270     280     290     300

              310     320     330     340     350     360
m929.pep      HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW
              |
a929           HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW
              310     320     330     340     350     360

              370     380     390     400     410     420
m929.pep      FSGVLAESVGGLGVSGTAAGVILVLAYMYAHYMFASSTAHAITAMFGAFFAAVSLNAPAM
              |
a929           FSGVLAESVGGLGVSGTAAGVILVLAYMYAHYMFASSTAHAITAMFGAFFAAVSLNAPAM
              370     380     390     400     410     420

              430     440     450     460     470     480
m929.pep      PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW
              |
a929           PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW
              430     440     450     460     470     480

m929.pep      WKVLGYW
              |

```

1341

a929 WKVLGYWX

g930.seq not found yet  
g930.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2851>:

m930.seq

```

1  ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTT TGCCATTAAC GAATGGGTGT TGGGAAGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAgTGG aAGCTTCAAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2852; ORF 930>:

m930.pep

```

1  MKLPLSYLPN IRFLSWCCLL AGIIPATLL ASPNP AEIRM QQDIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EWLVEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGSFN *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2853>:

g930-1.seq (partial)

```

1  GGCAAGTGTC TGCATGCGGG CGACATTAAT CAAATCATGT CCTTAGCACA
51  AAATGCTTTG ATCGGCAGGG GATATACCAC GACCCGTATC TTGGCTGCGC
101 CACAGGATTG GAATAGTGGC AAGCTTCAAT TAACCCGTAT ACCGGGTAT
151 CTGCGCTCCA TACGAATCGA TCGGTCCAAC GATGATCAAA CCCATGCAGG
201 ACGTATTGCA GCATTCCAAA ACAAAATTTCC CACCCGCTCG AACGATCTGT
251 TGAATCTGGC TGATTGGAA CAAGGACTGG AAAATCTCAA ATGTCTCCCG
301 ACTGCGGAAG CCGATCTCCA AATCGTTCCC GTAGAGAGAG AACCAAACCA
351 AAGTGATGTC GTGGTGCAAT GGCGGTAACG TCTGCTGCCC TACTGTGTGA
401 GTGTGGGGAT GGATAATTCG GGTAGTGAGG CGACAGGAAA ATACCAAGGA
451 AATATCACTT TCTCTGCCGA CAATCCTTTT GGACTGAGTG ATATGTTCTA
501 TGTAATTATG GGACGTTCAA TTGGCGGTAC GCCCGATGAG GAAAATTTTG
551 ACGGCCATCG CAAAGAAGGC GGATCAAACA ATTACGCCGT ACATTATTCA
601 GCCCCTTTTC GTAAATGGAC ATGGGCATTG AATCACAATG GCTACCGTTA
651 CCATCAGGCG GTTTCGGGAT TATCGGAAGT CTATGACTAT AATGGAAAAA
701 GTTACAACAC TGATTTCGGC TTCAACCGCC TGTGTATCG TGATGCCAAA
751 CGCAAAACCT ATCTCAGTGT AAAACTGTGG ACGAGGGAAA CAAAAAGTTA
801 CATTGATGAT GCCGAAGTGA CTGTACAACG GCGTAAAACC ACAGGTTGGT
851 TGGCAGAACT TTCCACAAA GGATATATCG GTCGCAGTAC GGCAGATTTT
901 AAGTTGAAAT ATAAACACGG CACCGCATG AAAGATGCTC TGCGCGCGCC
951 TGAAGAAGCC TTTGGCGAAG GCACGTCACG TATGAAAATT TGGACGGCAT
1001 CGGCTGATGT AAATACTCCT TTTCAAATCG GTAAACAGCT ATTTGCCTAT
1051 GACACATCCG TTCATGCACA ATGGAACAAA ACCCCGCTAA CATCGCAAGA
1101 CAAACTGGCT ATCGGCGGAC ACCACACCGT ACGTGGCTTC GACGGTGAAA
1151 TGAGTTTGCC TGCCGAGCGG GGATGGTATT GGCGCAACGA TTTGAGCTGG
1201 CAATTAAAC CAGGCCATCA GCTTTATCTT GGGGCTGATG TAGGACATGT
1251 TTCAGGACAA TCCGCCAAAT GGTTATCGGG CCAAACTCTA GCCGGCACAG
1301 CAATTGGGAT ACGCGGGCAG ATAAAGCTTG GCGGCAACCT GCATTACGAT
1351 ATATTTACCG GCCGTGCATT GAAAAAGCCC GAATATTTTC AGACGAAGAA
1401 ATGGGTAACG GGGTTTCAGG TGGGTTATTC GTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2854; ORF 930-1.ng>:

g930-1.pep (partial)

```

1  GKCLHAGDIN QIMSLAQNAL IGRGYTTTRI LAAPQDLNSG KLQTLMPGY
51  LRSIRIDRSN DDOTHAGRIA AFQNKFPTRS NDLLNLRDLE QGLENLKCLP
101 TAEADLQIVP VEREPNQSDV VVQWR*RLLP YCVSVGMDNS GSEATGKYQG
151 NITFSADNPF GLSDMFYVNY GRSIGGTPDE ENFDGHRKEG GSNNYAVHYS
201 APFGKWTWAF NHNGYRYHQA VSGLSEVYDY NGKSYNTDFG FNRLLYRDAK
251 RKTYLSVKLW TRETKSYIDD AELTVQRRKT TGWLAELSHK GYIGRSTADF
301 KLKYKHGTGM KDALRAPEEA FEGGTSRMKI WTASADVNTF FQIGKQLFAY
351 DTSVHAQWNK TPLTSQDKLA IGGHHTVRGI DGEMSLPAER GWYWRNDLSW
401 QFKPGHQLYL GADVGHVSGQ SAKWLSGQTL AGTAIGIRGQ IKLGGNLHYD

```



1342

451 IFTGRALKKP EYFQTKKVV T GFQVGYSF\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2855>:

m930-1.seq

```

1   ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTC TGCCATTAAC GAAGTGGTGT TGGAAAGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAGTGG CAAGCTTCAA TTAACCTGTA TACCGAGCTA
501 TCTGCGCTCC ATACGAATCG ATCGGTCTAA CGATGATCAA ACCCATGCAG
551 GACGTATTGC AGCATTCCAG AACAAATTC CCACCCGCTC GAACGATCTG
601 TTGAATCTGC GTGATTTGGA ACAAGGACTG GAAAATCTCA AACGCTCTCC
651 GACTGCGGAA GCCGATCTCC AAATCGTTCC CGTAGAGGGA GAACCAAACC
701 AAAGTGATGT CGTGGTGCAA TGGCGGCAAC GTCTGCTGCC CTACCGTGTG
751 AGTGTGGGGA TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG
801 AAATATCACT TTCTCTGCCG ACAATCCTTT GGGACTGAGT GATATGTTCT
851 ATGTAAATTA TGGACGTCG ATTGGCGGTA CGCCCGATGA GGAAAGTTTT
901 GACGGCCATC GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC
951 AGCCCTTTTC GTTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT
1001 ACCATCAGGC AGTTTCCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA
1051 AGTTACAATA CTGATTTCCG CTTCAACCGC CTGTTGTATC GTGATGCCAA
1101 ACGCAAAACC TATCTCGGTG TAAAACTGTG GATGAGGGAA ACAAAAAGTT
1151 ACATTGATGA TGCCGAACG ACTGTACAAC GCGGTAAAAC TGCGGGTTGG
1201 TTGGCAGAAC TTTCCACAA AGAATATATC GGTCGCAGTA CGGCAGATTT
1251 TAAGTTGAAA TATAAACGCG GCACCGGCAT GAAAGATGCT CTGCGCGCGC
1301 CTGAAGAAGC CTTTGGCGAA GGCACGTCAC GTATGAAAAT TTGGACGGCA
1351 TCGGCTGATG TAAATACTCC TTTTCAAATC GGTAAACAGC TATTTGCCTA
1401 TGACACATCC GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG
1451 ACAAACCTGG TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA
1501 ATGAGTTTGT CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG
1551 GCAATTTAAA CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG
1601 TTTCAGGACA ATCCGCCAAA TGGTTATCGG GCCAAACTCT AGTCGGCACA
1651 GCAATTGGGA TACGCGGGCA GATAAAGCTT GCGGCAACG TGCATTACGA
1701 TATATTTACC GCGCGCGCAT TGAAAAAGCC CGAATTTTTC CAATCAAGGA
1751 AATGGGCAAG CGGTTTTCAG GTAGGCTATA CGTTTTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2856; ORF 930-1&gt;:

m930-1.pep

```

1   MKLPLSYLPN IRLSWCCLL AGIIAPATLL ASPNPAEIRM QQDIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EVVLEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGKLQ LTLIPSYLRS IRIIDRSNDDQ THAGRIAAFQ NKFPTRSNDL
201 LNLRLDLEQL ENLKLRLPTAE ADLQIVPVEG EPNQSDVVVQ WRQRLPYRV
251 SVGMDSNGSE ATGKYQGNIT FSADNPLGLS DMFYVNYGRS IGGTPDEESF
301 DGHRKEGGSN NYAVHYSAPF GKWTWAFNHN GYRYHQA VSG LSEVYDYNK
351 SYNTDFGFNR LLYRDAKRKT YLGVKLWMRE TKS YIDDAEL TVQRRKTAGW
401 LAELSHKEYI GRSTADFKLK YKRGTMKDA LRAPEEAFGE GTSRMKIWTA
451 SADVNTPFQI GKQLFAYDTS VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE
501 MSLSAERGWY WRNDLSWQFK PGHQLYLGAD VGHVSGQSAK WLSGQTLVGT
551 AIGIRGQIKL GGNLHYDIFT GRALKKPEFF QSRKWASGFQ VGYTF*

```

m930-1/g930-1 95.4% identity in 478 aa overlap

	90	100	110	120	130	140
m930-1.pep	AINEVVLEGEH	HARFQFALKRAL	RETGFQAGKCL	LHAGNINQIM	SLAQNALIGR	GYTTTRII
g930-1.pep				:		
				GKCLHAGDINQIM	SLAQNALIGR	GYTTTRII
				10	20	30
	150	160	170	180	190	200
m930-1.pep	LAAPQDLNSGKL	QTLTIPSYLRS	IRIIDRSNDDQ	THAGRIAAFQ	NKFPTRSN	DLNLRDLE
g930-1.pep	:					
	LAAPQDLNSGKL	QTLTIPSYLRS	IRIIDRSNDDQ	THAGRIAAFQ	NKFPTRSN	DLNLRDLE
	40	50	60	70	80	90
	210	220	230	240	250	260
m930-1.pep	QGLENLKRLPTA	EADLQIVPVEG	EPNQSDVVVQ	WRQRLPYRV	SVGMDSNGSE	ATGKYQG

[illegible]

a930-1.pep not yet found

```
g931.seq
1  ATGAAACCCA AATTCAAAC CGTTTTAAAC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAG CCGCGTCCTT CATGGAACCC GATATGGGCA
101 ATATCGGTTT GGTTTTGAC  AATCCAAAG CATTCCAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACAACACGA TTTTCCACCG
201 CGTcatCGGC GGCTTCGTCA TCCAAGGCGA CGGATTGACC GAGGACTTGG
251 TGCAAAAGGC AACCGATAAG GCCGTTGCCA ACGAATCCGG caacgGCTTG
301 AAAAAACCCG TCGGCACCAT CGCAATGGCG CGGACGGCAG CCCCCGATTG
351 CGCCGCGGCC CAATTCTTTA TCAATCTGGC GGACAACGGT TCGCTCGACT
401 ACAAAAACGG ACAATACGGC TACACCGTTT TCGGCAGGGT AGAAAGCGGA
451 ATGGACACCG TTTCCAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTTGTCTG
551 GGCAGTAACA GCAGACAGA  CGTTCAGACG GCGTCGCCCC TTTCCAAAAA
601 AACGCCGTTT AA
```

g931.pep

1	<u>MKP</u> KFKTVLT	<u>ALL</u> VLVSLPS	<u>MA</u> ATRVLMET	DMGNIRLVLD	ESKASKTVAN
51	FVRYARKGFY	DNTIFHRVIG	GFVIQDGDLT	EDLVQKATDK	AVANESGNGL
101	KNTVGTIAMA	RTAAPDSAAA	QFFINLADNG	SLDYKNGQYG	YTVFGRVESG
151	MDTVSKIARV	KTATRGFYQN	VVPQPVKIRR	VVVGQ*	

1	ATGAAACCCA	AATTCAAAAC	CGTTTTAACC	GCGTGCTTT	TGGCGGTTTC
51	CCTGCCGTCT	ATGGCGGCAA	CCCATGTTT	GATGAAACC	GATATGGGCA
101	ATATCCGTT	GGTTTTGAC	GAATCCAAAG	CCCCCAAAAC	CGTTGCTAAT
151	TTCGTGCCT	ATGCCCCGAA	AGGCTTTAC	GACGACACCG	TTTTTACCCG
201	CGTTATCGAC	GGTTTTGTTA	TCCAGGCGCG	TGGATTGAC	GAGGACTTGG
251	CACAAAAGGC	AAGCGATAAG	CGCGTTGCCA	ACGAATCCGG	CAACGGCTTG
301	AAAAACACCG	CCGGCACCAT	CGCCATGGCG	CGGACGACAG	CCCCCGATTG
351	CGCCACCAGC	CAATTCTTTA	TCAATCTGGC	GGACCA . kCT	TCGTCGACT
401	ACAAAACCG	ACAATACGCG	TATACCGTTT	TCGGCAGGGT	CGAAAGCGGC
451	ATGAACACCC	TTTCCAAAAT	CGCCC GCGTC	AAAACCGCCA	CGCGCGGCTT
501	TTATCAAAAC	GTACCCGTAC	AGCCC GTCAA	AATCCGTCG	GTTGTTGTCTG
551	GGCAGTAA				

m931.pap..

```

1  MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
51  FVRYARKGPFY DDTVFHRVID GFVIQGGGLT EDLAQKASDK AVANESGNGL
101 KNTAGTIAMA RTTAPDSATS QFFINLADXX SLDYKNGQYG YTVFGRVESG
151 MNTVSKIARV KTATRGEFYON VPVQPVKIRR VVVGQ*

```

Homology with a predicted ORF from *N.gonorrhoeae*

q931/m931

		10	20	30	40	50	60
g931.pep		MKPKFKTVLTALLAVSLPSMAATRVL	METDMGNIRLVL	DESKASKTVANFVRYARKGFY			
m931		MKPKFKTVLTALLAVSLPSMAATHVL	METDMGNIRLVL	DESKAPKTVANFVRYARKGFY			
		10	20	30	40	50	60
		70	80	90	100	110	120
g931.pep		DNTIFHRVIGGFVIQ	GDGLTEDLVQKATDKAVANESGNGLKNT	VGTIAMARTAAPDSAAA			
		:   :					
m931		DDTVFHRVIDGFVIQ	GGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS				
		70	80	90	100	110	120
		130	140	150	160	170	180
g931.pep		QFFINLADNGSLDYKNGQYGYTVFGRV	ESGMDTVSKIARVKTATRGFYQNPVPQPVKIRR				
m931		QFFINLADXXSLDYKNGQYGYTVFGRV	ESGMNTVSKIARVKTATRGFYQNPVPQPVKIRR				
		130	140	150	160	170	180
g931.pep		VVVGQX					
m931		VVVGQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2861>:

1	ATGAAACCCA	AATTCAAAAC	CGTTTTAACC	GCGCTGCTTT	TGGCGGTTTC
51	CCTGCGTCT	ATGGCGCAA	CCCATGTTT	GATGAAACC	GATATGGGCA
101	ATATCCGTTT	GGTTTTGGAC	GAATCCAAAT	CACCCAAAAC	CTTTGCCAAT
151	TTCTGCGCT	ATGCCGAAA	AGGCTTTTAC	GACAAATCGA	TTTTTACCCG
201	CGTCATCGGC	GGCTTCGTTA	TCCAAGGCGG	CGGATTGACC	GAGGACTTGG
251	CACAAAAGGC	AAGCGATAAG	GCCGTTGCCA	ACGAATCCGG	CAACGGCTTG
301	AAAAACACTG	TCGGACCAAT	CGCCATGGCG	CGGACGGCCG	ATCCGGATTTC
351	CGCCACCACG	CAATTCTTTA	TCAATCTGGT	GGACAATGAT	TCGCTCAACT
401	ACAAAAACGG	ACAATACGGC	TATACCGTTT	TCGCGAGGGT	CGAAAGCGGG

1345

451 ATGAACACCG TTTCCAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT  
 501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG  
 551 GGCAGTAA

This corresponds to the amino acid sequence <SEQ ID 2862; ORF 931.a>:

a931.pep  
 1 MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN  
 51 FVRYARKGFY DNTIFHRVIG GFVIQGGGLT EDLAQKASDK AVANESGNGL  
 101 KNTVGTIAMA RTADPDSATS QFFINLVDND SLNYKNGQYG YTVFGRVESG  
 151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ\*

m931/a931 94.6% identity in 185 aa overlap

	10	20	30	40	50	60
m931.pep	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
a931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m931.pep	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
a931	DNTIFHRVIGGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTVGTIAMARTADPDSATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m931.pep	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR					
a931	QFFINLVDNDSLNYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR					
	130	140	150	160	170	180
m931.pep	VVVGQX					
a931	VVVGQX					

g932.seq not found yet

g932.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2863>:

m932.seq  
 1 ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC  
 51 GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCCGTCA TTTTGGGAAT  
 101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCATTGAC  
 151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG  
 201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA  
 251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAACAAA  
 301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAATGA

This corresponds to the amino acid sequence <SEQ ID 2864; ORF 932>:

m932.pep  
 1 MKYIVSISLA MGLAACSFEGG FKPNPWDAAS FWELKNYANP YPGSASAALD  
 51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDYPENK  
 101 KYEWPREEGK TK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 932 shows \_\_\_% identity over a \_\_\_ aa overlap with a predicted ORF (ORF 932.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2865>:

g934.seq  
 1 ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCT CACTCACCGC

q934 . pep

```

1  MKKIIASALI ATFALTACQD DTQARLERQQ KQIEALQQQL AQQADDTVYQ
51  LTPEAVKDTI PAQAQANGNN GQPVTKGKRA AVYLRPIDRK LAAAKPDWRG
101 GRRVYRQAG KQIHDTGQPR QPRRPSRACC LPSVRTPQCA HQQGFHAQPF
151 PCKTITGGAGA ALPPDNAPR QLPSPRYARF RQKAVNPARQ CRLKGFQTAF
201 LYLILGALLCC RLIFRRHFVS KRLMSGWF*

```

m934.seq (partial)

```

seq (pair1)
1      . . CCGGCTCGAAC AGCAGCAGAA ACAGATTGAA GCCCTGCAAC AGCAGCTCGC
51     ACAGCAGGCA GACGATACGG TTTACCAACT GACTCCCGAA GCAGTCAAAG
101    ACACCATTC C TGCCGGAAGCA CAGGCAAACG GCAACCAACg GCAACCCGTT
151    ACCGGTAA . A CAGGGCAGC AGTATTTTA CGACCAATCG ACAGAGAAGT
201    GGCTGCTGCA AAGCCTGGTC GGC GCGCGCGG CAGGCGCGTT TATCGGCAAC
251    GCGCTGGCAA ACAAATTCAC ACGGGCAGC AACCAAGACA GTCCCGTCGC
301    CCGGCGCGCG CGTGACAGCT ACCATCAGTC CGCACGCCCC AATGCGCGCA
351    yCAGCAGGGA TTTGAACACG CGCAGCTCC GTGCAAAAACA ACAGGCGCGG
401    CAkGCGCAGC GTTACCGCCC GACAACGCGC CCGsCCGsCA ATTACCGCGG
451    CCCCCTATG CGCGGTTTCG GCAGGAGCG GTAAACCCGG CGCGCCAATG
501    CCGTCTGAAG AGCTTTTACA CGGCATTThT GCATTGTGTA GGGACATTGT
551    TATGTTGCCG TTTGATTTC AGACGGCATT TTGTTTCCA GCGTTTGATG
601    TCGGGATGGC AATTCTGA

```

m934.pep (partial)

```

1      RLEQQQKQIE ALQQQLAQQA DDTVYQLTPE AVKDTIPAEA QANGNNGQPV
51     TGXRRAAVYL RPIDRKLAAA KPGRRGRRRV YRQRAGKQIH TGRQPROSRR
101    PARACSLFSV RTPQCAHQQG FEHAQPPCKT TGGAXAALPP DNAPXRQLPP
151    PRYARFQREA VNPARQCRLK SFQTAFXHLL GTLLCCRLIF RRHFVSKRLM
201    SGWQF*

```

Homology with a predicted ORF from *N.gonorrhoeae*

from *N. gonorrhoeae*:

m934/g934

[illegible]

```
m934.pep      QSRRPARACSLPSVRTPQCAHQGFHAQPCKTTGGAXAALPPDNAPXRQLPPPRYARF  
                |||::|||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
g934          QPRRPSRACLPSVRTPQCAHQGFHAQPCKTTGGAGAALPPDNAPARQLPPSRYARF  
               130       140       150       160       170       180  
  
              160        170         180          190           200  
m934.pep      RQEAVNPARQCRLKSFQTAFXHLGLTLLCCRLIFRRHFVSKRLMSGWQFX  
                |||:|||||:|||:|||||:|||||:|||||:|||||:|||||:|||||:  
g934          RQKAVNPARQCRLKGFQTAFLYLLGALLCCRLIFRRHFVSKRLMSGWQFX  
               190        200        210        220        230
```

```
a934.seq
1  ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCG CACTCGCCGC
51  CTGCCAAGAC GACGCGCAGG CGCGGCTCGA ACAGCAGCAG AAACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCGAAG CACAGGCAAA
201 CGGCAACAAC GGGCAACCCG TTACCGG.TA AAGACGGGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGG TCGGCGCGCG
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTG ACACGGGCGA
351 GCAACCAAGA CAGTCCCGTC GCCCGGCGCG CGCGTGCCGC TACCATCAG
401 TCCGCACATC CCAATGCGCG CACCAGCAGG GATTTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
501 GCCCGCCCGC CAATTACCGC CGCCCCGCCA TGC CGCGGTTT CGGCAGAAGG
551 CGGTA AATTC GGC GTGCCAA TGCCGTCTGA AGGGCTTTCA GACGGCATTG
601 TTGTATTTGT TAGGGACATT GTTATGTTGC CGTTTGATTT TTAGACGGCA
651 TTTTGTTTCC AAGAGTTTGA TGTCGGGATG GCAATTCTGA
```

a934.pep

1	<u>MKKIIASALI</u>	<u>ATFALAACQD</u>	DAQARLEQQQ	KQIEALQQQL	AQQADDTVYQ
51	LTPEAVKDTI	PAEAQANGNN	GQPVTX*RR	AVYLRPIDRK	LAAAKPGRRG
101	GRRVYRQAG	KQIHTGRQP	QSRPARACR	LPSVRTSQCA	HQQGFHAQP
151	PCKTTGGAGA	ALPPDNAPAR	QLPPRHARF	RQKAVNPACQ	CRLKGFQTAF
201	LYLLGTLLCC	RLIFRRHFVS	KSLMSGWQF*		

```

m934.pep      10      20      30
               RLEQQQKQIEALQQQLAQQAADDTVYQLTPEAVKDTI
               |||
a934          MKKIIASALIATFALAACQDDAQARLEQQQKQIEALQQQLAQQAADDTVYQLTPEAVKDTI
               10      20      30      40      50      60

               40      50      60      70      80      90
m934.pep      PAEAQANGNNGQPVTGXRRAAVYLRPIDRKLAAAKPGRRGRRVYRQRAGKQIHTGRQPR
               |||
a934          PAEAQANGNNGQPVTXXRRAAVYLRPIDRKLAAAKPGRRGRRVYRQRAGKQIHTGRQPR
               70      80      90      100     110     120

               100     110     120     130     140     150
m934.pep      QSRRPARACSLPSVRTPQCAHQGGFEHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF
               |||
a934          QSRRPARACRLPSVRTSQCAHQGGFEHAQPPCKTTGGAGAALPPDNAPARQLPPPRHARF
               130     140     150     160     170     180

               160     170     180     190     200
m934.pep      RQEAVNPARQCRLKSFQTAFXHLGLTLLCCRLIFRRHFVSKRLMSGWQFX
               |||
a934          RQKAVNPACQCRLKGFQTAFLYLLGLTLLCCRLIFRRHFVSKSLMSGWQFX
               190     200     210     220     230

```

q935.seq not found yet

1348

g935.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2871>:

m935.seq

```

1  ATGTTGTATT TCAGATACGG CTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGAGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCAGATTGG
151 AAAGTTGAAA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGCG CGACGCGCTC AACGGCAATC
251 AGGCGGATTT AATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAGTG CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCGGAGG CGGCAAAATT
501 GGATTTGCCG GCACCGGTTT TGGAAAATGT GGGGCGTTTT CGGAAAAAAA
551 CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC
601 AATAGAAATG CCAATAATGC CGCGCCGCAA TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCGGGCGGCA GGGTTGAATT
701 ATGAAATCGA GCGGAAAAAG CTGACGCCGT TGGCAGATAA TCATTATTTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCA GTAAAAAATC
801 AGCTTATGAT GACGGGTTCG GCAGGGCGTA TTTGGGTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCTG
901 GGCAGCGACG GCTTTGATGC GAAAAACAAA CGGGTAAACA ACCGCCGCTT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGCTG TCCCATACTT
1001 ACCGCCCAAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GCAGGCAGGA
1101 CGGGTTTTAT GTTTCGTCTG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GGCAGCGTCA ATAATGCCGC CTACCGGCGC AACGGTGTTT ATGCCGGTTG
1251 GGCAGCAGAG TGGCGGCAGT TGGCGGTTT GAACAGTCGG GTTCCGCTG
1301 CTTATGCCCG CCGCAACTAT AAGGGCATTG CGGCTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CGGCGTTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCTG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID.2872; ORF 935&gt;:

m935.pep

```

1  MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51  KVENDAPRVV DGDFLLAHPK MLEHSLRDAL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVERYREL HGENAADERI LLDLAAAEFD
151 DFRLKSAERH FAEAAKL DLP APVLENVGRF RKKTEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTPLADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDATK RVNNRRLPPY MLAGHVGVLQ SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAE WRQLGGLNSR VSASYARRNY KGIAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPYA KRRNSEVFVS
501 ADWRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2873>:

a935.seq

```

1  ATGTTGTATT TCAGATACGG TTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGAGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCGGATTGG
151 AAAGTTGACA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGCG CGACGTGCTC AACGGCAATC
251 AGGCGGATTT GATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAGTG CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCCGAGG CGGAAAAAAT
501 GGATTTGCCG GCGCCGTTTT TGGAAAATGT GGGGCGTTTT CGGAAAAAAG
551 CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC

```

1349

```

601 AATAGAAATG CCAATAATGC CGCGCCGCAG TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCGGGCGGCA GGCTTGAATT
701 ATGAAATCGA GGCGGAAAAA CTGACGGCGT TGGCAGATAA TCATTATTTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCA GTAAAAAATC
801 AGCTTATGAC GACGGGTTCG GCAGAGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCTG
901 GGCAGCGACG GCTTTGATGC GAAAACAAA CGGGTAAACA ACCGCCGCCT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGTTG TCCCATACTT
1001 ACCGCCCCAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GTCGGCAGGA
1101 CGGGTTTTAT GTTTCGTCGG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GGCGCGGTCA ATAATGCCGC CTACCGGCGC AACGGTGTTT ATGCCGGCTG
1251 GGCGCAGGAG TGGCGGCACT TGGGCGGTTT GAACAGTCGG GTTCCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCGTTG CGGCTTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CCGCGTTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCTG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2874; ORF 935.a>:

a935.pep

```

1 MLYFRYGFV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51 KVDNDAPRVV DGDFLLAHPK MLEHSLRDVL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRKLSAERH FAEAEKLDLP APVLENVGRF RKKAEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTALADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDATK RVNNRRLPPY MLAGHGVGVQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAE WRQLGGLNSR VSASYARRNY KGVAEFSTE
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPIYA KRRNSEVFVS
501 ADWRF*

```

m935/a935 98.8% identity in 505 aa overlap

	10	20	30	40	50	60
m935.pep	MLYFRYGFV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW KVDNDAPRVV					
a935	MLYFRYGFV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW KVDNDAPRVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m935.pep	DGDFLLAHPK MLEHSLRDALNGNQADLIAS LADLYAKLPD YDAVLYGRAR ALLAKLAGRP					
a935	DGDFLLAHPK MLEHSLRDALNGNQADLIAS LADLYAKLPD YDAVLYGRAR ALLAKLAGRP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m935.pep	AEAVARYREL HGENAADERI LLDLAAAEFD DFRKLSAERH FAEAEKLDLP APVLENVGRF					
a935	AEAVARYREL HGENAADERI LLDLAAAEFD DFRKLSAERH FAEAEKLDLP APVLENVGRF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m935.pep	RKKTEGLTGW RFSGGISPAV NRNANNAAPQ YCRQNGGRQI CSVSRAERAAGL NYEIEAEK					
a935	RKKAEGLTGW RFSGGISPAV NRNANNAAPQ YCRQNGGRQI CSVSRAERAAGL NYEIEAEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m935.pep	LTPLADNHYL LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS					
a935	LTALADNHYL LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS					
	250	260	270	280	290	300



1350

	310	320	330	340	350	360
m935.pep	GSDGFDAKTKRVNNRRLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
a935	GSDGFDAKTKRVNNRRLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
	310	320	330	340	350	360
	370	380	390	400	410	420
m935.pep	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFVFPKRETVGGAVNNAAYRRNGVYAGWAQE					
a935	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFVFPKRETVGGAVNNAAYRRNGVYAGWAQE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m935.pep	WRQLGGLNSRVASASYARRNYKGIAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
a935	WRQLGGLNSRVASASYARRNYKGIAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
	430	440	450	460	470	480
	490	500				
m935.pep	GRTESNVPYAKRRNSEVFVSADWRFX					
a935	GRTESNVPYAKRRNSEVFVSADWRFX					
	490	500				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2875>:

g936.seq

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51  CCTTGCCCTC GCGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGcgcAACCA CCGgcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCCGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACTTGGA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAccgT CGGCGTACAA AAAGTCATTA CCCTCTACCA AAACCTACGT
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2876; ORF 936.ng>:

g936.pep

```

1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL QGVATEGEKQ
101 FVGQIARSEQ AAEVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2877>:

m936.seq (partial)

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51  CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCCGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCC...

```

This corresponds to the amino acid sequence <SEQ ID 2878; ORF 936>:

m936.pep (partial)

```

1  MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL QGVATEGEKQ
101 FVGQIARSEQ AAEVYNYIT VASLPRTA...

```

Homology with a predicted ORF from *N.gonorrhoeae*

m936/q936

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT					
	:: :     : :     :: :					
g936	MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAKSVIDRRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLQNNTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVNYIT					
	:     :     :     :     :     :     :     :     :     :					
g936	ARSYLQNNTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVNYIT					
	70	80	90	100	110	120
	130					
m936.pep	VASLPRTAXXX					
g936	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAIT					
	130	140	150	160	170	180

a936.seq

1	ATGAAACCCA	AACCGCACAC	CGTCCGCACC	CTGACTGCCG	CCGTCTCAG
51	CCTTGCCCTC	GGCGGTCTGC	TCAGCGCAGT	CGTGGCGCG	GCGCGGCTCG
101	CGCGGAAATC	CGCCGTCGAT	CGCCGAACCA	CCGCGCGCA	AACCGACGAC
151	AACGTAATGG	CGCTCGGTAT	GCAAAACACC	GCCGCTCCT	ATCTGCGCCA
201	AAACAACCAA	ACCAAAGGCT	ACACGCCCCA	AATCTCCGTT	GTCGGCTACA
251	ACCGCCACCT	GCTGCTGCTC	GGACAAGTCG	CCACGGAAG	CGAGAAACAG
301	TTCGTGCGTC	AGATTGCACG	TTCCGAACAG	GCCGCCGAAG	GCGTGTACAA
351	CTACATTACC	GTCCGCTCCC	TGCCCGGCAC	TGCCGGCGAC	ATCCGCGGCG
401	ACACTTTGGA	CACATCCAAA	GTCCGCGCCA	CGCTGTTGGG	CATCAGCCCC
451	GCCACACAGG	CGCGCGTCAA	AATCGTTACC	TACGGCAACG	TAACCTACGT
501	TATGGGCATC	CTACCCCCG	AAGAACAGGC	GCAGATTACC	CAAAAAGTCA
551	GCAACCACGT	CGGCGTACAA	AAAGTCATCA	CCCTTACCA	AAACTACGTC
601	CAACCTGTA				

a936.pgp

1	MKPKPHTVRT	<u>LTA</u> AVLSLAL	GGCVSAVVGG	AAVGAksAVD	RRTTGAQTDD
51	NVMALRIETT	ARSYL <u>RQ</u> NNQ	TKGYTPQISV	VGYNRHLLLL	GQVATEGEKQ
101	FVGQIARSEQ	AAEGVYNYIT	VASLPRTAGD	IAGDTWNTSK	VRATLLGISP
151	ATQARVKIVT	YGNVTYVMGI	LTPEEQAQIT	QKVSTTVGVQ	KVITLYQNYV
201	OR*				

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT					
		::   :	:			
a936	MKPKPHTVRTLTAAVLSLALGGCVSAVVGGAAVGAKSAVDRRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLQRNNQTKGYTPQISVVGYNRHLALLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
a936	ARSYLQRNNQTKGYTPQISVVGYNRHLALLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
m936.pep	VASLPRTA					

1352

a936                    |||||  
 VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT  
                       130                140                150                160                170                180

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2881>:

## g936-1.seq

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51 CCTTGCCCTC GCGGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGccgAACCA CCGgcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCCGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACCTGGAA CACGTCCAAA GTCCGCGCca cgCTGTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAcggT CGGCGTACAA AAAGTCATTA CCCTCTACCA AAACCTACGTC
601 CAACGCTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2882; ORF 936-1.ng>:

## g936-1.pep

```

1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2883>:

## m936-1.seq

```

1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51 CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC GCCTGTCGAC CGCCGAACCA CCGCGCGGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCCGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACACCTGGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAACCGT CGGCGTACAA AAAGTCATCA CCCTCTACCA AAACCTACGTC
601 CAACGCTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2884; ORF 936-1>:

## m936-1.pep

```

1  MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIV YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*
  
```

m936-1/g936-1      95.5% identity in 202 aa overlap

	10	20	30	40	50	60
m936-1.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGA	SAVDRRTTGAQTDDNV	MALRIETT			
g936-1	MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGA	KSVIDRRTTGAQTDDNV	MALRIETT			
	10	20	30	40	50	60
m936-1.pep	ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
g936-1	ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
m936-1.pep	ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
g936-1	ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
m936-1.pep	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT					
g936-1	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT					

1353

```

g936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              130      140      150      160      170      180

              190      200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
g936-1      QKVSTTVGVQKVITLYQNYVQRX
              190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2885>:

```

a936-1.seq
1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGACTGCCG CCGTCCTCAG
51 CCTTGCCCTC GCGGCTGCG TCAGCGCAGT CGTCGGCGGC GCGGCGGTCTG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTAATGG CGCTGCGTAT CGAAACCACC GCCCGCTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCAA AATCTCCGTT GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAAGTC CCACCGAAGG CGAGAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACACTTGGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCGTC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACGTC CGGCGTACAA AAAGTCATCA CCCTCTACCA AAACACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2886; ORF 936-1.a>:

```

a936-1.pep
1  MKPKPHTVRT LTA AVLSLAL GGC VSAVVG AAVGAKSAVD RRTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIVT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

a936-1/m936-1 97.0% identity in 202 aa overlap

```

              10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVD RRTGAQTDD NVMALRIETT
              |||||
a936-1      MKPKPHTVRTLTA AVLSLALGGCVSAVVGGA AVGAKSAVD RRTGAQTDD NVMALRIETT
              10      20      30      40      50      60

              70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTKGYTPQISV VGYNRHLLL GQVATEGEKQ FVGQIARSEQAAEGVYNYIT
              |||||
a936-1      ARSYLRQNNQTKGYTPQISV VGYNRHLLL GQVATEGEKQ FVGQIARSEQAAEGVYNYIT
              70      80      90      100     110     120

              130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
              |||||
a936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
              130     140     150     160     170     180

              190     200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
a936-1      QKVSTTVGVQKVITLYQNYVQRX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2887>:

```

g937.seq
1  atGAAAAATA TTCTCTAgT ATTTGTTAGC TTTGTGCCAT TATGTGTCCG
51 CACTGATCTG CCGCTGAata tCGAAGACAT AATGaccgAC AAGGGAAAAT
101 GGAAactGGA AACTTccctt acctacctgA acaGCGAAAA cagCCGCGCC
151 GCACTTGCCT CACCGGTTTA CATTcAGACC GGCTCCGCTT CCTTTATCCC
201 CGTCCCgACC GAAATTCAGG AAAACGGCAG CAATACCGAT ATGCTCGCCG
251 GCACGCTCGG TTTGCGCTAC GGACTGAccg GCAataccgA CATTTACGGC
301 AGCGGCAGCT ATCTGTGGCA CGAAGAACGC AAACTCGacg GCAACGGCAA

```

1354

```

351  AACCCGCAAC  AAACGGATGT  CCGACATATC  CGCCGGCATC  AGCCACACCT
401  TCCTtaAAGA  cgGCAAAAAT  CCCGCACTCA  TCGCTTTCCT  CGAAAGCAGC
451  GTTTACGAAA  AATCGCGCAA  CAAAGCCTCG  TCGGGAAAAT  CGTGGCTCAT
501  CGGCGCCACC  ACCTACAAAG  CCATAGATCC  GATTGTCCTT  TCCCTCACCG
551  CCGCCTACCG  CATCAACGGC  AGCAAAACCC  TTTGAGACGA  CGTCAAATAC
601  AAAGCAGGCA  ATTACTGGAT  GCTGAATCCC  AACATCTCAT  TTGCCGCCAA
651  CGACAGAATC  AGCCTGACCG  GAGGCATCCA  ATGGCTGGGC  AAACAGCCCC
701  ACCGCATAGA  CGGCAAAAAA  GAATCCGCAA  GAAACACATC  CACCTACGCC
751  CATTTCCGCG  CAGGTTTCGG  TTTCAACCAA  ACCGCGGCTT  TAAACGCATC
801  CGCAGCTTTC  AACGTTTCAG  GGCAAAGCAG  TTCCGAAGTG  AAATTGGGCG
851  TACAGCATAC  ATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2888; ORF 937.ng>:

g937.pep

```

1  MKNILLVFVS  FVPLCVRTDL  PLNIEDIMTD  KGKWKLETS  TYLNSENSRA
51  ALASPVYIQ  GSASFIPVPT  EIQENGSTND  MLAGTLGLRY  GLTGNTDIYG
101  SGSYLWHEER  KLDGNGKTRN  KRMSDISAGI  SHTFLKDGKN  PALIAFLEST
151  VYEKSRNKAS  SGKSWLIGAT  TYKAIDPIVL  SLTAAYRING  SKTLSDDVKY
201  KAGNYWMLNP  NISFAANDRI  SLTGGIQWL  KQPDRIKGG  ESARNTSTYA
251  HFGAGFGFTK  TAALNASARF  NVSGQSSSEL  KLGVQHTF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2889>:

m937.seq

```

1  ATGAAGCGCA  TCTTTTGCC  CGCCTTGCCC  GCCATCCTGC  CTTTATCCAC
51  TTATGCCGAC  CTGCCCTTGA  CGATTGAAGA  CATAATGACC  GACAAGGGAA
101  AATGGAAACT  GGAACTTCC  CTTACCTACC  TGAACAGCGA  AAACAACCGC
151  GCCGAACCTT  GCGCACCGET  TTACATTCAA  ACCGGCGCAA  CCTCGTTTAT
201  CCCCATTCCG  ACCGAAATCC  AAGAAAACGG  CAGCAATACC  GATATGCTCG
251  TCGGCACGCT  CGGTTTGCGC  TACGGACTGA  CCGGGAATAC  CGACATTTAC
301  GGCAGCGGCA  GCTATCTGTG  GCACGAAGAA  CGCAAACCTG  ACGGCAACAG
351  CAAAACCCGC  AACAAACGGA  TGTCCGACGT  ATCCCTCGGC  ATCAGCCACA
401  CTTTCCTTAA  AGACGACAAA  AACCCCGCCC  TAATCAGCTT  TCTTGAAAGC
451  ACGGTTTACG  AAAAATCGCG  CAACAAAGCC  TCGTCGGGAA  AATCCTGGCT
501  CATCGCGGCC  ACCACCTACA  AAGCCATAGA  TCCGATTGTC  CTTTCCCTCA
551  CCGCCGCTTA  CCGCATCAAC  GGCAGCAAAA  CCCTTTCAGA  CGGCATCCGC
601  TACAAATCGG  GCAACTACCT  GCTGCTCAAC  CCCAACATCT  CATTTGCTGC
651  CAACGACAGA  ATCAGCCTGA  CCGGAGGCAT  CCAATGGCTG  GGCAGGCAGC
701  CCGACCGGAC  GGACGGCAAA  CGGGAATCCT  CCAGAAACAC  ATCCACCTAC
751  GCCCATTTTC  GCGCAGGTTT  CGGTTTCACC  AAAACCACGG  CTTTAAACGC
801  ATCCGCACGT  TTCAACGTTT  CAGGGCAAAG  CAGTTCCGAA  CTGAAATTTG
851  GCGTACAGCA  TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2890; ORF 937>:

m937.pep..

```

1  MKRIFLPALP  AILPLSTYAD  LPLTIEDIMT  DKGKWKLETS  LTYLNSENNR
51  AELAAPVYIQ  TGATSFIPIP  TEIQENGSTN  DMLVGTGLRL  YGLTGNTDIY
101  GSGSYLWHEE  RKLDGNSKTR  NKMSDVSLG  ISHTFLKDDK  NPALISFLES
151  TVYEKSRNKA  SSGKSWLIGA  TTYKAIDPIV  LSLTAAYRIN  GSKTLDGIR
201  YKSGNYLLLN  PNISFAANDR  ISLTGGIQL  GRQPDRTDGK  RESSRNTSTY
251  AHFGAGFGFT  KTTALNASAR  FNVSGQSSSE  LKFGVQHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 937 shows 86.9% identity over a 289 aa overlap with a predicted ORF (ORF 937.ng) from *N. gonorrhoeae*:

g937/m937

```

          10      20      30      40      50      59
g937.pep  MKNILL-VFVSFVPLCVRTDLPLNIEDIMTDKGKWKLETS LTYLNSENSRAALASPVYIQ
          || :| :: ::::| : :|||:|||||:|||||:|||||:| :| :| :|
m937      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETS LTYLNSENNRAELAAPVYIQ
          10      20      30      40      50      60
g937.pep  60      70      80      90      100     110     119
          TGSASFIPVPTTEIQENGSTNDMLAGTLGLRYGLTGNTDIY GSGSYLWHEERKLDGNGKTR

```

[illegible]

```
a937.seq
1 ATGAAGCGCA TCTTTTTGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACACCGA AAACAACCGC
151 CCGCAACTTG CGCACCCGGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTTCC ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCACGCT CGGTTTGCGC TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAACTTCG ACGGCAACCG
351 CAAAACCCGA AACAACCGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CCTTCCTTAA AGACGACAAA AACCCTGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCCCTCGTC CTCTCATTTG
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCTTTTCAAG CAACACCAAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCAATATATAT CCTTCGCGCG
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTTC GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTTAA
```

```
a937.pep
1 MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNRR
51 AELAAPVYIQ TGATSFIPIP TEIQENGSTNT DMLVGTGLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPVP LSLTAAYRIN GSKTLLSNTK
201 YKAGNYWMLN PNISFAANDR ISLTGGIQWL GKQPDRLDGK KESARNTSTY
251 AHFGAGGFET KTTALNASAR FNVSGQSSE LKFGVQHTF*
```

	10	20	30	40	50	60
m937.pep	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSEN	NRAELAAPVYIQ				
a937	MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSEN	NRAELAAPVYIQ				
	10	20	30	40	50	60
	70	80	90	100	110	120
m937.pep	TGATSFIPIPTEIQENG	SNTDMLVGTGLGRYGLTGNTDIYSGSYLWHEERKLDGNSKTR				
a937	TGATSFIPIPTEIQENG	SNTDMLVGTGLGRYGLTGNTDIYSGSYLWHEERKLDGNGKTR				
	70	80	90	100	110	120

1356

	130	140	150	160	170	180
m937.pep	NKRMSDVSLSGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a937	NKRMSDVSLSGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m937.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a937	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m937.pep	RESSRNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
a937	KESARNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

g939.seq not found yet

g939.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2893>:

m939.seq (partial)

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCCTCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAATATCGG
201 CATCCGCGAC GTAAACGCAC CC...
```

This corresponds to the amino acid sequence &lt;SEQ ID 2894; ORF 939&gt;:

m939.pep (partial)

```

1  MKRLTLLAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD VNAP...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2895>:

a939.seq

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCATCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACCATCGG
201 CATCCGCGAC GGTAACGCAC CCCACGGTTC GGCAGCTGTG ATGAAACCGG
251 TGGTAATGAA TTTGAGCGAT CAGGATATTT TGAACGTATC CGCATTCTAT
301 GCCAAACAGC AGCCCAAATC CGGTGAAGCC AATCCTAAGG AAAATCCCGA
351 ATTGGGTGCG AAAATCTATC GCGGCGGTTT GAGCGATAAA AAAGTGCCGG
401 CGTGTATGTC CTGCCACGGT CCGAGCGGTG CGGGTATGCC GGGGGGCGGA
451 AGCGAAATTC AGGCTTATCC GCGTTTGGGC GGTCAGCATC AGGCATATAT
501 TGTGTAACAG ATGAATGCCT ACAAGTCCGG TCAGCGTAAA AATACCATCA
551 TGGAAGATAT TGCAAACCGT ATGTCTGAAG AAGATTGAA AGCGGTGCGC
601 AACTTTATCC AAGGTTTGCG TTA
```

This corresponds to the amino acid sequence &lt;SEQ ID 2896; ORF 939.a&gt;:

a939.pep

```

1  MKRLTLLAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD GKRTGSAAV MKPVVMNLSQ QDILNVSAFY
101 AKQPKSGEA NPKENPELGA KIYRGGLSDK KVPACMSCHG PSGAGMPGGG
151 SEIQAYPRLG GQHQAIVEQ MNAYKSGQRK NTIMEDIANR MSEEDLKAVA
201 NFIQGLR*
```

m939/a939 100.0% identity in 70 aa overlap

	10	20	30	40	50	60
m939.pep	MKRLTLLAFVLAAGAVSASPKADVEKGKQVAATVCAACHAADGNSGIAMYPRLAAQHTAY					
a939	MKRLTLLAFVLAAGAVSASPKADVEKGKQVAATVCAACHAADGNSGIAMYPRLAAQHTAY					

1357

```

              10      20      30      40      50      60
              70
m939.pep      IYHQTIGIRDVNAP
              |||||
a939          IYHQTIGIRDGKRTHGSAAVMKPVVMNLSQDILNVSAFYAKQPKSGEANPKENPELGA
              70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2897>:

```

g950.seq
1  ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
51 GGCCGCCCGGC GCCGTTGCTGC CCCACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
251 AAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2898; ORF 950.ng>:

```

g950.pep
1  MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA
101 EGKCGEGKCG SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2899>:

```

m950.seq
1  ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCCGGT GCAGTTGCTGC CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2900; ORF 950>:

```

m950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 950 shows 86.6% identity over a 112 aa overlap with a predicted ORF (ORF 950) from *N. gonorrhoeae*

m950/g950 86.6% identity in 112 aa overlap

```

              10      20      30      40      50
m950.pep      MNKNIAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----
              |||||
g950          MNKNIAALAGALSLSLAAGAVAANKPASNATGVQKSAQSGCASKSAEGSCGASKSAEG
              10      20      30      40      50      60

              60      70      80      90      100
m950.pep      ----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
              |||||
g950          SCGAAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2901>:

```

a950.seq
1  ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCCGGT GCAGTTGCTGC CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```



1358

This corresponds to the amino acid sequence <SEQ ID 2902; ORF 950.a>:

```
a950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 950 shows 100.0% identity over a 102 aa overlap with a predicted ORF (ORF 950) from *N. meningitidis*

```
a950/m950    100.0% identity in 102 aa overlap

              10      20      30      40      50      60
a950.pep      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG
              |||||
m950           MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG
              10      20      30      40      50      60

              70      80      90      100
a950.pep      EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
              |||||
m950           EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
              70      80      90      100
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2903>:

```
g951.seq
1  ATGATTATGT TACCCGCCCG TTCACTATT TTATCTGTCC TCGCAGCAGC
51  CCTGCTTGCC GGACAGGCGT ATGCTGCCCG CGCGGCGGAT GTGGAGCTGC
101 CGAAGGAAGT CGGAAAGGTT TTAAGGAAAC ATCGGCGTTA CAGCGAGGAA
151 GAAATCAAAA ACGAACGCGC ACGGCTTGCG GCAGTGGGCG AACGGGTCAA
201 CAGGGTGTGT ACCTGTGTGG GCGGTGAAAC GGCTTTGCAG AAAGGGCAGG
251 CGGGAACGGC TCTGGCAACC TATATGCTGA TGTGGAACG CACAAAATCC
301 CCCGAAGTCG CCGAACGCGC CTTGGAATG GCCGTGTCGC TGAACGCGTT
351 TGAACAGGCG GAAATGATTT ATCAGAAATG GCGGCAGATC GAGCCTATAC
401 CGGGTGAGGC GCAAAAACGG GCGGGGTGGC TGCAGAACGT ATTGAGGGAA
451 GGGGGAATC AGCATCTGGA CGGGTGGAAG GAGGTGCTGG CGCAATCGGA
501 CGATGTGCAA AAACGCAGGA TATTTTGTCT GCTGGTGCAA GCCGCCGTGC
551 AGCAGGGTGG GGTGGCTCAA AAAGCATCGA AAGCGGTTCC CGGTGCGGCG
601 TTGAAGTATG AACATCTGCC CGAAGCGGCG GTTGCCGATG CGGTGTTCCG
651 CGTACAGGGA CGCGAAAAGG AAAAGGCAAT CGAAGCTTTG CAGCGTTTGG
701 CGAAGCTCGA TACGGAATA TTGCCCCCA CTTAATGAC GTTGCCTCTG
751 ACTGCACGCA AATATCCCGA AATACTCGAC GGCTTTTTCG AGCAGACAGA
801 CACCCAAAAC CTTTCGGCCG TCTGGCAGGA AATGGAAATT ATGAATCTGG
851 TTTCCTGCG TAAGCCGGAT GATGCCTATG CGCGTTTGA CGTGCTGTTG
901 GAACACAACC CGAATGCAAA CCTGTATATT CAGGCGGCGA TATTGGCGGC
951 AAACCGAAAA GAAGTGCGT CCGTTATCGA CGGCTACGCC GAAAAGGCAT
1001 ACGGCAGGGG GACGGGGGAA CAGCGGGGCA GGGCGGCAAT GACGGCGGCG
1051 ATGATATATG CCGACGCGAG GGATTACGCC AAAGTCAGGC AGTGTTGAA
1101 AAAAGTGTCC GCGCCGGAAT ACCTGTTCGA CAAAGGCGTG CTGGCGGCTG
1151 CGGCGGCTGC CGAATTGGAC GGAGGCCGGG CGGCTTTGCG GCAGATCGGC
1201 AGGGTGC GGA AACTTCCCGA ACAGCAGGGG CGGTATTTTA CGGCAGACAA
1251 TTTGTCCAAA ATACAGATGC TCGCCCTGTC GAAGCTGCCC GACAAACGGG
1301 AAGCCCTGAT CGGGCTGAAC AACATCATCG CCAAACTTTC GGCGGCGGGA
1351 AGCACGGAAC CTTTGGCGGA AGCATTGGCA CAGCGTTCCA TTATTTACGA
1401 ACAGTTCGGC AAACGGGGA AAATGATTGC CGACCTTGAA ACCGCGCTCA
1451 AACTTACGCC CGATAATGCA CAAATTATGA ATAATCTGGG CTACAGCCTG
1501 CTTTCCGATT CCAAACGTTT GGACGAGGGT TTCGCCCTGC TTCAGACGGC
1551 ATACCAATC AACC CGGACG ATACCGCCGT TAACGACAGC ATAGGCTGGG
1601 CGTATTACCT GAAAGGCGAC GCGGAAAGCG CGCTGCCGTA TCTGCGGTAT
1651 TCGTTTGAAA ACGACCCCGA GCCCGAAGTT GCCGCCCAT TGGGCGAAGT
1701 GTTGTGGGCA TTGGGCGAAC GCGATCAGGC GGTGACGTA TGGACGAGG
1751 CGGCACACCT TAGGGGAGAC AAGAAAATAT GCGGGGAGAC GCTCAAACGC
1801 TACGGAATCG CCTTGCCCGA GCCTTCCCGA AAACCCCGGA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2904; ORF 951.ng>:

```
g951.pep
1  MIMLPARFTI LSVLAAALLA GQAYAAGAAD VELPKEVGKV LRKHRRYSEE
```

1359

```

51  EIKNERARLA  AVGERVNRVF  TLLGGETALQ  KGQAGTALAT  YMLMLERTKS
101 PEVAERALEM  AVSLNAFEQA  EMIYQKWRQI  EPIPGEAQKR  AGWLRNVLRE
151 GGNQHLDGLE  EVLAQSDDVQ  KRRIFLLLVQ  AAVQQGGVAQ  KASKAVRRRA
201 LKYEHLPEAA  VADAVFGVQG  REKEKAIEAL  QRLAKLDTEI  LPPTLMTLRL
251 TARKYPEILD  GFFEQTDTQN  LSAVWQEMEI  MNLVSLRKP  DAYARLNVLL
301 EHNPNANLYI  QAAILAANRK  EGASVIDGYA  EKAYGRGTGE  QRGRAAMTAA
351 MIYADRRDYA  KVRQWLKKVS  APEYLFDKGV  LAAAAAAELD  GGRAALRQIG
401 RVRKLPQQG  RYFTADNLSK  IQMLALSCLP  DKREALIGLN  NIIAKLSAAG
451 STEPLAEALA  QRSIIYEQFG  KRGMIAADLE  TALKLTPDNA  QIMNNLGYSL
501 LSDSKRLDEG  FALLQTAYQI  NPDDTAVNDS  IGWAYYLGKD  AESALPYLRY
551 SFENDPEPEV  AAHLGEVLWA  LGERDQAVDV  WTQAAHLRGD  KKIWRETLKR
601 YGIALPEPSR  KPRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2905>:

```

m951.seq
1  ATGATTATGT  TACCTAACCG  TTTCAAAATG  TTAAGTGTGT  TGACGGCAAC
51  CTTGATTGCC  GGACAGGTAT  CTGCCGCCGG  AGGCGGTGCG  GGGGATATGA
101 AACAGCCGAA  GGAAGTCGGA  AAGGTTTTC  GAAAGCAGCA  GCGTTACAGC
151 GAGGAAGAAA  TCAAAAACGA  ACGCGCACGG  CTTGCGGCAG  TGGGCGAGCG
201 GGTAAATCAG  ATATTTACGT  TGCTGGGAGG  GGAACCGGCC  TTGCAAAAGG
251 GGCAGGCGGG  AACGGCTCTG  GCAACCTATA  TGCTGATGTT  GGAACGCACA
301 AAATCCCCCG  AAGTCGCCGA  ACGCGCCTTG  GAAATGGCCG  TGTCGCTGAA
351 CGCGTTTGAA  CAGGCGGAAA  TGATTATCA  GAAATGGCCG  CAGATTGAGC
401 CTATACCGGG  TAAGCGCAA  AAACGGGCGG  GGTGGCTGCG  GAACGTGCTG
451 AGGGAAAGAG  GAAATCAGCA  TCTGGACGGA  CTGGAAGAAG  TGCTGGCTCA
501 GGCAGGACGA  GGACAGAAC  GCAGGCTGTT  TTTATTGTTG  GCACAAGCCG
551 CCGTGCAACA  GGACGGGTTG  GCGCAAAAAG  CATCGAAAGC  GGTTCGCCGC
601 GCGGCGTTGA  AATATGAACA  TCTGCCCGAA  GCGGCGGTTG  CCGATGTGGT
651 GTTCAGCGTA  CAGGGACGCG  AAAAGGAAAA  GGCAATCGGA  GCTTTGCAGC
701 GTTTGGCGAA  GCTCGATACG  GAAATATTGC  CCCCCACTTT  AATGACGTTG
751 CGCTGACTG  CACGCAAATA  TCCCGAAATA  CTCGACGGCT  TTTTCGAGCA
801 GACAGACACC  CAAAACCTTT  CGGCCGTCTG  GCAGGAAATG  GAAATTATGA
851 ATCTGGTTTC  CCTGCACAGG  CTGGATGATG  CCTATGCGCG  TTTGAACGTG
901 CTGTTGGAAC  GCAATCCGAA  TGCAGACCTG  TATATTCAGG  CAGCGATATT
951 GGCGGCAAA  CGAAAAGAAG  GTGCTTCCGT  TATCGACGGC  TACGCCGAAA
1001 AGGCATACGG  CAGGGGACG  GAGGAACAGC  GGAGCAGGGC  GGCCTAACG
1051 GCGGCGATGA  TGTATGCCGA  CCGCAGGGAT  TACGCCAAAG  TCAGGCAGTG
1101 GCTGAAAAAA  GTATCCGCGC  CGGAATACCT  GTTCGACAAA  GGTGTGCTGG
1151 CGGCTGCGGC  GGCTGTGAG  TTGGACGGCG  GCAGGGCGGC  TTTGCGGCAG
1201 ATCGGCGAGG  TCGGGAACCT  TCCCGAACAG  CAGGGGCGGT  ATTTTACGGC
1251 AGACAATTGT  TCCAAAATAC  AGATGCTCGC  CCTGTGCAAG  CTGCCCAGTA
1301 AACGGGAGGC  TTTGAGGGGG  TTGGACAAGA  TTATCGAAAA  ACCGCCGTGC
1351 GGCAGTAATA  CAGAGTTACA  GGCAGAGGCA  TTGGTACAGC  GGTCAAGTTG
1401 TTACGATCGG  CTTGGCAAGC  GGAAGAAAT  GATTTCAGAT  CTGAAAGGG
1451 CGTTCAGGCT  TGCACCCGAT  AACGCTCAGA  TTATGAATAA  TCTGGGCTAC
1501 AGCCTGCTGA  CCGATTCCAA  ACGTTTGGAC  GAAGGTTTCG  CCCTGCTTCA
1551 GACGGCATA  CAAATCAACC  CGGACGATAC  CGCTGTCAAC  GACAGCATAG
1601 GCTGGGCGTA  TTACCTGAAA  GGCGACGCGG  AAAGCGCGCT  GCCGTATCTG
1651 CCGTATTCGT  TTGAAACGA  CCCCAGCCC  GAAGTTGCCG  CCCATTGGG
1701 CGAAGTGTG  TGGGCATTGG  GCGAACGCGA  TCAGGCGGTT  GACGTATGGA
1751 CGCAGGCGG  ACACCTTACG  GGAGACAAGA  AAATATGGCG  GGAAACGCTC
1801 AAACGTCACG  GCATCGCATT  GCCCCAACCT  TCCCGAAAC  CTCGAAATA
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 2906; ORF 791>:

```

m951.pep
1  MIMLPNRFKM  LTVLTATLIA  QVSAAGGGA  GDMKQPEVG  KVFRKQQRYS
51  EEEIKNERAR  LAAVGERVNQ  IFTLLGGETA  LQKQAGTAL  ATYMLMLERT
101 KSPEVAERAL  EMAVSLNAFE  QAEMIYQKWR  QIEPIPGKAQ  KRAGWLRNVL
151 RERNQHLDG  LEEVLAQADE  GQNRVFLLL  AQAQVQDGL  AQKASKAVRR
201 AALKYEHLPE  AAVADVFSV  QGREKEKAIG  ALQRLAKLDT  EILPPTLMTL
251 RLRTARKYPEI  LDGFFEQTDT  QNLSAVWQEM  EIMNLVSLHR  LDDAYARLNV
301 LLERNPNADL  YIQAILAAN  RKEGASVIDG  YAEKAYGRGT  EEQRSRAALT
351 AAMMYADRRD  YAKVRQWLKK  VSAPEYLFDK  GVLAAGAAVE  LDGGRAALRQ
401 IGRVRKLPQ  QGRYFTADNL  SKIQMLALS  LPDKREALRG  LDKIIEKPPA
451 GSNTLQAEA  LVQRSVVYDR  LGRKKMISD  LERAFRLAPD  NAQIMNNLGY
501 SLLTDSKRLD  EGFALLQTAY  QINPDDTAVN  DSIGWAYYLK  GDAESALPYL
551 RYSFENDPEP  EVAHLGEVL  WALGERDQAV  DVWTQAAHLT  GDKKIWRETL
601 KRHGIALPQP  SRKPRK*

```

Computer analysis of this amino acid sequence gave the following results:

1360

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 951 shows 88.6% identity over a 616 aa overlap with a predicted ORF (ORF 951) from *N. gonorrhoeae*

m951/g951 88.6% identity in 616 aa overlap

	10	20	30	40	50	60
m951.pep	MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKVEGKVFRKQORYSEEEIKNERAR					
g951	MIMLPARFTILSVLAAALLAGQAYAA--GAADVLPKEVGKVLKRRYSEEEIKNERAR					
	10	20	30	40	50	
	70	80	90	100	110	120
m951.pep	LAAVGERVNIQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
g951	LAAVGERVNRVFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
	60	70	80	90	100	110
	130	140	150	160	170	180
m951.pep	QAEMIQKWRQIEPIPGKAQKRAGWLRNVLRRGNQHLDGLEEVLAQADEGQNRVFLLL					
g951	QAEMIQKWRQIEPIGGAQKRAGWLRNVLREGGNQHLDGLEEVLAQSDDVQKRRIFLLL					
	120	130	140	150	160	170
	190	200	210	220	230	240
m951.pep	AQAAVQQDGLAQKASKAVRRRAALKYEHLPAAVADVVSQGREKEKAIGALQRLAKLDT					
g951	VQAAVQQGGVAQKASKAVRRRAALKYEHLPAAVADAVFGVQGREKEKAIEALQRLAKLDT					
	180	190	200	210	220	230
	250	260	270	280	290	300
m951.pep	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVWQEMEIMNLVSLHRLDDAYARLNV					
g951	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVWQEMEIMNLVSLRKPDDAYARLNV					
	240	250	260	270	280	290
	310	320	330	340	350	360
m951.pep	LLERNPNADLYIQAAILAANRKEGASVIDGYAEKAYGRGTTEEQRSRAALTAAMMYADRRD					
g951	LLEHNPNANLYIQAAILAANRKEGASVIDGYAEKAYGRGTGEQGRGAAMTAAMIYADRRD					
	300	310	320	330	340	350
	370	380	390	400	410	420
m951.pep	YAKVRQWLKKVSAPEYLFDKGVLA AAAAELDGGRAALRQIGRVKRLPEQQGRYFTADNL					
g951	YAKVRQWLKKVSAPEYLFDKGVLA AAAAELDGGRAALRQIGRVKRLPEQQGRYFTADNL					
	360	370	380	390	400	410
	430	440	450	460	470	480
m951.pep	SKIQMLALS KLDPKREALRGLDKII EKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD					
g951	SKIQMLALS KLDPKREALIGLNNII AKLSAAGSTEPLAEALQRSIIYEQFGKRGKMIAD					
	420	430	440	450	460	470
	490	500	510	520	530	540
m951.pep	LERAFRLAPDNAQIMNNLGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
g951	LETALKLTPDNAQIMNNLGYSLLS DSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
	480	490	500	510	520	530
	550	560	570	580	590	600
m951.pep	GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL					
g951	GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLRGDKKIWRETL					
	540	550	560	570	580	590
	610					
m951.pep	KRHGIALPQPSRKPRK					
g951	KRYGIALPEPSRKPRKX					
	600	610				

1	ATGTTACCCG	CCCGTTTCAC	CATTTTATCT	GTGCTCGCGG	CAGCCCTGCT
51	TGCCGGGCAG	GCGTATGCCG	CCCGCGCGCG	GGATGCGAAG	CCGCGCAAGG
101	AAGTCGGAA	GGTTTTCAGA	AAGCAGCAG	GTTCACAGGA	CGGAAGAACT
151	AAAAACGAA	CGCGACGGCT	TGCGGCAGTG	GGCGAGCGGG	TTAATCAGAT
201	ATTACGTTG	CTGGGAGGGG	AAACCGCCCT	GCAAAAGGGG	CAGCGCGGGAA
251	CGGCTCTGGC	AACCTATATG	CTATGCTTGG	AACGCACAAA	ATCCCCCGAA
301	GTCCGCCGAA	CGCCCTTGG	CATGCGCGTG	TGCGTGAACG	CGCTTGAACA
351	GGCGGAAATG	ATTTATCAGA	AATGCGCGCA	GATTGAGCCT	ATACCGGGTA
401	AGGCGCAAAA	ACGGCGCGGG	TGGCTCGGGA	ACGTGCTGAG	GGAAAGAGGA
451	AATCAGCATC	TAGACGGACT	GGAAGAACTG	CTGGCTCAGG	CGGACGAAGG
501	ACAGAACC GC	AGGGTGTTTT	TATTGTTGGC	ACAAGCCGCC	GTGCAACAGG
551	ACGGGTGGC	GCAAAAAGCA	TCCGAAGCGT	TTCCGCGCGC	GGCGTTGAGA
601	TATGAACATC	TGCCCGAAGC	GGCGGCTGGC	GATGTGGTGT	TACGCGTACA
651	GGGACGCGAA	AGGAAAAGG	CAATCGGAGC	TTTGACGCGT	TTGGCGAAGC
701	TCGATACGGA	AATATTGCC	CCCACTTTAA	TGACGTTGCG	TCTGACTGCA
751	CGCAAAATATC	CCGAAATACT	CGACGGCTTT	TTCGAGCACA	CAGACACCCA
801	AAACCTTTTCG	CGCGCTTGGC	AGGAATAATG	AATATGAAAT	CTGTTTTCCT
851	TGCACAGGCT	GGATGATGCT	TATGCGCGTT	TGAACGTGGT	GTGGAACGCG
901	AATCCGAATG	CAGACCTGCA	TATTCAGGCA	CGCATATTGG	CGGCAAAACG
951	AAAAGAAAGT	GCTTCCGTTA	TCGACGGCTA	CGCCGAAAAG	CAGATACGGCA
1001	GGGGACGGG	GGAACAGCGG	GGCAGGGCGG	CAATGACGGC	GGCGATGATA
1051	TATGCCGACG	GAAGGGATTA	CACCAAAGCT	AGGCAGTGCT	TGAAAAAAGT
1101	GTCCGCGCGC	GAATACCTGT	TCGACAAAAG	TGTGCTGGCG	GCTCGCGCGG
1151	CTGTGAGATT	GACGCGCGCG	AGGGCGGCTT	TGCGGCAGAT	CGGCAGGGTG
1201	CGGAAACTTC	CGGAACAGCA	GGGCGGGTAT	TTTACGGCAG	ACAATTTGTC
1251	CAAAATACAG	ATGTTTCGCC	TGTCGAAGCT	GCCCGACAAA	CGGAGGTTCT
1301	TGAGGGGGTT	GACAGAAGAT	ATCGAAAAC	CGCCTGCCCG	CAGTAATACA
1351	GAGTTACAGG	CAGAGGCATT	GGTACAGCGG	TCAGTTGTTT	ACGATCGGCT
1401	TGGCAAGCGG	AAAAAATGTA	TTTCAGATCT	TGAAAGGGCG	TTCAGGCTTG
1451	CACCCGATAA	CGCTCAGATT	ATGAATAATC	TGGGCTACAG	CTCGCTTTCC
1501	GATTCCAAAC	GTTTGGACGA	AGGCTTCGCC	CTGCTTCAGA	CGGCATACCA
1551	AATCAACCCG	GACGATACCG	CTGTCACAGA	CAGCATAGGC	TGGGCGTATT
1601	ACCTGAAAGG	CGACGCGGGA	AGTCGCGTGC	GCTATCTGCG	GTATTCTGTT
1651	GAAGACGACC	CGGAGCCCGA	AGTTGCCGCC	CATTTGGGCG	AAGTGTGTGT
1701	GGCATTTGGC	GAACCGCATC	AGGCGGTTGA	CGTATGGACG	CAGGCGGCAC
1751	ACCTTACGGG	AGACAAGAAA	ATATGGCGGG	AAACGCTCAA	ACGTACGGGC
1801	ATCGCATTTG	CCCAACCTTC	CCGAAAACCT	CGGAAATAA	

a951.pap

1	per	MLPARFTILS	VLAALLAGO	AYAAGAADAK	PPKEVGKVFR	KQQRYSSEEI
51		KNERARLAHV	GERVNVQIFTL	LGGETALQKG	QAGTALATYM	LMLERTKSPE
101		VAERALEMAV	SLNAFEQAM	IYQKWRQIEP	IPGKAQKRAG	WLRNVLRERG
151		NOHLDGLEEV	LAQADEQONR	KVFLLAQAA	VQODGLAQKA	SKAVRRALR
201		YEHLEPAAVA	DVVSQVQGR	KEAIGALGR	LAKLDTEILP	PTLMTLRLTA
251		RKYPEILDGF	FEQTDTONLS	AVWQEMEIMN	LVSLHRLDDA	YARLNVLLER
301		NPNADLYTQA	AIIAANRRKEG	ASVIDGYAEK	AYGRGTGEOR	GRAAMTAAMI
351		YADRRDYTKV	RQWLKKVSAP	EYLFDKGVLV	AAAAGVLDGG	RAALRQIGRV
401		RKLPPEQQGR	FTADNLSIKQ	MFALSCLKDPK	REALRGLDKI	IEKPPAGSNT
451		ELQAEALVQR	SVVYDRLGKR	KKMISDLERA	FRLAPDNAQI	MNNLGYSLLS
501		DSKRLDEGFA	LLGTAYQINP	DDTAVNDSIG	WAYYLKGDAG	SALPYLRYSF
551		ENDPEPEVAA	HQEVWLWALG	ERDQAVDVWT	QAAHLTGDDK	IWRETLKRHG
600		IALPQPSRKP	RK*			

Homology with a predicted ORF from *N. meningitidis*

ORF 951 shows 96.4% identity over a 614 aa overlap with a predicted ORF (ORF 951) from *N. meningitidis*

a951/m951 96.4% identity in 614 aa overlap

```

          10      20      30      40      50
a951.pep    MLPARFTILSVLAAALLAGQAYAG--AADAKPPKEVGKVFRKQQRYSSEEIKNERAR
          ||| || :|:|:|:|:|:| ||| :| | | | | | | | | | | | | | | | | | | |
m951        MIMLPNRFKMLTTLVLTATLIAGQVSAAGGGAGDMKQPKVEVGKVFRKQQRYSSEEIKNERAR
          10      20      30      40      50      60
          60      70      80      90     100     110
a951.pep    LAAGVERVNIQIFTLGGETALQKGQAGTALATYMLMLERTKSPVAERALEMAVSLNAFE

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1362

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|||||
m951      LAAVGERVNQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
              70          80          90          100          110          120

a951.pep  120          130          140          150          160          170
QAEMIQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLDGLEEVLAQADEGQNRVFLLL
|||||
m951      QAEMIQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLDGLEEVLAQADEGQNRVFLLL
              130          140          150          160          170          180

a951.pep  180          190          200          210          220          230
AQAAVQQDGLAQKASKAVRRAALRYEHLPEAAVADVVSVOGREKEKAIGALQRLAKLDT
|||||
m951      AQAAVQQDGLAQKASKAVRRAALRYEHLPEAAVADVVSVOGREKEKAIGALQRLAKLDT
              190          200          210          220          230          240

a951.pep  240          250          260          270          280          290
EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
|||||
m951      EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
              250          260          270          280          290          300

a951.pep  300          310          320          330          340          350
LLERNPNADLYIQAAILAANKREGASVIDGYAEKAYGRGTGEQGRGAAMTAAMIYADRRD
|||||
m951      LLERNPNADLYIQAAILAANKREGASVIDGYAEKAYGRGTGEQGRGAAMTAAMIYADRRD
              310          320          330          340          350          360

a951.pep  360          370          380          390          400          410
YTKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRKLPEQQGRYFTADNL
|:|||||
m951      YAKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRKLPEQQGRYFTADNL
              370          380          390          400          410          420

a951.pep  420          430          440          450          460          470
SKIQMFALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD
|||||
m951      SKIQMLALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD
              430          440          450          460          470          480

a951.pep  480          490          500          510          520          530
LERAFRLAPDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK
|||||
m951      LERAFRLAPDNAQIMNNLGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK
              490          500          510          520          530          540

a951.pep  540          550          560          570          580          590
GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
|||||
m951      GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
              550          560          570          580          590          600

a951.pep  600          610
KRHGIALPQPSRKPRK
|||||
m951      KRHGIALPQPSRKPRK
              610

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2909>:

g952.seq (partial)

```

1  ..TTGTCTTATC GTTTGAATGC TGCACCGATG TTTAACGATA ATCCTGTTGT
51  TTACGGAAAA ATCAAATTGC AGAGTTGGAA AGCGCGGCGG GATTCAATA
101 TTGTAAAGCA GGATTTGGAT TTTCTCTGCG GGGCGGCTTC GGTGGCGACG
151 CTTTTGAACA ATTTTACGG GCAAAAGCTG ACGGAAGAAG AAGTGTTGGA
201 AAAACTGGGT AAGGAACAGA TCGCGCGCTC GTTTGAGGAT ATGCGGCGCA
251 TTATGCCCGA TTGGGTTT GAGGCGAAAG GCTATGCCCT GTCTTTCGAA
301 CAGCTCGCGC AGTTGAAAT CCCCCTCATC GTGTATCTGA AATACCGCAA
351 AGACGACCAT TTTTCGGTAT TCGCGGGAGT GGATGGCAAT ACGGTTTTGC
401 TTGCCGACCC GTCGCGGGT CATGTTTCGA TGAGCAGGGC GCAGTTTTTG
451 GAGGCTTGGC AAACCCGTA GGGAAATTG GCAGGCAAAA TTTTGGCGGT
501 CGTGCCGAAA AAAGCGGAGG CGATTTCAAA TAAATTGTTT TTCACACATC
551 ATCCCAAGCG GCAGACGGAG TTTGCAGTCG GACAGGTAAA ATGGTGGCGT

```

1363

601 GCTTATTGA

This corresponds to the amino acid sequence <SEQ ID 2910; ORF 952.ng>:

g952.pep (partial)

```

1  ..LSYRLNAAPM FNDNPVVYVK IKLQSWKARR DFNIVKQDLDFSCGAASVAT
51  LLNNFYGQKL TEEEVLEKLG KEQMRASFED MRRIMPD LGF EAKGYALSFE
101 QLAQLKIPVI VYLKVRKDDH FSVLRGVDGN TVLLADPS PG HVSMSRAQFL
151 EAWQTREGNL AGKILAVVPK KAEAISNKL FTHHPKRQTE FAVGQVKWWR
201 AY*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2911>:

m952.seq

```

1  ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT
51  ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTGTTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG CGCGGCGGGA TTTCAATATT
151 GTAAAGCAGG ATTTGGATTT TTCCTGTGGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT GCGGCGCATT
301 ATGCCTGATT TGGGTTTTGA GGCGAAGGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCGCAG TTGAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAAG
401 ACGACCATTT TTCGGTATTG CGCGGTATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGGCA TGTTTCAATG AGCAGGGCGC AGTTTTTGGA
501 TGCTTGCAA ACCCGTGAGG GAAATTGGC AGGTAAGATT TTGGCTGTCA
551 TACCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACAACAC
601 CCAAAACGGC AGACGGAGTT TACAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2912; ORF 952>:

m952.pep

```

1  MMKFYVFL ACVVVLSYR LNAAPMFNDN PVVYGKIKVQ SWKARRDFNI
51  VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKKLDKEQM RASFEDMRRRI
101 MPDLGF EAKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFLDAWQ TREGNLAGKI LAVIPKKAET ISNKLFTQH
201 PKRQTEFTVG QIRQARAE*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 952 shows 92.5% identity over a 201 aa overlap with a predicted ORF (ORF 952) from *N. gonorrhoeae*

g952/m952: 92.5% identity in 201 aa overlap

		10	20	30	40		
g952.pep		LSYRLNAAPMFNDNPVVYVGKIKLQSWKARRDFNIVKQDLDFSCG					
m952	MMKFYVFLACVVVLSYRLNAAPMFNDNPVVYVGKIKVQSWKARRDFNIVKQDLDFSCG						
		10	20	30	40	50	60
g952.pep	AASVATLLNNFYGQKLTEEEVLEKLGKEQMRASFEDMRRIMPD LGF EAKGYALSFEQLAQ						
m952	AASVATLLNNFYGQTLTEEEVLKKLDKEQMRASFEDMRRIMPD LGF EAKGYALSFEQLAQ						
		70	80	90	100	110	120
g952.pep	LKIPVIVYLKVRKDDHFSVLRGVDGNTVLLADPS PGHVSMSRAQFLEAWQTREGNLAGKI						
m952	LKIPVIVYLKVRKDDHFSVLRGIDGNTVLLADPSLGHVSMSRAQFLDAWQTREGNLAGKI						
		130	140	150	160	170	180
g952.pep	LAVVPKKA E A I S N K L F F T H H P K R Q T E F A V G Q V K W W R A Y X						
m952	LAVIPKKAETISNKLFFTHHPKRQTEFTVGQIRQARAE						
		190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2913>:

a952.seq

```

1  ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT
```

1364

```

51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG AAAGGCGGGA TTTCATATT
151 GTAAAGCAGG ATTTGGATTT TTCCTGCGGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT GCGGCGCATT
301 ATGCCAGATT TGGGTTTGA AGCGAAAGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCACAG TTGAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAGG
401 ATGATCATTT CTCGGTATTG CGCGGGATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGTCA TGTTTCAATG AGCAGGGCGC AGTTTNGGA
501 TGCTTGCAA ACCCGTGAGG GAAATTGGC AGGTAAGATT TTGGCGGTCG
551 TGCCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACATCAT
601 CCCAAGCGGC AGACGGAGTT TGCAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2914; ORF 952.a>:

```

a952.pep
1  MMKFYVFL ACVVVSLSYR LNAAPMFNDN PVVYGKIKVQ SWKERRDFNI
51  VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKKLDKEQM RASFEDMRRI
101 MPDLGFEEKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFXDAWQ TREGNLAGKI LAVVPKKAET ISNKLFFTHH
201 PKRQTEFAVG QIRQARAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 952 shows 97.7% identity over a 218 aa overlap with a predicted ORF (ORF 952) from *N. meningitidis*

a952/m952 97.7% identity in 218 aa overlap

a952.pep	10	20	30	40	50	60
m952	10	20	30	40	50	60
a952.pep	70	80	90	100	110	120
m952	70	80	90	100	110	120
a952.pep	130	140	150	160	170	180
m952	130	140	150	160	170	180
a952.pep	190	200	210	219		
m952	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2915>:

```

g953.seq
1  ATGAAAAAAA TCATCTTCGC CGCGCTCGCA GCGGCAGCCG TCGGCACTGC
51  CTCCGCCACC TACAAAGTGG ACGAATATCA CGCCAACGTC CGTTTCGCCA
101 TCGACCACTT CAACACCAGC ACCAACGTCG GCGGTTTTTA CGGTCTGACC
151 GGTTCGCTCG AGTTCGATCA AGCAAAACGC GACGGCAAAA TCGACATCAC
201 CATTCCCGTC GCCAACCTGC AAAGCGGTTT GCAACCCTTC ACCGGCCACC
251 TGAAATCCGC CGACATCTTC GATGCCGCTC AATATCCGGA CATCCGCTTC
301 GTTTCACCA AATTCAACTT CAACGGCAAA AAAGTGTGTT CCGTTGACGG
351 CAACCTGACC ATGCGGGGCA AAACCGCCCG CGTCAAACTC AAAGCCGAAA
401 AATTCAACTG CTACCAAAGC CCGATGGCGG AAACCGAAGT TTGCGGCGGC
451 GACTTCAGCA CCACCATCGA CCGCACCAAA TGGGCGGTGG ACTACCTCGT
501 TAACGCCGGT ATGACCAAAA ACGTCCGCAT CGACATCCAA ATCGAAGCTG
551 CAAAAAATA A

```

1365

This corresponds to the amino acid sequence <SEQ ID 2916; ORF 953.ng>:

g953.pep  
 1 MKKIIFAALA AAAVGTASAT YKVDEYHANV RFAIDHFNST TNVGGFYGLT  
 51 GSVEFDQAKR DGKIDITIPV ANLQSGSQPF TGHLSADIF DAAQYPDIRF  
 101 VSTKFNFNKG KLVSV DGNLT MRGKTAPVKL KAEKFNCYQS PMAETEVC GG  
 151 DFSTTIDRTK WGV DYL V NAG MTKNVRIDIQ IEAAKQ\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2917>:

m953.seq  
 1 ATGAAAAAAA TCATCTTCGC CGCACTCGCA GCCGCCGCCA TCAGTACTGC  
 51 CTCCGCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCG  
 101 CCATCGACCA TTTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG  
 151 ACCGGTTCGG TCGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT  
 201 CACCATCCCC ATTGCCAACC TGCAAAGCGG TTCGCAACAC TTTACCGACC  
 251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC  
 301 TTTGTTTCCA CCAAAATCAA CTTCAACGGC AAAAAACTGG TTTCCGTTGA  
 351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAA CTCAAAGCCG  
 401 AAAAAATCAA CTGCTACCAA AGCCCGATGG AGAAAACCGA AGTTTGTGGC  
 451 GGCGACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT  
 501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG  
 551 CAGCCAAACA ATAA

This corresponds to the amino acid sequence <SEQ ID 2918; ORF 953>:

m953.pep  
 1 MKKIIFAALA AAAISTASAA TYKVDEYHAN RFAIDHFNST STNVGGFYGL  
 51 TGSVEFDQAK RDGKIDITIP IANLQSGSQH FTDHLKSADI FDAAQYPDIR  
 101 FVSTKFNFNK KLVSV DGNLT TMHGKTAPVK LKAEKFNCYQ SPMEKTEVCG  
 151 GDFSTTIDRT KWGM DYL V NVV GMTKSVRID I QIEAAKQ\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 953 shows 93.0% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. gonorrhoeae*

m953/g953 93.0% identity in 187 aa overlap

	10	20	30	40	50	60
m953.pep	MKKIIFAALAAAAAISTASAA TYKVDEYHANRFAIDHFNSTSTNVGGFYGLTGSVEFDQAK					
g953	MKKIIFAALAAAAAVGTASA-TYKVDEYHANVRFAIDHFNSTSTNVGGFYGLTGSVEFDQAK					
	10	20	30	40	50	
	70	80	90	100	110	120
m953.pep	RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFNKKLVSV DGNL					
g953	RDGKIDITIPVANLQSGSQPF TGHLSADIFDAAQYPDIRFVSTKFNFNKKLVSV DGNL					
	60	70	80	90	100	110
	130	140	150	160	170	180
m953.pep	TMHGKTAPVKLKA EKFN CYQSPMEKTEVC GDFSTTIDRTKWGM DYL V NVV GMTKSVRID I					
g953	TMRGKTAPVKLKA EKFN CYQSPMAETEVC GDFSTTIDRTKWGV DYL V NAG MTKNVRID I					
	120	130	140	150	160	170
m953.pep	QIEAAKQX					
g953	QIEAAKQX					
	180					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2919>:

a953.seq  
 1 ATGAAAAAAA TCATCATCGC CGCGCTCGCA GCAGCCGCCA TCGGCACTGC  
 51 CTCCGCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCT  
 101 CTATCGACCA TTTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG  
 151 ACCGGTTCGG TTGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT  
 201 CACCATCCCC GTTGCCAACC TGCAAAGCGG TTCGCAACAC TTTACCGACC  
 251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC  
 301 TTTGTTTCCA CCAAAATCAA CTTCAACGGC AAAAAACTGG TTTCCGTTGA



a953.pcp

pep	1	2	3	4	5
51	MKKIIIAALA	AAAIQTASAA	TYKVD EYHAN	ARFSIDHFNT	STNVGGFFYGL
101	TGSVEFDQAK	RDGKIDITIP	VANLQSGSQS	FTDHLKSADI	FDAAQYPPDIR
151	GVSTKIDFNG	KKLVSDVGNL	TMHGKTAPVK	LKAEKFCYQI	SPMLKTEVCG
151	FGDSTTIDRT	KWGM DYLVNV	GMTKSVRIDI	QIEAAKQ*	

Homology with a predicted ORF from *N. meningitidis*

ORF 953 shows 97.3% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. meningitidis*

a953/m953 97.3% identity in 187 aa overlap

		10	20	30	40	50	60
a953.pep		MKKIIIAALAAAA	IGTASAATYKVDEYHANARFSIDH	ENTSTNVGGFYGLTGSVEFDQAK			
		:	:	:	:	:	:
m953		MKKIIFAALAAAA	ISTASAATYKVDEYHANARFAIDH	ENTSTNVGGFYGLTGSVEFDQAK			
		10	20	30	40	50	60
		70	80	90	100	110	120
a953.pep		RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQY	PDIRFVSTKFNENGKKLV	SV	DG	NL	
		:	:	:	:	:	:
m953		RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQY	PDIRFVSTKFNENGKKLV	SV	DG	NL	
		70	80	90	100	110	120
		130	140	150	160	170	180
a953.pep		TMHGKTAPVKLKA	EKFNCYQSPMLKTEVCGGDFSTTIDRTKWGM	DYLVN	VG	MTKSV	RIDI
		:	:	:	:	:	:
m953		TMHGKTAPVKLKA	EKFNCYQSPMEKTEVCGGDFSTTIDRTKWGM	DYLVN	VG	MTKSV	RIDI
		130	140	150	160	170	180
a953.pep		QIEAAKQX					
m953		QIEAAKQX					

g954.seq not found yet

g954.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2921>:

m954.seq

1	ATGAAAAAGT	TTTATTTTGT	GCTGCTGGCG	TTGGGTTTGG	CAGCGTGTGG
51	GCAAGAACAA	TCGCAAGAA	CTGATGCGGA	GCAGATTTT	TTTGCCAAAT
101	CAATATCAAT	TGCAGATGAG	AAACAGGCTT	TTTATTTTGA	ATCGCGCGCC
151	CGTTTCCGTG	TATTGCAACA	AGGCCCTTGGC	GGGGATTTTG	AGAGGTTTTT
201	AAAAGGAGAA	ATACCTAATC	AAGAAAATCT	TGCAAAAGTAT	CGTGAAAAAT
251	TTACTCAAGC	AGTCGCTTAT	TATGCGGACA	CGAATGGAGA	TGATGACCCA
301	TACCGCGCTC	GCAAAACAGC	TGCGCAAGAT	GCAGAAATCC	TGATGAAGAG
351	TATGGTAAAC	AGCGGTGGAG	CGCGTACAAC	TGATTTAGAT	AAGGAAAGTT
401	ATCAAAATTA	CCGAAAATCA	ATGCAAGAA	CCCGTAAAA	AATAACGGAA
451	GCTGAAGCCA	ATTTGCCGAA	AAAAATAA		

This corresponds to the amino acid sequence <SEQ ID 2922; ORF 954>:

m954 . pep

1 MKKFYFVLLA LGLAACGQEQ SQKADAEQYF FANKYQFADE KQAFYFERAA  
51 RFRVLQOGLG GDFERFLKGE IPNQENLAKY RENITQAVAY YADTNGDDDP  
101 YRVCKQAAQD AEILMKSMVT SGGGGTTDLD KESYQNYRKS MQECRKITE  
151 AEANLPLK\*

a954.seq not found yet

a954.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2923>:

g957.seq (partial)

```

1 ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGATT
51 TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGTAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CCGGGAAAAA TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTTCGGT ATTTGATGCG GCGGGGCGCG GGAAAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG GGGGatgaaG gcgaacagtc ttgtggtcgg
801 ctatgatgcg gacggtCtgc CgcaAAAagt ctattggagt gtcgacaatg
851 gaaaaaaacc ccaaagtgtc gaatattatt tgaaaaacgg aaatcttttt
901 attgcccaat cttcgacggt aaccttgaaa acggatggcg taacggcgga
951 tatgcaaaacc tatcatgcmc aacaaacgtt gtatttggat ggg...
```

This corresponds to the amino acid sequence <SEQ ID 2924; ORF 957.ng>:

g957.pep (partial)

```

1 MFKKFKPVLL SFFALVFVFW LGTGIAYEIN PRWFLSDTAT EVPENPNFAV
51 AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFVSV VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHLGICYQM AQVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS VDNGKKPQSV EYYLKNLNL
301 IAQSSTVTLK TDGVTADMQT YHAQQTLYLD G...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2925>:

m957.seq

```

1 ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGATT
51 TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGTAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAATCT TGCCGGAAT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA
501 CCGGGAAAAA TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTTCGGT ATTTGATGCG GCGGGGCGCG GGAAAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG AGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGCACAAAT CTTGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTTGGAT GGCGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCTTGATTT TCCTTTGAAC
1051 TTGGAAAAAT TGAAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCCGGC GGCAGGCGCG ACCTTTCTCA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 2926; ORF 957>:

m957.pep

```

1 MFKKFKPVLL SFFALVFVFW LGTGIAYEIN PRWFLSDTAT EVKPNPNFAV
51 AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFVSV VYGGTVHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHLGICYQM AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVFYQN
```

1368

251 MRELMPRGMK ANSLVVGYDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF  
 301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN  
 351 LENLEKEVRR YAEAAARRSG GRRDLSH\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 957 shows 95.2% identity over a 331 aa overlap with a predicted ORF (ORF 957) from *N. gonorrhoeae*

g957/m957 95.2% identity in 331 aa overlap

	10	20	30	40	50	60
g957.pep	MFKKFKPVLLSFFALVF	FWLGTG	IAYEINPRWFLSD	TATEV	PENPN	AFVAKLARLFRNA
m957	MFKKFKPVLLSFFALVF	FWLGTG	IAYEINPRWFLSD	TATEV	PKPN	AFVAKLARLFRNA
	70	80	90	100	110	120
g957.pep	DRAVVIVKESMRTEES	LAGAVDDG	PLQSEKDYLA	LAIRLSRLKEKAKW	FHVTEQ	EHGEEV
m957	DRAVVIVKESIRTEEN	LAGTVDDG	PLQSEKDYLA	LAIRLSRLKEKAKW	FHVTEQ	EHGKEV
	130	140	150	160	170	180
g957.pep	WLDYIIGEGGLVAVS	LSQRSPEAFV	NAEYLYRND	RPFSVNVYGGTA	HGENYETT	TGEYRVV
m957	WLDYHIGEGGLVAVS	LSQRSPEAFV	NAEYLYRND	RPFSVNVYGGT	VHGENYETT	TGEYRVV
	190	200	210	220	230	240
g957.pep	WQPDGSVFDAAAGRG	KIGEDVYEH	CLGCYQMAQV	YLAKYRDVANDE	QKVWDFR	ESNRIAS
m957	WQPDGSVFDAAAGRG	KIGEDVYEH	CLGCYQMAQV	YLAKYRDVANDE	QKVWDFR	KESNRIAS
	250	260	270	280	290	300
g957.pep	DSRDYVFYQNMREL	MPRGMKAN	SLVVGYDAD	GLPQKVYWSV	DNGKKPQS	VEYYLKNGNLF
m957	DSRSNVFYQNMREL	MPRGMKAN	SLVVGYDAD	GLPQKVYWSF	DNGKKRQS	FEYYLKNGNLF
	310	320	330			
g957.pep	IAQSSTVT	LKT	DGVTADMOTY	HAQQTLYLDG		
m957	IAQSSTVALK	ADGVTADMOTY	HAQQTWYLDG	GGRIVREEKQ	GDRLPDFPLN	LENLEKEVRR
	310	320	330	340	350	360
m957	YAEAAARRSG	GRRDLSHX				
	280	290	300			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2927>:

a957.seq  
 1 ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT  
 51 TGCCTTTTGG CTGGGAACGG GTATTGCCA TGAGATTAAT CCGCGTTGGT  
 101 TTTTGAGCGA TACGGCAACT GAAATCCGA ATGCTTTTGT GGCGAACTT  
 151 GCCCGCCTGT TCCGAAATGC CGACAGGGCG GTTGTCATCG TGAAGGAATC  
 201 GATGAGGACG GAGGAAAGTC TTGCCGGAGC TGTGGATGAC GGTCCGTTGC  
 251 AGTCGGAGAA GGATTATCTT GCACTCGCTG TCCGGCTCAG TCGTTTGAAA  
 301 GAAAGGCGA AATGGTTTCA CGTAACGGAG CAGGAACATG GGGAAAGAGT  
 351 TTGGCTGGAT TACTATATCG GCGAGGGCGG TTTGTTGCG GTTTCGCTTT  
 401 CGCAACGCTC GCCGGAAGCG TTTGTTAATG CCGAATATCT GTATCGGAAC  
 451 GATCGTCCGT TTTCTGTAAA TGTGTACGGC GGAACGGTTC ACGGGGAAAA  
 501 TTATGAAACG ACAGGAGAAT ATCGGGTTGT TTGGCAACCG GACGGTTCGG  
 551 TATTGTATGC GTCGGGGCGC GGGAAAATCG GGAAGATGT TTATGAGCAT  
 601 TGCCCTCGGT GTTATCAGAT GGCCAGGTA TATTGGCGA AATATCGGGA  
 651 TGTCGCGAAT GATGAGCAGA AGGTTTGGGA CTTCCGCGAA GAGAGTAACC  
 701 GGATTGCGTC GGAATCGCGC GATTCTGTGT TTTATCAGAA TATGCGGGAA  
 751 TTGATGCCCC GAGGGATGAA GGCAAACAGT CTTGTGGTCG GCTATGATGC  
 801 GGACGGTCTG CCGCAGAAAG TCTATTGGAG TTTTCGACAAT GGGAAAAAAC  
 851 GCCAGAGTTT CGAATATTAT TTGAAAAACG GAAATCTTTT TATTGCACAA  
 901 TCTTCGACGG TAGCATTGAA AGCGGATGGC GTAACGGCGG ATATGCAGAC

1369

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951 CTATCATGCG CAACAGACGT GGTATTTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTTGAA CTTGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCGGG
1101 CGGCAGCGCG GACCTTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2928; ORF 957.a>:

```

a957.pep
1 MFKKFKPVLL SFFALVFVAFW LGTGIAYEIN PRWFSLDTAT ENPNAFVAKL
51 ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGCVQMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL PQKVYWSFDN GKKRQSFEEY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a957/m957 96.3% identity in 377 aa overlap

a957.pep	10	20	30	40	50
m957	10	20	30	40	50
a957.pep	60	70	80	90	100
m957	60	70	80	90	100
a957.pep	120	130	140	150	160
m957	120	130	140	150	160
a957.pep	180	190	200	210	220
m957	180	190	200	210	220
a957.pep	240	250	260	270	280
m957	240	250	260	270	280
a957.pep	300	310	320	330	340
m957	300	310	320	330	340
a957.pep	360	370			
m957	360	370			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2929>:

```

g958.seq
1 TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51 TTTCGGCACG CATTGCGCCG CCGATACCGT TCGGGCGGAA GAGGCGGACG

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1370

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101 GGC GTGTCGC AGAAGGCGGT GCGCAGGGCG CGTCCGAATC CGCACAAAGCT
151 TCCGATTGGA CCTCGGTTTC GACCTGCCTG TTTTGCACTA ACGAAAGCGG
201 CAGCCCCGAG AGAACCGAAG CCGCCGTCCA AGGCAGCGGC GAAGCATCCG
251 TCCCCGAAGA CTATACGCGC ATTGTGCGCG ACAGGATGGA AGGACAGTCG
301 AAGGTTAAGG TCGCGCGCGA AGGAAGCGTT ATCATCGAAC GGGACGGCGC
351 AGTCCTCAAT ACCGATTGGG CGGATTACGA CCAGTCGGGC GACACCGTTA
401 CCGTAGGCGA CCGGTTTCGCC CTCCAACAGG ACGGTACGCT GATTCCGGGC
451 GAAACCTGTA CCTACAATCT CGATCAGCAG ACCGGCGAAG CGCACAACTG
501 CCGTATGGAA ACCGAACAAG GCGGACGGCG GCTGCAAAGC GTCAGCCGCA
551 CCGCCGAAAT GTTGGGCGAA GGGCGTTACA AACTGACGGA AACCAATTC
601 AACACCTGTT CCGCCGGAGA TGCCGGCTGG TATGTCAAAG CCGCCTCTGT
651 CGAAGCGGAT CGGGGAAAAG GCATAGGCGT TGCCAAACAC GCCGCCTTCG
701 TGTTCCGGCG CGTTCCCTTT TCTATACGC CTTGGGCGGA CTTCCCGCTT
751 GACGGCAACC GCAAAAGCGG ACTGCTCGTC CCGTCCGTAT CTGCCGGTTC
801 GGACGGCGTT TCCCTTTCCG TCCCCTATTA TTTCAACCTT GCCCCCAACT
851 TCGATGCCAC TTTCGCCCCC GGCATTATCG GCGAACGCGG CGCGACGTTT
901 GACGGACAAA TCCGTTACCT GCGTCCCGAT TACAGCGGAC AGACCGACCT
951 GACCTGGTTG CCGCAGGATA AGAAAAGCGG CAGGAACAAC CGCTATCAGG
1001 CAAAATGGCA GACCCGGCAC GACATTTCCG ACACGCTTCA GCGGGGTGTC
1051 GATTTCAACC AAGTCTCCGA CAGCGGCTAC TACCGCGACT TTTACGGCGG
1101 CGAAGAAATC GCGGGCAACG TCAACCTCAA CCGCCGCGTA TGGCTGGATT
1151 ATGGCGGCGG GCGGGCGGGA GCGAGCCTGA ATGCCGGCCT TTCGGTTCAG
1201 AAATACGAGA CGCTGGCAAA CCAAAGCGGC TACAAAGACG AACCTTACGC
1251 CATCATCCCC CGCCTTTCTG CCGATTGGCA TAAAAACGCA GGCAGGGCGC
1301 AAATCGGCGT GTCCGCACAA TTTACCCGCT TCAGCCACGA CGGCCGCCAA
1351 GACGGCAGCC GACTGGTCGT GTATCCCGGT ATCAAATGGG ATTTACAGCA
1401 CAGCTGGGGC TACGTCCGCC CCAAACCTCG GCTGCAGGCC ACTTATTACA
1451 GCCTCGACAG TTTCGGCGGC AAAGCATCCC GCAGCGTCGG GCGCGTTTTG
1501 CCCGTTGTCA ATATCGACGG CGGCACAACC TTCGAACGCA ATACGCGCCT
1551 GTTCGGCGGC GGAGTCGTGC AAACCATCGA GCGCGCGCTG TTCTACAAC
1601 ATATTCTGTC CAAATCTCAA AACGACCTGC CCAATTTCTG TTCGTCGGAA
1651 AGCAGCTTCG GCTACGGGCA GCTTTTCCGC GAAAACCTCT ATTACGGCAA
1701 CGACCGCATC AACGCCGCCA ACAGCCTTTC CACCGCGGTG CAGAGCCGTA
1751 TTTTGGACGG CGCGACGGGG GAGGAGCGTT TCCGCGCCGG TATCGGTCAG
1801 AAATTCTATT TCAAGGATGA TGCGGTGATG CTTGACGGCA GCGTCGGCAA
1851 AATCCGCGC AGCCGTTCCG ACTGGGTGGC ATTCGCTCC GCGGCGATAG
1901 CGGGCGGTTT CACCCTCGAC AGCAGCATCC ACTACAACCA AAACGACAAA
1951 CGCGCCGAAC ATTACGCGGT CGGCGCAGGC TACCGCCCGG CCCCCGAAA
2001 AGTGTGAAC GCCCGCTACA AATACGGGCG CAACGAAAAA ATCTACCTGC
2051 AGCGCGACGG TTCTATTTT TACGACAAAC TCAGCCAGCT CGACCTGTCC
2101 GCACAATGGC CGCTGACGCG CAACCTGTCT GCCGTCGTCC GTACAACTA
2151 CGGTTTTGAA GCCAAAAAAC CGATAGAAAT GCTTGCCGGT GCAGAATACA
2201 AAAGCAGTTG CGGCTGCTGG GCGCGGGGCG TGTACGCCA ACGCTACGTT
2251 ACCGGCGAAA ACACCTACAA AAACGCCGTC TTTTTCAC TTCAAGTGAA
2301 AGACCTCAGC AGCGTCGGCA GAAACCCGCG AGGCAGGATG GATGTCGCCG
2351 TTCCCGGCTA CATCCCCGCC CACTCTCTTT CCGCCGACG CAACAAACGG
2401 CCCTGA

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This corresponds to the amino acid sequence <SEQ ID 2930; ORF 958.ng>:

g958.pep

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1  LARLFSLKPL VLALGFCEGT HCAADTVAAE EADGRVAEGG AQGASESAQA
51  SDLTLGSTCL FCSNESGSPE RTEAAVQSGS EASVPEDYTR IVADRMEGQS
101 KVKVRAEGSV IIERDGAVALN TDWADYDQSG DTVTVGDRFA LQQDGLTIRG
151 ETLTYNLDQQ TGEAHNVNME TEQGGRRLOS VSRTAEMLGE GRYKLTETQF
201 NTCSAGDAGW YVKAASVEAD RGKGIGVAKH AAFVFGGVPL FYTPWADFPL
251 DGNRKSGLLV PSVSAGSDGV SLSVPYYFNL APNFDATFAP GIIGERGATF
301 DQQIRYLRPD YSGQTDLTWL PHDKKSGRNN RYQAKWQHRH DISDTLQAGV
351 DFNQVSDSGY YRDFYGGEEI AGNVNLNRRV WLDYGGRAAG GSLNAGLSVQ
401 KYQTLANQSG YKDEPYAIMP RLSADWHKNA GRAQIGVSAQ FTRFSDHGRQ
451 DGSRLVVYPG IKWDFSNSWG YVRPKLGLHA TYYSLDSFGG KASRSVGRVL
501 PVVNDGGTT FERNTRLFGG GVVQTIPEPL FNYIIPAKSQ NDLPNFDSSSE
551 SSFGYGQLFR ENLYYGNDR I NAANSLSTAV QSRILDGATG EERFRAGIGQ
601 KFYFKDDAVM LDGVSQKNPR SRSDWVAFAS GGIGGRFTLD SSIHYNQNDK
651 RAEHYAVGAG YRPAPGKVLN ARYKYGRNEK IYLOADGSYF YDKLSQLDLS
701 AQWPLTRNLS AVVRYNYGFE AKKPIEMLAG AEYKSSCGCW GAGVYAQRVY
751 TGENTYKNAV FFSLLQLKDL SVGRNPAGRM DVAVPGYIPA HSLSAGRNKR
801 P*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2931>:

m958.seq

```

1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCCTCTG
51  CTTCCGACAG CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGAA AGCGTTCGGA GCGGTCCGA ACCCATAACG

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1371

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151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTGCA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTCG AACGCAACCG
351 GACGACCTC AATACCGATT GGGCGGATTA CGACCAAGTCG GGCAGACACCG
401 TTACCGCAGG CGACCGGTTT GCCCTCCAAC AGGACGGTAC GCTGATTCCG
451 GGGCAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 GCCTCCGATG GAAATCGAAC AAGCGCGACG GCGGTGCAA AGCGTCAGCC
551 CACCGGCCGA AATGTTGGGC GAAGGCGATT ACAAACTGAC GGAACCCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCAGCCTC
651 TGTGCAAGCG GATCGGGAAG AAGGCATAGG CGTTGCCAAA CACGCCGCCCT
701 TCGTGTTCGG CGGCGTTCCC ATTTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTTGACGGCA ACCGCAAAAG CGGCCTGCTT GTTCCCTCAC TGTCCGCCGG
801 TTCGGACGGC GTTTCCTCTT CCGTTCCTTA TTATTTC AAC CTGCCCCCA
851 ATCTCGATGC CAGGTTCCGG CCCAGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTTGACGGGC AGGTACGCTA CCTGCGGCCG GATTATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCGGCACG ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCGAAATG GCAGCATCGG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTCGATTGGA ACCAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTAGGGCGG CAGGGCGGCG GGGCGCAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAAGC GGCTACAAAG ACAAAACCGTA
1251 TGCCCTCATG CCGCGCCTTT CGGTGCGAGT GCGTAAAAAC ACCGGCAGGG
1301 CGCAATACGG CGTGTCGCA CAATTTACCC GATTACAGCA CGACAGCCGC
1351 CAAGACGGCA GCCGCTGGT CGTCTATCCC GACATCAAT GGGATTTCAG
1401 CAACAGCTGG GGCTATGTCC GTCCCAAAC TCGGCTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCGCAGT
1501 CTGCCCATTG TCAACATCGA CAGCGGCGCA ACTTTTGAGC GGAATACGCG
1551 GATGTTCGGC GGAGAAGTCC TGCAAACCT CGAGCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTGCTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTCTTT CGCGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAAGCC
1751 GTATTTTGGG CCGCGCGACG GGGGAAGAGC GTTTCGCGC CGGCATCGGT
1801 CAGAAATTCT ATTTCAAGGA TGATGCGGTG ATGCTTGACG GCAGCGTCGG
1851 CAAAAAACCG CGCAACCGTT CCGACTGGGT GGCATTTGCC TCCGGCAGCA
1901 TCGGAGCCG CTTCATCCTC GACAGCAGCA TCCACTACAA CCAAACGAC
1951 AAACGCGCGC AGAATACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGCTG AACGCCGCT ACAAAATACG CGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAAT GGCCGCTGAC GCGCAACCTG TCGGCGCTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCAAAA AACCAGATAG GGTGCTGGCG GGTGCGGAAT
2201 ACAAAAGCAG TTGCGGCTGC TGGGGCGCGG GCGGTGACGC CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTGC GCAGAAACCC CGCAGACAGG ATGGATGTGC
2351 CCGTTCGCGG CTATATCACC GCCACTCTC TTTCCGCCG ACGCAACAAA
2401 CGACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2932; ORF 958>:

```

m958.pep
1 LARLFSLKPL VLALGLCFGT HCAAADAVAA EETDNPTAGE SVRSVSEPIQ
51 PLSLSLGSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEOQ
101 SQVQVRAEGN VVVERNRTTL NTDWADYDQS GDTVTAGDRF ALQODGTLIR
151 GETLTYNLEQ QTGEAHNVLM EIEQGGRRLO SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKIGIVAK HAAAFVGGVP IFYTPWADFP
251 LDGNRKSGLL VPSLSAGSDG VLSVPPYFN LAPNLDATFA PSVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLOAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGS LNAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSVEWRKN TGRAQIGVSA QFTRFSDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSRT
501 LPIVNI DSGA TFERNTRMFG GEVLQTLLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGQLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKDDAV MLDGSVGKKP RNRSDWVAFA SGSIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVKL NARYKYGRNE KIYLSKDSGY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVL GA EYKSSCGC WGAGVYAORY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIT AHSLSAGRNK
801 RP*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 958 shows 89.3% identity over a 802 aa overlap with a predicted ORF (ORF 958) from *N. gonorrhoeae*

1372

m958/g958 89.3% identity in 802 aa overlap

	10	20	30	40	50	60
m958.pep	LARLFSLKPLVLALGLCFGTHCAAA	DAVAEEETDNPTAGESVRSVSEPIQ	PTSLSLG	STC		
g958	LARLFSLKPLVLALGFCFGTHCAA	-DTVAEEADGRVAEGGAQGASESAQ	ASDLTLG	STC		
	10	20	30	40	50	
	70	80	90	100	110	120
m958.pep	LFCSNESGSPERTEAAVQGS	GEASIPEDYTRIVADRMEG	QSQVQVRAEGNVVVERN	RTTL		
g958	LFCSNESGSPERTEAAVQGS	GEASVPEDYTRIVADRMEG	QSKVKVRAEGSVI	IERDGA	VL	
	60	70	80	90	100	110
	130	140	150	160	170	180
m958.pep	NTDWADYDQSGD	TVTAGDRFALQQD	GTIRGETLTYNLE	QQTGEAHNV	RMEIEQGGRR	LQ
g958	NTDWADYDQSGD	TVTVGDRFALQQD	GTIRGETLTYNLD	QQTGEAHNV	RMETEQGGRR	LQ
	120	130	140	150	160	170
	190	200	210	220	230	240
m958.pep	SVSRTAEMLGEGHY	KLTETQFNTCSAGD	AGWYVKAASVEAD	REKIGVAKHAA	FVFGGVP	
g958	SVSRTAEMLGEGRY	KLTETQFNTCSAGD	AGWYVKAASVEAD	RKGKIGVAKHAA	FVFGGVP	
	180	190	200	210	220	230
	250	260	270	280	290	300
m958.pep	IFYTPWADFPLDGN	RKSGLLVPSLSAGS	DGVSLSVPYFNL	APNLDATFAP	SVIGERGAV	
g958	IFYTPWADFPLDGN	RKSGLLVPSVSAGS	DGVSLSVPYFNL	APNFDATFAP	GIIGERGAT	
	240	250	260	270	280	290
	310	320	330	340	350	360
m958.pep	FDGQVRYLRPDY	AGQSDLTWLP	HDKKSGRNNRY	QAKWQHRH	DISDTLQAG	VDFNQVSDSG
g958	FDGQIRYLRPDY	SGQDLTWLP	HDKKSGRNNRY	QAKWQHRH	DISDTLQAG	VDFNQVSDSG
	300	310	320	330	340	350
	370	380	390	400	410	420
m958.pep	YYRDFYGNKEI	AGNVNLRVWLDY	GGRAAGGSLN	AGLSVLKYQ	TLANQSGYK	DKPYALM
g958	YYRDFYGGEEI	AGNVNLRVWLDY	GGRAAGGSLN	AGLSVQKYQ	TLANQSGYK	DEPYAIM
	360	370	380	390	400	410
	430	440	450	460	470	480
m958.pep	PRLSVEWRKNT	GRAQIGVSAQ	TRFSDSRQD	GSRLVVYP	DIKWDFS	NSWGYVRPKLGLH
g958	PRLSADWHKN	AGRAQIGVSAQ	TRFSDGRQD	GSRLVVYP	GIKWDFS	NSWGYVRPKLGLH
	420	430	440	450	460	470
	490	500	510	520	530	540
m958.pep	ATYYSLNRF	GSQEARVSR	TLPIVNID	SGATFERN	TRMFGGEV	LQTLFNYI
g958	ATYYSLDS	FSGKASRS	VGRVLPV	VNIDGGT	TFERNTR	LFGGGVQ
	480	490	500	510	520	530
	550	560	570	580	590	600
m958.pep	QNDLPNFD	SSSESSFGY	GQLFREN	LYGNDRI	TANSLSA	AVQSRILD
g958	QNDLPNFD	SSSESSFGY	GQLFREN	LYGNDRI	ANAANSL	STAVQSRILD
	540	550	560	570	580	590
	610	620	630	640	650	660
m958.pep	QKFYFKDD	AVMLDGS	VGKPRN	RSRWVAF	ASGSIGS	RFI
g958	QKFYFKDD	AVMLDGS	VGNPRN	RSRWVAF	ASGGIGR	FTLDSSI
	600	610	620	630	640	650
	670	680	690	700	710	720
m958.pep	SYRPAQ	GKVLNARY	KYGRNE	KIYLKSD	GSYFYDK	LSQLDL
g958	GYRPA	GKVLNARY	KYGRNE	KIYLQAD	GSYFYDK	LSQLDL
	660	670	680	690	700	710

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              730      740      750      760      770      780
m958.pep      EAKKPIEVLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g958           EAKKPIEMLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPAGR
              720      730      740      750      760      770

              790      800
m958.pep      MDVAVPGYITAHSLSAGRNRKP
              |||||:|||||:|||||:|||||:
g958           MDVAVPGYIPAHSLSAGRNRKRP
              780      790      800

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2933>:

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a958.seq
1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTCGGCAGC CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGGA AGCGTTCGGA GCGTGTCCGA ACCCATAACG
151 CCTACCAAGC TGAGCCTCGG TTCGACCTGC CTGTTTTCGA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCAGACAT
251 CCATCCCCGA AGACTATACG CGCATTGTGT CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCTGTC AACGCAATCG
351 GACGACCCCTC AATGCCGATT GGGCGGATTA CGACCACTCG GGCACACCCG
401 TTACCGCAGG CGACCGGTTC GCCCTCCAAC AGGACGGTAC GCTGATTCCG
451 GGCGAACCCG TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGTATG GAAACCGAAC ACGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAACCCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCCGCTTC
651 CGTCGAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCT
701 TCGTGTTCGG CGGCGTTCCC ATTTTCTACA CCCCTTGGGC GGAATTCCCG
751 CTTGACGGCA ACCGCAAAAG CGGCCTGTCT GTTCCCTCAC TGTCCGCCGG
801 TTCCGACGGC GTTTCCTTTT CCGTTCCTTA TTTATTTCAAC CTGCCCCCA
851 ATCTCGATGC CACGTTTCGG CCGGCGTGA TCGGCGAACG CGGCGCGGTC
901 TTTGACGGGC AGGTACGCTA CTGCGGCCG GATTATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCCGCACG ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCGAAATG GCAGCACCGG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTCGATTTCA ACCAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTATGGCGC CAGGCGGGCG GCGGCGAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAAGC GGCTACAAAG ACAAAACGTA
1251 TGCCCTGATG CCGCGCCTTT CCGCCGATTG GCGCAAAAC ACCGGCAGGG
1301 CGCAAATCGG CGTGTCCGCC CAATTTACCC GCTTCAGCCA CGACAGCCGC
1351 CAAGACGGCA GCGCCTCGT CGTCTATCCC GACATCAAAT GGGATTTCAG
1401 CAACAGCTGG GGTACGTCC GTCCAAACT CCGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCCGCACT
1501 CTGCCCATCG TCAACATCGA CAGCGGCATG ACCTTCGAAC GCAATACGCG
1551 GATGTTTCGG GCGGAGTCC TGCAAACCCCT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTCTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTTTTT CGTGAAACCC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCGGCC GTGCAAGGCC
1751 GTATTTTGGG CCGCGCGACG GGGGAAGAGC GTTCCGCGC CGGCATCGGG
1801 CAGAAATTCT ACTTCAAAAA CGACGCAGTC ATGCTTGACG GCAGTGTCGG
1851 CAAAAAACC GCGAGCCGTT CCGACTGGGT GGCATTGCGC TCCAGCGGCA
1901 TCGGACGCGC CTTATCCTC GACAGCAGCA TCCACTACAA CAAAACGAC
1951 AAACGCGCCG AGAAGTACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGCTG AACGCCCGCT ACAAATACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GGCCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAAGCAG TTGCGGCTGC TGGGGCGCGG GCGGTGTACG CCAACGCTAC
2251 GTTACGCGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTCT GCAGAAACCC CGCAGACAGG ATGGATGTCG
2351 CCGTTCCCGG CTATATCCCC GCGCACTCTC TTCCGCGCGG ACGCAACAAA
2401 CGGCCCTGA

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This corresponds to the amino acid sequence <SEQ ID 2934; ORF 958.a>:

```

a958.pep
1  LARLFSLKPL VLALGFCEFGT HCAAADAVAA EETDNPTAGG SVRSVSEPIQ
51  PTSLSLSTGC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMREGQ
101 SQVQVRAEEN VVERNRRTL NADWADYDQS GDTVTAGDRF ALQQDGTLLIR
151 GETLTYNLEQ QTGEAHNVRM ETEHGRRLO SVSRTEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFFVGGVP IFYTPWADFP

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1374

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251 LDGNRKSGLL VPSLSAGSDG VSLSVPIYFN LAPNLDTFA PGVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSNLAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSADWRKN TGRAQIGVSA QFTRFSHDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSRT
501 LPIVNIDSGM TFERNTRMFG GGVLTQLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGOLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKNDV MLDGSVGKKP RSRSDWVAF SSGIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVK NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVL GAEEKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIP AHSLSAGRNK
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a958/m958 98.1% identity in 802 aa overlap

```

          10      20      30      40      50      60
a958.pep  LARLFSLKPLVLALGFCFGTHCAAADAVAAEETDNPTAGGSVRSVSEPIQPTSLSLGSTC
m958      LARLFSLKPLVLALGFCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC
          10      20      30      40      50      60

          70      80      90      100     110     120
a958.pep  LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTTL
m958      LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTTL
          70      80      90      100     110     120

          130     140     150     160     170     180
a958.pep  NADWADYDQSGDVTAGDRFALQODGTLIRGETLTYNLEQQTGEAHNVRMETEHGGRRLQ
m958      NTDWADYDQSGDVTAGDRFALQODGTLIRGETLTYNLEQQTGEAHNVRMEIEQGGRRLQ
          130     140     150     160     170     180

          190     200     210     220     230     240
a958.pep  SVSRTAEMLGEGHYKLTETQFNTCESAGDAGWYVKAASVEADREKGIGVAKHAAFFVGGVP
m958      SVSRTAEMLGEGHYKLTETQFNTCESAGDAGWYVKAASVEADREKGIGVAKHAAFFVGGVP
          190     200     210     220     230     240

          250     260     270     280     290     300
a958.pep  IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSVPIYFNLAAPNLDTFAPGVIGERGAV
m958      IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSVPIYFNLAAPNLDTFAPSVIGERGAV
          250     260     270     280     290     300

          310     320     330     340     350     360
a958.pep  FDGQVRYLRPDYAGQSDLTWLPDCKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG
m958      FDGQVRYLRPDYAGQSDLTWLPDCKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG
          310     320     330     340     350     360

          370     380     390     400     410     420
a958.pep  YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM
m958      YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM
          370     380     390     400     410     420

          430     440     450     460     470     480
a958.pep  PRLSADWRKNTGTRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH
m958      PRLSVEWRKNTGTRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH
          430     440     450     460     470     480

          490     500     510     520     530     540
a958.pep  ATYYSLNRFSGQEARRVSRTLPIVNIDSGMTFERNTRMFGGGVLQTLERLFYNYIPAKS
m958      ATYYSLNRFSGQEARRVSRTLPIVNIDSGMTFERNTRMFGGEVLQTLERLFYNYIPAKS

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1375

	490	500	510	520	530	540
	550	560	570	580	590	600
a958.pep	QNDLPNFDSSSESGYQQLFRENLYYGNDRIANTANSLSAAVQSRILDGATGEERFRAGIG					
m958	QNDLPNFDSSSESGYQQLFRENLYYGNDRIANTANSLSAAVQSRILDGATGEERFRAGIG					
	550	560	570	580	590	600
	610	620	630	640	650	660
a958.pep	QKFYFKNDVAVMLDGSVGKKPRSRSDWVAFASSGIGSRFILDSSIHYNQNDKRAENYAVGA					
m958	QKFYFKNDVAVMLDGSVGKKPRSRSDWVAFASSGIGSRFILDSSIHYNQNDKRAENYAVGA					
	610	620	630	640	650	660
	670	680	690	700	710	720
a958.pep	SYRPAQGGKVLNARYKYGRNEKIYKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF					
m958	SYRPAQGGKVLNARYKYGRNEKIYKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF					
	670	680	690	700	710	720
	730	740	750	760	770	780
a958.pep	EAKKPIEVLAGAIEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR					
m958	EAKKPIEVLAGAIEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR					
	730	740	750	760	770	780
	790	800				
a958.pep	MDVAVPGYIPAHSLSAGRNRKPX					
m958	MDVAVPGYITAHSLSAGRNRKP					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2935>:

g959.seq

```

1 ATGAACATCA AACACCTTCT CTGACCGCC GCCGCAACCG CACTGTTGGG
51 CATTTCGGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2936; ORF 959.ng>:

g959.pep

```

1 MNIKHL LLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51 AQAEKA AAWAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2937>:

m959.seq

```

1 ATGAACATCA AACACCTTCT CTGACCTCC GCCGCAACCG CACTGCTGAG
51 CATTTCGGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2938; ORF 959>:

m959.pep

```

1 MNIKHL LLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51 AQAEKA ALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 959 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. gonorrhoeae*

1376

m959/g959 95.4% identity in 108 aa overlap

	10	20	30	40	50	60
m959.pep	MN	IK	HL	LL	TS	AAT
g959	MN	IK	HL	LL	TS	AAT

	70	80	90	100	109
m959.pep	VGG	KIT	DID	LE	HD
g959	VGG	KIT	DID	LE	HD

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2939>:

a959.seq

```

1  ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51  CATTTCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2940; ORF 959.a&gt;:

a959.pep

```

1  MNFKRLLLLTA AATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*ORF 959 shows 94.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. meningitidis*

a959/m959 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a959.pep	MN	FK	RL	LL	LT	AA
m959	MN	IK	HL	LL	TS	AA

	70	80	90	100	109
a959.pep	VGG	KIT	DID	LE	HD
m959	VGG	KIT	DID	LE	HD

g960.seq not found yet

g960.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2941>:

m960.seq

```

1  ATGCAAGTAA ATATTCAGAT TCCCTGTATG CTGTACAGAC GCGGGAGTGT
51  TAAGCCCCC TTGTTGAAG CTCCGCGGCT CCTGCCGAGC TTCACCGACC
101 CCGTTGTGCC CAAGCTCTCT GCTCCCGGCG GCTACATTGT CGACATCCCC
151 AAAGGCAATC TGAAAACCGA AATCGAAAAG CTGGCCAAAC AGCCCGAGTA
201 TGCCTATCTG AACAGCTCC AAGTAGCGAA AAACGTCAAC TGGAAACCAGG
251 TGCAACTGGC TTACGATAAA TGGGACTATA AGCAGGAAGG CTTAACCAGA
301 GCCGCTGCAG CGATTATCGC GCTGGCTGTT ACCGTGGTTA CTGCGGGCGC
351 GGGAGTCGGA GCCGCACTAG GCTTAAACGG CGCAGCCGCA GCAGCGGCCG
401 ATGCCGCCTT TGCCCTCACTC GCTTCTCAGG CTTCCGTATC GCTCATCAAC
451 AATAAAGGCG ATGTCGGCAA AACCCTGAAG GAACTGGGCA GAAGCCGCAC
501 GGTAAAAAAT CTGGTTGTAG CGGCGGCAAC GGCAGGCGTA TCCAACAAC

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1377

```

551 TCGGTGCCTC TTCCCTTGCC ACTTGGAGCG AAACCCCTTG GGTAAACAAC
601 CTC AACGTTA ACCTGGCCAA TGCGGGCAGT GCCGCGCTGA TCAACACCGC
651 TGTTAACGGC GGCAGCCTGA AAGACAATCT GGAGGCAAAT ATCCTGGCGG
701 CATTGGTGAA TACCGCGCAT GGGGAGGCGG CGAGTAAGAT CAAAGGACTG
751 GATCAGCACT ATGTCGCCCA CAAAATCGCT CATGCCGTAG CGGGCTGTGC
801 GGCTGCAGCG GCGAATAAGG GCAATGTCA GGACGGCGCG ATCGGTGCGG
851 CTGTGGGTGA GATTGTCGGG GAGGCTTTGG TTAAAATAC CGATTTTAGC
901 GATATGACCC CGGAACAATT AGATCTGGAA GTTAAGAAAA TTACCGCCTA
951 TGCCAAACTT GCGGCAGGTA CAGTTGCAGG CGTAACGGGA GGAGATGTCA
1001 ATACTGCTGC ACAAACCGCA CAAAACGCGG TAGAAAATAA TGCGGTAAAA
1051 GCTGTTGTAA CTGCTGCAAA AGTGGTTTAT AAGGTAGCCA GAAAAGGATT
1101 AAAAAACGGG AAAATCAACG TTAGAGATT AAAACAGACG TTGAAAGACG
1151 AAGGTTATAA TTTAGCCGAC AACCTGACCA CTTATTTCGA CGAAACATTG
1201 GATTGGAACG ATGCCAAAGC CGTTATTGAT ATTGTCGTCG GAACAGAGCT
1251 GAATCGCGCT AATAAAGGGG AAGCGGCACA AAAGGTCAAG GAAGTTTAG
1301 AAAAAAATCG TCCTTATATC CCTAATAAAG GTGCTGTACC GAATATGAGT
1351 ACATACATGA AAAATAATCC TTTTGAAAA CAGCTGGCTC AAATTTCAGA
1401 AAAGACAACG CTTCCGACGC AGCAAGGGCA GTCTGTCTTC TTGGTAAAAA
1451 GAAACCAAGG GTTATTAAAA ACCGGTGATA GGTTTTATTT AGATGGCCAA
1501 CATAAAATC ATTTAGAGGT TTTTGATAAA AATGGGAACT TTAAGTTTGT
1551 TCTAAATATG GATGGTTCGC TTAACCAAT GAAACTGGG GCAGCAAAAG
1601 GTCGTAAATT AAACTTAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2942; ORF 960>:

m960.pep

```

1 MQVNIQIPCM LYRRGSVKPP LFEAPRLPS FTDPVVPKLS APGGYIVDIP
51 KGNLKEIEK LAKQPEYAYL KQLQVAKNVN WNQVQLAYDK WDKQEGLTR
101 AGAAIALAV TVVTAGAGVG AALGLNGAAA AAADAAFASL ASQASVSLIN
151 NKGDVGKTLK ELGRSRTVKN LVVAATAGV SNKLGASSLA TWSETPWVNN
201 LNVNLANAGS AALINTAVNG GSLKDNLEAN ILAALVNTAH GEAASKIKGL
251 DQHYVAHKIA HAVAGCAAAA ANKGKQDGA IGAAVGEIVG EALVKNTDFS
301 DMTPEQLDLE VKKITAYAKL AAGTVAGVTG GDVNTAAQTA QNAVENNAVK
351 AVVTAAKVVY KVARGLKNG KINVRDLKQT LKDEGYNLAD NLTTLEFDEL
401 DWNDAKAVID IVVGTELNRA NKGEAAQKVK EVLEKNRPYI PNKGAVPNMS
451 TYMKNNPFKG QLAQISEKTT LPTQQGQSVF LVKRNQGLLK TGDRFYLDGQ
501 HKNHLEVFDK NGNFKEVLNM DGSLNQMKTG AAKGRKLNLK *

```

a960.seq not found yet

a960.pep not found yet

g961.seq not found yet

g961.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2943>:

m961.seq

```

1 ATGAGCATGA AACACTTTCC AGCCAAAGTA CTGACCACAG CCATCCTTGC
51 CACTTTCTGT AGCGGCGCAC TGGCAGCCAC AAGCGACGAC GATGTTAAAA
101 AAGCTGCCAC TGTGGCCATT GTTGCTGCCT ACAACAATGG CCAAGAAATC
151 AACGGTTTCA AAGCTGGAGA GACCATCTAC GACATTGGTG AAGACGGCAC
201 AATTACCCAA AAAGACGCAA CTGCAGCCGA TGTGAAGCC GACGACTTTA
251 AAGGTCTGGG TCTGAAAAAA GTCGTGACTA ACCTGACCAA AACCGTCAAT
301 GAAAACAACG AAAACGTCGA TGCCAAAGTA AAAGCTGCAG AATCTGAAAT
351 AGAAAAGTTA ACAACCAAGT TAGCAGACAC TGATGCCGCT TTAGCAGATA
401 CTGATGCCGC TCTGGATGAA ACCACCAACG CCTTGAATAA ATTGGGAGAA
451 AATATAACGA CATTTGCTGA AGAGACTAAG ACAAAATATC TAAAAATTGA
501 TGAAAAATTA GAAGCCGTGG CTGATACCGT CGACAAGCAT GCCGAAGCAT
551 TCAACGATAT CGCCGATTCA TTGGATGAAA CCAACACTAA GGCAGACGAA
601 GCCGTCAAAA CCGCCAATGA AGCCAAACAG ACGGCCGAAG AAACCAAACA
651 AAACGTCGAT GCCAAAGTAA AAGCTGCAGA AACTGCAGCA GGCAAAGCCG
701 AAGCTGCCGC TGGCACAGCT AATACTGCAG CCGACAAGGC CGAAGCTGTC
751 GCTGCAAAAG TTACCGACAT CAAAGCTGAT ATCGCTACGA ACAAGCTGA
801 TATTGCTAAA AACTCAGCAC GCATCGACAG CTGGACAAA AACGTAGCTA
851 ATCTGCGCAA AGAAACCCGC CAAGGCCTTG CAGAACAAGC CGCGCTCTCC
901 GGCCTGTTC AACTTACAA CGTGGGTCGG TTCAATGTAA CGGCTGCAGT
951 CGCGGGCTAC AAATCCGAAT CGGCAGTCGC CATCGGTACC GGCTTCGCT
1001 TTACCGAAAA CTTTGCCGCC AAAGCAGGCG TGGCAGTCGG CACTTCGTCC
1051 GGTCTTCCG CAGCCTACCA TGTCGGCGTC AATTACGAGT GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 2944>:

m961.pep

```

1 MSMKHFPKAV LTTAILATEFC SGALAATSDD DVKKAATVAI VAAYNNGQEI

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1378

```

51  NGFKAGETIY DIGEDGTITQ KDATAADVEA DDFKGLGLKK VVTNLTKTVN
101 ENKQNVDAKV KAAESEIEKL TTKLADTDAA LAOTDAALDE TTNALNKLGE
151 NITTFAEETK TNIVKIDEKL EAVADTVDKH AEA FN DIADS LDETNTKADE
201 AVKTANEAKQ TAEETKQNV AKVKAETA A GKAEAAAGTA NTAADKAEAV
251 AAKVTDIKAD IATNKADIAK NSARIDSLDK NVANLRKETR QGLAEQAALS
301 GLFQPYNVGR FNVTAAVGGY KSESAVAIGT GFRFTENFAA KAGVAVGTSS
351 GSSAAYHVG V NYEW*

```

a961.seq not found yet  
a961.pep not found yet

g972.seq not found yet  
g972.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2945>:

```

m972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCArTTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA
251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTCG GArGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTGTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGCGG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTATTAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAAGAA AGCAAATGGG TAAGGTTCTGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTCTGTG GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCCGAAAG GTTTGATCAG AGAAAGAAAA AGCTTAATTT AACTTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTCAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCTGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAATG GAACTTGATG AATTGGGGGT TATTGCTTTT AAAAATTCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTGA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAAATGT
1251 AGATTATGAT TATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2946; ORF 972>:

```

m972.pep
1  LTNRGGAKLK TXSKSSERMS EVEYFSHFIS DGKGKLEIP QRRGKQDGVF
51  VDWISFTFHE DTLLKVS GCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFGXQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RT RITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNE D GSGKTFYVGR KKNRFRVRY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQSYFC GAFFICKRKF NMPVPERFDQ RKKKLNLTFE
301 HKLHYAKNAV GKLNVNFIEM GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKYQEYLS KVVHQNVDDYD YF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2947>:

```

a972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATCCG CAGCGAAGAG GTAAGCAAGA CGGGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA

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1379

```

251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTTC GAGGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGCTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTATTAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAAGAA AGCAATGGG TAAGGTTCTGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTGTAG AAAATTTAAA AATATGCCCG
851 TTCCCGAAG GTTTGATCAG AGAAAGAAAA CGCTTAATTT AACTTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAAATT GAACTTGATG AATTGGGGGT TATTGCTTTT AAAAATCTCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTGA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAAATGT
1251 AGATTATGAT TATTTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2948; ORF 972.a>:

```

a972.pep
  1 LTNRGGAKLK TNSKSSERMS EVEYFSHFIS DGK GK LLEIP QRRGKQDGVF
 51 VDWISFTFHE DTLLKVSGCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFGGQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RT RITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNED GSGKTFYVGR KKNRSRFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFICRKFK NMPVPERFDQ RKKTNLNLTFE
301 HKLHYAKNAV GKLVNFMIE M GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKYQEYLS KVIHQNVVDYD YF*

```

m972/a972 99.3% identity in 422 aa overlap

```

              10      20      30      40      50      60
m972.pep      LTNRGGAKLKTXSKSSERMSEVEYFSHFISDGK GK LLEIPQRRGKQDGVFVDWISFTFHE
              |||||
a972           LTNRGGAKLKTNSKSSERMSEVEYFSHFISDGK GK LLEIPQRRGKQDGVFVDWISFTFHE
              10      20      30      40      50      60

              70      80      90      100     110     120
m972.pep      DTLLKVSGCPLFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDVDYGE
              |||||
a972           DTLLKVSGCPLFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDVDYGE
              70      80      90      100     110     120

              130     140     150     160     170     180
m972.pep      VHFGXQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RT RITRIDLALDFFDGEYTPDQ
              |||||
a972           VHFGGQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RT RITRIDLALDFFDGEYTPDQ
              130     140     150     160     170     180

              190     200     210     220     230     240
m972.pep      ALLDHDNGFFDNSNQRPKSETIGTAWRNEDGSGKTFYVGRKKNRSRFVRVYEKGRQLGDKE
              |||||
a972           ALLDHDNGFFDNSNQRPKSETIGTAWRNEDGSGKTFYVGRKKNRSRFVRVYEKGRQLGDKE
              190     200     210     220     230     240

              250     260     270     280     290     300
m972.pep      SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFICRKFKNMPVPERFDQRKKNLNLTFE
              |||||
a972           SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFICRKFKNMPVPERFDQRKKNLNLTFE
              250     260     270     280     290     300

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1380

	310	320	330	340	350	360
m972 . pep	HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI					
a972	HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m972 . pep	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKYQEYLSKVYHQNVDDYD					
a972	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKYQEYLSKVYHQNVDDYD					
	370	380	390	400	410	420
m972 . pep	YFX					
a972	YFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2949>:

```

g973 . seq
1  ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCCG
51  actCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA ACAGGAAGTT TTTGATGCCG ACACACTGAC CCGGCTGGAA
151 AAAGTATTGG ACTTTGCCGA GCTGGAAGTG CGCGATGCGA TGATTACGCG
201 CAGCCGCATG AACGTATTGA AAGAAAACGA CAGCATCGAA CGCATCACCG
251 CCTACGTCAT CGATACCGCC CATTCGCGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTCAACCCC GAGCAGTTCC ACCTGAAATC CGTCTTGCGC CCTGCCGTTT
401 TCGTGCCCCG AGGCAAATCT TTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
501 TTTGGTCACC TTTGAAGACA TCATCGAGCa aatcgtcggt gacaTCGAAG
551 ACGAGTTTGA CGAAGACGAA AGCGccgacg acatCCACTC cgTTTccgCC
601 GAACGCTGGC GCATCCacgc ggctaCCGAA ATCGAAGaca TCAACGCCTT
651 TTTCCGTACG GAatacggca gcaagaagc cgacaccatc ggcggctTGG
701 TCATTACAGGA ATTGGGACAC CTGCCCGTGC GCGCGAAAA AGTCCTTAtc
751 ggcgGTTTGC agttcaccgt CGCCCGCGCC GACAACCGCC GCCTGCACAC
801 GCTGATGGCG ACCCGCGTGA AGTAAGCAGA GCCTGCCcgc accgccgttT
851 CTGCacAGTT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2950; ORF 973.ng>:

```

g973 . pep
1  MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLTRLE
51  KVLDFAELEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFPN EQFHLKSVLR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGGLVT FEDIIEQIVG DIEDEFDEDE SADDIHSVSA
201 ERWRIHAATE IEDINAFFGT EYGSEEADTI GGLVIQELGH LPVRGEKVL I
251 GGLQFTVARA DNRRLHTLMA TRVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2951>:

```

m973 . seq
1  ATGGACGGCG CACAACCGAA AACGAATTTT TTTGAACGCC TGATTGCCCCG
51  ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA GCAGGAAGTT TTTGATGCCG ATACGCTTTT AAGATTGGAA
151 AAAGTCCTCG ATTTTTCGGA TTTGGAAGTG CGGACGCGA TGATTACGCG
201 CAGCCGTATG AACGTTTTAA AAGAAAACGA CAGCATCGAG CGCATCACCG
251 CCTACGTTAT CGATACCGCC CATTCGCGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTTAACCCC GAGCAGTTCC ACCTCAAATC CATTCCTCGC CCCGCCGTCT
401 TCGTCCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCGAT TGTCATCGAC GAATACGGCG GCACATCCGG
501 CTTGGTCACC TTTGAAGACA TCATCGAGCA AATCGTCGGC GAAATCGAAG
551 ACGAGTTTGA CGAAGACGAT AGCGCCGACA ATATCCATGC CGTTTCTTcm
601 GaACGcTGGC GCATCCATGC AGCTACCGAA ATCGAAGACA TCAACACCTT

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651 CTTCCGGCAGC GAATACAGCA KCGAAGAAGC CGACACCATT GGCGGCCTGG  
 701 TCATTCAAGA GTTGGGACAT CTGCCCGTGC GCGGCGAAAA AGTCCTTATC  
 751 GGCGGTTTGC AGTTCACCGT CGCACGCGCC GACAACCGCC GCCTGCATAC  
 801 GCTGATGGCG ACCCGCGTGA AGTAA

This corresponds to the amino acid sequence <SEQ ID 2952; ORF 973>:

m973 . pep

1 MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLRLLE  
 51 KVLDFSLEVD RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED  
 101 KDEVLGILHA KDLLKYMFPN EQFHLKSILR PAVFVPEGKS LTALLKEFRE  
 151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG EIEDEFDEDD SADNIHAVSS  
 201 ERWRIHAATE IEDINTFFGT EYSXEEADTI GGLVIQELGH LPVRGEKVL  
 251 GGLQFTVARA DNRRLHTLMA TRVK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 973 shows 95.6% identity over a 274 aa overlap with a predicted ORF (ORF 973.ng) from *N. gonorrhoeae*:

m973/g973

	10	20	30	40	50	60
m973 . pep	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFSLEVD					
g973	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFAELEV					
	10	20	30	40	50	60
m973 . pep	RDAMITRSRMNVLKENDSIE RITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFPN					
g973	RDAMITRSRMNVLKENDSIE RITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFPN					
	70	80	90	100	110	120
m973 . pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
g973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
	130	140	150	160	170	180
m973 . pep	EIEDEFDEDD SADNIHAVSS ERWRIHAATE IEDINTFFGT EYSXEEADTI GGLVIQELGH					
g973	DIEDEFDEDESADDIHSVSAERWRIHAATE IEDINAFGT EYGSEEADTI GGLVIQELGH					
	190	200	210	220	230	240
m973 . pep	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
g973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2953>:

a973 . seq

1 ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCG  
 51 ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTGACC CTGTTGCGCC  
 101 AAGCGCACGA ACAGGAAGTA TTTGATGCGG ATACGCTTTT AAGATTGGAA  
 151 AAAGTCCTCG ATTTTCTGA TTTGGAAGTG CGCGACGCGA TGATTACGCG  
 201 CAGCCGTATG AACGTTTTAA AAGAAAACGA CAGCATCGAA CGCATCACCG  
 251 CCTACGTTAT CGATACCGCC CATTGCGGCT TCCCCGTCAT CCGTGAAGAC  
 301 AAAGACGAAG TTTTGGGTAT TTTGCACGCC AAAGACCTGC TCAAATATAT  
 351 GTTCAACCCC GAGCAGTTCC ACCTCAAATC GATATTGCGC CTGCGCGTCT  
 401 TCGTCCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA  
 451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG  
 501 TTTGGTAACT TTTGAAGACA TCATCGAGCA AATCGTCGGC GACATCGAAG  
 551 ATGAGTTTGA CGAAGACGAA AGCGCGGACA ACATCCACGC CGTTTCCGCC



1382

```

601 GAACGCTGGC GCATCCACGC GGCTACCGAA ATCGAAGACA TCAACGCCTT
651 TTTCCGGCACG GAATACAGCA GCGAAGAAGC CGACACCATC GGCGGCCTGG
701 TCATTACAGGA ATTGGGACAC CTGCCCCTGTC GCGGCGAAAA AGTCCTTATC
751 GGCGGTTTGC AGTTCACCGT CGCCCGCGCC GACAACCGCC GCCTGCATAC
801 GCTGATGGCG ACCCGCGTGA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2954; ORF 973.a>:

```

a973.pep
  1 MDGAQPKTNF FERLIARLAR EPDSAEDVLT LLRQAHEQEV FDADTLRLLE
 51 KVLDFSDLEV RDAMITSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGLVF FEDIIEQIVG DIEDEFDEDE SADNIHAVSA
201 ERWRIHAATE IEDINAFFGT EYSSEADTI GGLVIQELGH LPVRGEKVL
251 GGLQFTVARA DNRRLHTLMA TRVK*

```

m973/a973 97.8% identity in 274 aa overlap

```

              10      20      30      40      50      60
m973.pep    MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFSDLEV
              |||||
a973         MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLRLLEKVLDFSDLEV
              10      20      30      40      50      60

              70      80      90     100     110     120
m973.pep    RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP
              |||||
a973         RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP
              70      80      90     100     110     120

              130     140     150     160     170     180
m973.pep    EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG
              |||||
a973         EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG
              130     140     150     160     170     180

              190     200     210     220     230     240
m973.pep    EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH
              :|||
a973         DIEDEFDEDESADNIHAVSAERWRIHAATEIEDINAFFGTEYSSEADTIGGLVIQELGH
              190     200     210     220     230     240

              250     260     270
m973.pep    LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX
              |||||
a973         LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX
              250     260     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2955>:

```

g981.seq
  1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCAC TCGCGCTGTC
 51 TGCCTGCGGC GGTACGGGCA AAGATGCCGC CGCGCCTGCC GCCAACCCCG
101 GCAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GACGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCGCCTTG AACAAACGGC ATGCGGACGT TGTGATGTCG
301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGATT TCAGCGACCC
351 GTATTTTGAA ATCACCACAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTTCTTCCGA AGATTTGAAA AAGATGAACA AAGTCGGCGT GGTACCGGC
451 CACACGGGCG ATTTCTCCGT TTCCAAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTCGAAAACG TCCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTCAATCG CAATTATGTG
601 AAAACAACCC CGGCCAAAGG AATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATCTACG CCAAATATTG TGCCAAAGAG GCGGACAGG CTGCGAAATA
801 A

```

1383

This corresponds to the amino acid sequence <SEQ ID 2956; ORF 981.ng>:

```

g981.pep
  1  MKKWIAAALA CSALALSACG GQGKDAAPA ANPGKVYRVA SNAEFAPFES
 51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101  GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KKVSSSEDLK KMNKVGVTG
151  HTGDFSUSKL LGNDNPFIAR FENVPLIIE LENGGLDSVV SDSAVIANVY
201  KNNPAKGMDV VTLPDFTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251  KIYAKYFAKE GGQAAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2957>:

```

m981.seq
  1  ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCCGC TCGCGCTGTC
 51  TGCCTGCGGC GGTCAGGGCA AAGATACCGC CGCGCCTGCC GCCAACCCCG
101  ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151  TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201  GATGGCGAAG GCGGGCAATT TAAAAATCGA ATCAAACAC CAGCCGTGGG
251  ACAGCCTTTT CCCCCTTTA AACAACGGCG ATGCGGACGT TGTGATGTCG
301  GCGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351  GTATTTTGAA ATCACCACAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401  CTTCTTCCGA AGATTTGAAA AACATGAACA AAGTCGCGCT GGTAACCGGC
451  TACACGGGCG ATTTCTCCGT ATCCAACTC TTGGGCAACG ACAATCCGAA
501  AATCGCGCGC TTTGAAAACG TTCCCTGAT TATCAAAGAA CTGGAAAACG
551  GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTATCGC CAATTATGTG
601  AAAAAACAAT CCGCCAAAGG GATGGACTTC GTTACCCTGC CCGACTTAC
651  CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701  AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751  AAGATTTACG CCAATATTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
801  A

```

This corresponds to the amino acid sequence <SEQ ID 2958; ORF 981>:

```

m981.pep
  1  MKKWIAAALA CSALALSACG GQGKDTAAPA ANPDKVYRVA SNAEFAPFES
 51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101  GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KKVSSSEDLK NMNKGVTG
151  YTGDFSUSKL LGNDNPFIAR FENVPLIIE LENGGLDSVV SDSAVIANVY
201  KNNPAKGMDV VTLPDFTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251  KIYAKYFAKE DGQAAK*

```

m981/g981 98.1% identity in 266 aa overlap

```

          10      20      30      40      50      60
981.pep  MKKWIAAALACSALALSACGGQGKDTAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF
          |||
g981      MKKWIAAALACSALALSACGGQGKDAAPAANPGKVYRVASNAEFAPFESLDSKGNVEGF
          10      20      30      40      50      60

          70      80      90      100     110     120
981.pep  DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE
          |||
g981      DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE
          70      80      90      100     110     120

          130     140     150     160     170     180
981.pep  ITQVVLVPKGKKVSSSEDLKMNKVGVTGTYTGDFSUSKLLGNDNPFIARFENVPLIIE
          |||
g981      ITQVVLVPKGKKVSSSEDLKMNKVGVTGHTGDFSUSKLLGNDNPFIARFENVPLIIE
          130     140     150     160     170     180

          190     200     210     220     230     240
981.pep  LENGGLDSVVSDSAVIANVYKNNPAKGMDVTLPDFTEHYGIAVRKGDEATVKMLNDAL
          |||
g981      LENGGLDSVVSDSAVIANVYKNNPAKGMDVTLPDFTEHYGIAVRKGDEATVKMLNDAL
          190     200     210     220     230     240

          250     260
981.pep  EKVRESGEYDKIYAKYFAKEDGQAAKX
          |||
g981      EKVRESGEYDKIYAKYFAKEGGQAAKX
          250     260

```

1384

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2959>:

```
a981.seq
1   ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGTCAGGGTA AAGATGCCGC CGCGCCCGCC GCAAATCCCG
101 ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCgcCTTG AACAAcGGCG ATGCGGACGT TGTGATGTCG
301 GGCGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCcAAG TCGTCTCTCGT TCCGAAAGGC AAAAAATAT
401 CTTCTTCCGA AGATTtGAAA AACATGAACA AAGTCGGCGT GGTAACCGGC
451 TACACGGGCG ATTTCTCCGT ATCCAAACTC TTGGGCAACG ACAACCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCcCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGA TTCCGTGGTC AGCGACAGCG CAGTCATCGC CAATTATGTG
601 AAAAAcAATC CGACCAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG AAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAAATCTACG CCAAATATTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2960; ORF 981.a>:

```
a981.pep
1   MKKWIAAALA CSALALSACG GQGKDAAAPA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVVMs
101 GVTITDDRQK SMDfSDPYFE ITQVVLVPKG KkISSeDLK NMNKVGvVTG
151 YTGDFSVSKL LGNDNPkIAR FENVPLIIE LENGGLDSV SDSAVIANyV
201 KNNPTKGMDf VTLpDFTTEH YGIAVRKGDE ATVKMLNDAL KKVRESGEyD
251 KIYAKYfAKE DGQAAX*
```

m981/a981 98.5% identity in 266 aa overlap

	10	20	30	40	50	60
m981.pep	MKKWIAAALACSALALSACGGQGKDTAAPANPDKVYRVASNAEFAPFESLDSKGNVEGF					
a981	MKKWIAAALACSALALSACGGQGKDAAPANPDKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
m981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMsGVTITDDRQKSMDfSDPYFE					
a981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMsGVTITDDRQKSMDfSDPYFE					
	70	80	90	100	110	120
m981.pep	ITQVVLVPKGKkVSSSEDlKNMNkVGvVTGYTGDFSVSKLLGNDNPkIARFENVPLIIE					
a981	ITQVVLVPKGKkISSSEDlKNMNkVGvVTGYTGDFSVSKLLGNDNPkIARFENVPLIIE					
	130	140	150	160	170	180
m981.pep	LENGGLDSVVSdSAVIANyVKNNpAKGMdFVTLpDFTTEHYGIAVRKGDEATVKMLNDAL					
a981	LENGGLDSVVSdSAVIANyVKNNPTKGMDfVTLpDFTTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
m981.pep	EKVRESGEYDKIYAKYfAKEDGQAAXX					
a981	KKVRESGEYDKIYAKYfAKEDGQAAXX					
	250	260				
m981.pep	EKVRESGEYDKIYAKYfAKEDGQAAXX					
a981	KKVRESGEYDKIYAKYfAKEDGQAAXX					
	250	260				

1385

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2961>:

```

g982.seq
1   atcgcatcgc aaaaaccttcg attcgacaat cgattcctcc aaaaaatggt
51  caacggcgTg aatatatttgc cggccgcCga ttgggtagcC ttgGGcgCgCA
101 AAGGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TAAAAGAAGT CGCGTCCAAA ACCAACgaCg
251 tagCCGgcga cggtagcact accgCCACCG TATTGGCACA ATCCATCGTT
301 GCCGAAGgcA TGAAATACGT TACCGCCGGC ATGAACCCGA CCGATCTGAA
351 ACGCGGCATC GACAAAGccg ttgCCGCTtt ggttgAAGAg cTGAAAAACA
401 TCGCCAAACC TTGCGATACT TCCAAAGAAA TCGCCCAAGT CGGCTCGATT
451 TCCGCCAACT CCGACGAACA AGtcgGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGgcg tgattacCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCCCCTTACT TTATCAACGA CGCGGAAAAA CAAATCGCCG GTCTGGACAA
651 TCCGTTTGTG TTGCTGTTCG ACAAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCCCGTGTG GGAACAAGTG GCGAAAGCCA GCCGCCGCTG GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATC CTGAAAACCG TTGCCGTCAA AGCccccggc tTCGGcGACC
851 GCCGCAAAGC GATgctgcaa gaCATCGCCA TCCTGACcgg cggcgTagtG
901 ATTtccGAAG Aagtccggcct GTCTTTGGAA AAAGcgactT TGgacgaCTT
951 Gggtcaaacc aaACGcatCG AAATCGGtga agaaaaact ACCGTCATcg
1001 acgGCTTCGG CGACGcagcC CAAAtcgaag cgCGTGTTCG CGAAATCCGCG
1051 CAACAAATCG AAACCGCGAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAAGTGGCAG GAGGCGTGGC AGTGATCAA GTCTGGCGCGG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCTGTTG CGCGCCCGTG CCGCTTGGGA AAACCTGCAC ACCGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTAT TGCGCGCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGA GAACCCAGCG TGGTGGTGAA
1401 CAAAGTGTTC GAAGGCAAAG GCAactacgG TTACAACGCa ggctcCGGCG
1451 AATACGgcga CATGATCGGA ATGGGCGTAC TCGACCCTGC CAAAGTAACC
1501 CGTTCCGCGC TGCAACACGC CGCGTCTAtC GCCGGTCTGA TGCTGACGAC
1551 CGACTGCATG ATTGCCGAAA TCCCTGAAGA AAAACCGGCT GTGCCCGATA
1601 TGGGGGGAAT GGGCGGTATG GCGGCATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2962; ORF 982.ng>:

```

g982.pep
1   IASQNLRFDN RFLQKMVNGV NILPAADWVA LGAKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGTT TATVLAQSI
101 AEGMKYVTAG MNPTDLKRG I DKAVAALVEE LKNIAPCDT SKEIAQVGS
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KSLLENLDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LFDKKISNI RDLLPVLEQV AKASRPLLI
251 AEDVEGEALA TLVNNIRGI LKTVAVKAPG FGDRRKAMLO DIAILTGGV
301 ISEEVGLSLE KATLDDLQGT KRIEIGEENT TVIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALNLH TGNADQDAGV QIVLRAVES
451 LRQIVANAGG EPSVVVNKVL EGKGNYGYN GSGEYDMIG MGVLDPKVT
501 RSALQHAASI AGLMLTTDCM IAEIPEEKPA VPDMGGMGGM GGMM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2963>:

```

m982.seq
1   ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
51  AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCGGCCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAAGAAGT TGCGTCCAAA ACCAACGACG
251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAATATGTT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTTGACGAA CTGAAAAACA
401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TGCGGAAAAA CAAATCGCTG CTTTGGACAA

```

651	TCCGTTTGTA	TTGTTGTTCG	ACAAAAAAT	CAGCAACATC	CGCGACCTGC
701	TGCCTGTTTT	GGAACAAGTG	GCAAAAGCCA	GCCGTCCGCT	GTTGATTATC
751	GCTGAAGACG	TAGAAGGGCA	AGCCTTGGCG	ACTTTGGTGC	TGAACAACAT
801	CCGAGGCATC	CTGAAACCG	TTGCCGTCAA	AGCCCCGGC	TTCCGCGACC
851	GCCGCAAGC	GATGTTGCA	GACATCGCCA	TCTGTACCGG	CGCGCTGGTG
901	ATTTCCGAAG	AAGTCGGTCT	GTCTTTGGAA	AAAGCGACTT	TGGACGACTT
951	GGGTCAAGCC	AAACGCATCG	AAATCGGTAA	AGAAAACACC	ACCATCATCG
1001	ACGGCTTTGG	CGACGCAACC	CAAATCGAAG	CGCGTGTTCG	CGAAATCCCG
1051	CAACAATTCG	AAACCGCAAC	CAGCGATTAC	AGCAAGAAA	AACTGCAAGA
1101	GCGCGTGCGT	AAATGGCAG	GCGGCGTGGC	AGTCATCAAA	TCGCGTGCCG
1151	CGACCGAAGT	CGAAATGAAA	GAGAAAAAAG	ACCGCGTGGG	AGACGCGCTG
1201	CACGCTACCC	GCGCAGCCGT	TGAAGAAGGC	GTGGTTGCAG	GCGGCGGCGT
1251	AGCCCTGTTG	CGTGCCCGTG	CTGCTTTGGA	AAACCTGCAC	ACCGGCAATG
1301	CCGACCAAGA	CGCAGGCGTA	CAAACTCGTT	TGCGCGCCGT	TGAGTCTCCG
1351	CTGCGCCAAA	TCGTTGCCAA	GCGAGGCGGC	GAACCCAGCG	TGGTTGTGAA
1401	CAAAGTATTG	GAAGGCAAAG	GCAACTACGG	TTACAACGCT	GGCAGCGGCG
1451	AATACGGCGA	TATGATCGAA	ATGGGCGTAC	TCGACCCCGC	CAAAGTAACC
1501	CGTTTTCGCG	TGCAACACGC	CGCATCTATC	GCCGGCTTGA	TGCTGACCAC
1551	TGATTGCTATG	ATCGTGTAAA	TCCCCGAAGA	CAAAACGGCT	GTGCCTGATA
1601	TGGGCGGCAT	GTCGTGGTATG	GGCGGCATGA	TGTAA	

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m982.seq
1 ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
51 AAACGGCGTA AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
101 AAGGTCCGAA CGTAGTCGTT GACCGCGCAT TCGGCGGGCC GCAGATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAAGAAGT TCGCTCCAAA ACCAACGACG
251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTGTACGAA CTGAAAAACA
401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGCG AAGTCTTTGG
551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TCGGAAAAAA CAAATCGCTG CTTTGGACAA
651 TCCGTTTGTA TTGTTGTTCTG ACAAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCCTGTTTT GGAACAAGTG GCAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGCGC ACTTTGGTCG TGAACAACAT
801 CCGAGGCATC CTGAAACCCG TTGCCGTCAA AGCCCCTGCC TTCGGCGACC
851 GCCGCAAGC GATGTTGCAA GACATCGCCA TCCTGACCGG CCGCGTGGTG
901 ATTTCCGAAG AAGTCGGTCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAAGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTTGG CGACGCAACC CAAATCGAAG CGCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAGAAA AACTGCAAGA
1101 GCGCGTGGCT AAATTGGCAG GCGCGTGGC AGTCAACAAA GTCGGTCCGC
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGTGCCCGTG CTGCTTTGGA AAACCTGCAC ACCGGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTCT TGCGCGCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTGTGAA
1401 CAAAGTATTG GAAGGCAAAG GCAACTACGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA TATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCTGC GC TGAACACGCG CGCATCTATC GCCGCTTGA TGCTGACCAC
1551 TGATTGTCATG ATCGTGTAAA TCCCCGAATG CAAACCGGCT GTGCCTGATA
1601 TGGGCGGCAT GGTGGTATG GCGGCGATGA TGTA
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Homology with a predicted ORF from *N. gonorrhoeae*

m982.pep MAAKDVFQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVVDRAFGGPHITKDGVTVAKEI  
:  
:

1387

g982	IASQNLRFDNRF	LQKMVNGVNIL	PAADWVALGAK	GRNVVVDRA	FGGPHITKDG	VTVAKEI
	10	20	30	40	50	60
	70	80	90	100	110	120
m982.pep	ELKDKFENMGAQ	MVKEVASKTND	VAGDGT	TTTATVLAQS	SIVAEGMKYV	TAGMNP
g982	ELKDKFENMGAQ	MVKEVASKTND	VAGDGT	TTTATVLAQS	SIVAEGMKYV	TAGMNP
	70	80	90	100	110	120
	130	140	150	160	170	180
m982.pep	DKAVAALVDELK	NIAPCDTSKEI	AQVGSISANS	DEQVGAI	IAEAMEKV	GKEGVIT
g982	DKAVAALVDELK	NIAPCDTSKEI	AQVGSISANS	DEQVGAI	IAEAMEKV	GKEGVIT
	130	140	150	160	170	180
	190	200	210	220	230	240
m982.pep	KSLENELDVVEG	MQFDRGYLSP	YFINDAEKQI	AALDNPFV	LLFDKKIS	NI
g982	KSLENELDVVEG	MQFDRGYLSP	YFINDAEKQI	AGLDNPFV	LLFDKKIS	NI
	190	200	210	220	230	240
	250	260	270	280	290	300
m982.pep	AKASRPLLI	IAEDVEGEAL	ATLVVNNIR	GILKTVAV	KAPGFGDR	RKAMLQD
g982	AKASRPLLI	IAEDVEGEAL	ATLVVNNIR	GILKTVAV	KAPGFGDR	RKAMLQD
	250	260	270	280	290	300
	310	320	330	340	350	360
m982.pep	ISEEVGLSLEK	ATLDDL	GQAKRIE	IGKENTTI	IDGFGDAA	QIEARVAE
g982	ISEEVGLSLEK	ATLDDL	GQAKRIE	IGKENTTI	IDGFGDAA	QIEARVAE
	310	320	330	340	350	360
	370	380	390	400	410	420
m982.pep	DKEKLQERVAK	LAGGVAVIK	VGAATEVEM	KEKKDRVE	DALHATRA	AVEEGV
g982	DKEKLQERVAK	LAGGVAVIK	VGAATEVEM	KEKKDRVE	DALHATRA	AVEEGV
	370	380	390	400	410	420
	430	440	450	460	470	480
m982.pep	RARAALENLHT	GNADQAGVQ	IVLRAVES	PLRQIVAN	AGGEP	SVVVNK
g982	RARAALENLHT	GNADQAGVQ	IVLRAVES	PLRQIVAN	AGGEP	SVVVNK
	430	440	450	460	470	480
	490	500	510	520	530	540
m982.pep	GSGEYGDM	IGMGLDPA	KVTR	SALQHAAS	IAGLMLT	DDCMIAE
g982	GSGEYGDM	IGMGLDPA	KVTR	SALQHAAS	IAGLMLT	DDCMIAE
	490	500	510	520	530	540
m982.pep	GGMMX					
g982	GGMMX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2965>:

a982.seq	1	ATGGCAGCAA	AAGACGTACA	ATTCGGCAAT	GAAGTCCGCC	AAAAAATGGT
	51	AAACGGCGTG	AACATTTTGG	CAAACGCCGT	GCGCGTAACC	TTGGGTCCCA
	101	AAGGCCGCAA	CGTGGTGGTT	GACCGCGCTT	TCGGCGGCCC	GCACATCACC
	151	AAAGACGGCG	TAACCGTCGC	CAAAGAAATC	GAACGTGAAAG	ACAAGTTTGA
	201	AAATATGGGC	GCGCAAATGG	TGAAAGAAGT	CGCGTCCAAA	ACCAACGACG
	251	TGGCGGGCGA	CGGTACGACT	ACCGCCACCG	TATTGGCGCA	ATCCATCGTT
	301	GCCGAAGGTA	TGAAATACGT	TACCGCCGGT	ATGAACCCGA	CCGACCTGAA
	351	ACGCGGTATC	GACAAAGCCG	TCGCCGCTTT	GGTTGAAGAG	CTGAAAAACA

1388

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401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CTGACGAACA AGTCGGCGCG ATTATTGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AATTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TCGCGAAAAA CAAATCGCCG GCTTGGACAA
651 TCCGTTTGTA TTGCTGTTTCG AAAAAAAAT CAGCAATATC CGCGACCTGC
701 TGCCTGTTTT GGAACAAGTG GCCAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATT CTGAAAACCG TTGCCGTTAA AGCTCCGGGC TTCGGCGACC
851 GCCGCAAAGC GATGCTGCAA GACATCGCTA TCCTGACCGG CGGCACAGTG
901 ATTTCCGAAG AAGTCGGCCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAGGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTCGG CGACGCAGCC CAAATCGAAG CGCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAATGGCAG GCGCGTGGC AGTAATCAAA GTCGGTGCCG
1151 CGACCGAAGT GGAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTCTGGA AAACCTGCAC ACCGGCAATG
1301 CAGACCAAGA CGCAGGCGTA CAAATCGTCT TGCGCGCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTGTTG GAAGGCAAAG GCAACTATGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA CATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCCGCGC TGCAACACGC CGCGTCTATC GCCGGCCTGA TGCTGACCAC
1551 AGACTGCATG ATTGCTGAAA TCCCTGAAGA CAAACCGGCT ATGCCTGATA
1601 TGGGCGGCAT GGGTGGTATG GGCGGCATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2966; ORF 982.a>:

```

a982.pep
1  MAAKDVQFGN EVRQKMVNGV NILANAVRVT LGPKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG I DKAAALVEE LKNIAPCDT SKEIAQVGS I
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KLENELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LFLDKKISNI RDLLPVLEQV AKASRPLLI I
251 AEDVEGEALA TLVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGGTV
301 ISEEVGLSLE KATLDDLQQA KRIEIGKENT TIIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALNLH TGNADQDAGV QIVLRAVESP
451 LRQIVANAGG EPSVVVNKVL EGKGNYGYN A GSGEYGMIE MGVLDPKAVT
501 RSALQHAASI AGLMLTTDCM IAEIPEDKPA MPDMGGMGGM GGMM*

m982/a982 99.3% identity in 544 aa overlap

10 20 30 40 50 60
m982.pep MAAKDVQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVVVDRAFGGPHITKDGVTVAKEI
|||||
a982 MAAKDVQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVVVDRAFGGPHITKDGVTVAKEI
10 20 30 40 50 60

70 80 90 100 110 120
m982.pep ELKDKFENMGAQMVKEVASKTNDVAGDGT TATVLAQSIVAEGMKYVTAGMNPTDLKRG I
|||||
a982 ELKDKFENMGAQMVKEVASKTNDVAGDGT TATVLAQSIVAEGMKYVTAGMNPTDLKRG I
70 80 90 100 110 120

130 140 150 160 170 180
m982.pep DKAAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG
|||||
a982 DKAAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG
130 140 150 160 170 180

190 200 210 220 230 240
m982.pep KLENELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFLDKKISNIRDLLPVLEQV
|||||
a982 KLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFLDKKISNIRDLLPVLEQV
190 200 210 220 230 240

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1389

m982.pep	250	260	270	280	290	300
	AKASRPLLI AEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV					
a982	AKASRPLLI AEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGTV					
	250	260	270	280	290	300
m982.pep	310	320	330	340	350	360
	ISEEVGLSLEKATLDDLGQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
a982	ISEEVGLSLEKATLDDLGQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
	310	320	330	340	350	360
m982.pep	370	380	390	400	410	420
	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
a982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
	370	380	390	400	410	420
m982.pep	430	440	450	460	470	480
	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEGKGNYGNA					
a982	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEGKGNYGNA					
	430	440	450	460	470	480
m982.pep	490	500	510	520	530	540
	GSGEYGDMIEMGVLDPAKVTRSALQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGGM					
a982	GSGEYGDMIEMGVLDPAKVTRSALQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGGM					
	490	500	510	520	530	540
m982.pep	GGMMX					
a982	GGMMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2967>:

g986.seq

1	GTGTTCAAAA	AATACCAATA	CTTCGCTTTG	GCGGCACTGT	GTGCCGCCTT
51	GCTGGCAGGC	TGCGAAAAGG	CAGGCAGCTT	TTTCGGTGCG	GACAAAAAAG
101	AAGCATCCTT	CGTAGAACGC	ATCGAACACA	CCAAAGACGA	CGGCAGTGTC
151	AGTATGCTGC	TGCCCGACTT	TGCCCAACTG	GTTCAAAGCG	AAGGCCCGGC
201	AGTCGTCAAT	ATTCAGGCAG	CCCCCGCCCC	GCGCACCCAA	AACGGCAGCG
251	GCAATGCCGA	AACCGATTCC	GACCCGCTTG	CCGACAGCGA	CCCGTTCTAC
301	GAATTTTCA	AACGCCTCGT	CCCGAACATG	CCCGAAATCC	CCCAAGAAGA
351	AGCAGATGAC	GGCGGATTGA	ACTTCGGTTC	GGGCTTCATC	ATCAGCAAAA
401	ACGGCTACAT	CCTGACCAAT	ACCCACGTCT	TTGCCGGTAT	GGGCAGTATC
451	AAAGTCCTGC	TCAACGACAA	GCGCGAATAT	ACCGCCAAAC	TCATCGGTTC
501	GGATGTCCAA	TCCGATGTCG	CCCTTCTGAA	AATCGACGCA	ACGGAAGAGC
551	TACCCGTCGT	CAAAATCGGC	AATCCCAAAA	ATTTGAAACC	GGGCGAATGG
601	GTCGCTGCCA	TCGGCGCGCC	CTTCGGCTTT	GACAACAGCG	TGACCGCCGG
651	CATCGTGTCC	GCCAAAGGCA	GAAGCCTGCC	CAACGAAAgc	tACACACCCT
701	TCATCCAAAC	CGACGTTGCC	ATCAATCCGG	GCAATTCCGG	CGGCCCGCTG
751	TTCAACTTAA	AAGGACAGGt	cgTCGGCATC	AATTCGCAAA	TATACAGCCG
801	CAGCGgcgga	ttCATGGGCA	TCTCCTTTGC	CATCCCGATT	GACGTTGCCA
851	TGAATGTGCG	CGAACAGCTG	AAAAACACCG	GCAAAGTCCA	ACGCGGACAA
901	CTGGGCGTGA	TTATTTCAGGA	AGTATCCTAC	GGTTTGGCAC	AGTCGTTCCG
951	TCTGGATAAA	GCCAGCGGCG	CATTGATTGC	CAAAATCCTT	CCCGGCAGCC
1001	CCGCAGAACG	TGCCGGCCTG	CAGGCGGGCG	ACATCGTCCT	CAGCCTCGAC
1051	GGCGGAGAAA	TACGTTCTTC	CGGCGACCTT	CCCCTCATGG	TCGGCGCCAT
1101	TACGCCGGGA	AAAGAAGTCA	GCCTCGGCGT	ATGGCGCAAA	GGCGAAGAAA
1151	TCACAATCAA	AGCCAAGCTG	GGCAACGCCg	ccgagcATAC	CGGCgcatCA
1201	TCCAAAACAG	ATGAAgcccc	ctacaccgAA	CAGCAATCCG	GTACGTTCTC
1251	GGTCGAATCC	GCAGGCATTA	CCCTTCAGAC	ACATACCGAC	AGCAGCGGca
1301	aacacctcgt	cgtcgtacgg	gtttccgacg	cggcagaacg	cGCAGGCTTA



1390

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1351 AGgcgcggcg acgaaatcct cgcggtcggg caagtccccg tcaatgacga
1401 agccgGTTTC cgcaaaGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGGTCatgcg ccgTGGCAAC ACGCTGTTCA TCGCATTAAA CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2968; ORF 986.ng>:

```

g986.pep
1  VFKKYQYFAL AALCAALLAG CEKAGSFFGA DKKEASFVER IEHTKDDGSV
51  SMLLPDFAQL VQSEGPVVN IQAAPAPRTQ NGSGNAETDS DPLADSDPFY
101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNGYILTN THVVAGMGSI
151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKNLKPGEW
201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
301 LGVIIQEVSY GLAQSFGLDK ASGALIAKIL PGSPAERAGL QAGDIVLSLD
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKAKL GNAAEHTGAS
401 SKTDEAPYTE QSGTFSVES AGITLQHTD SSGKHLVVVR VSDAERAGL
451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLVMRRGN TLFIALNLQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2969>:

```

m986.seq
1  GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCAGCCTC
51  GCTGGCAGGC TGCACAAGG CAGGCAGCTT CTTCGTGGCG GACAAAAAAG
101 AAGCATCCTT CGTAGAACGC ATCGAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGCCCAACTG GTTCAAAGTG AAGGTCCGGC
201 AGTCGTCAAT ATTCAGGCAG CCCC CGCCCC GCGCACCCAA AACGGCAGCG
251 GCAATGCCGA AAACGATTCC GACCCGATTG CCGACAACGA CCCGTTCTAC
301 GAATTTTTCA AACGCCTCGT CCCGAATATG CCCGAAATCC CCCAAGAAGA
351 AGCAGATGAC GCGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGCTACAT CCTGACCAAT ACCCAGCTCG TTACCGGCAT GGGCAGTATC
451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTC
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAATCCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCGCCA TCGGCGCGCC CTTCGGCTTC GACAACAGCG TGACCGCCGG
651 CATCGTCTGC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
801 CAGCGGCGGA TTCTAGGGCA TTTCCTTCGC CATCCCGATT GACGTTGCCA
851 TGAATGTGCG CGAACAGCTG AAAACACCCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTTGGCAG AATCGTTCGG
951 TTTGGACAAA GCCGGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
1001 CCGCAGAACG TGCCGGCCTG CAGGCGGGCG ACATCGTCCT CAGCCTCGAC
1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
1101 TACGCCGGGA AAAGAACTCA GCCTCGCGGT ATGGCGCAA GCGGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCGG CCGAGCATAT CGGCGCATCA
1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTCGAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTCCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAA CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2970; ORF 986>:

```

m986.pep.
1  VFKKYQYLAL AALCAASLAG CDKAGSFFVA DKKEASFVER IEHTKDDGSV
51  SMLLPDFAQL VQSEGPVVN IQAAPAPRTQ NGSGNAENDS DPIADNDPFY
101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNGYILTN THVVTGMGSI
151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL QAGDIVLSLD
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
401 SKTDEAPYTE QSGTFSVES AGITLQHTD SSGHLLVVVR VSDAERAGL
451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

```

Computer analysis of this amino acid sequence gave the following results:

1391

Homology with a predicted ORF from *N. gonorrhoeae*

m986/g986 97.0% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
	:     :     :     :     :     :					
g986	VFKKYQYFALAALCAALLAGCEKAGSFFGADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m986.pep	VQSEGPVAVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPMPEIPQEEADD					
	:     :     :     :     :     :					
g986	VQSEGPVAVNIQAAPAPRTQNGSGNAETDSDPLADSDPFYEFFKRLVPMPEIPQEEADD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	:     :     :     :     :     :					
g986	GGLNFGSGFIISKNGYILTNTHVVAGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	:     :     :     :     :     :					
g986	TEELPVVKIGNPKNLKPGEWVAAIGAPFGDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	:     :     :     :     :     :					
g986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300

1392

	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
g986	LGVIIQEVSYGLAQSFGLDKASGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
g986	PVMVGAITPGKEVSLGVWRKGEEITIKAKLGNAAEHTGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQTHTDSSGGHLVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
g986	AGITLQTHTDSSGKHLVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
g986	VPLLVMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2971>:

```

a986.seq
1  GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCCGCCCTC
51  GCTGGCAGGC TGCACAAAAG CCGGCAGCTT TTTCGGTGCG GACAAAAAAG
101 AAGCATCCTT TGTAGAACGC ATCAAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGTCCAACGT GTTCAAAGCG AAGGCCCGGC
201 AGTCGTCAAT ATTCAGGCAG CCCC CGCCCC GCGCACCCAA AACGGCAGCA
251 GCAATGCCGA AACCGATTCC GACCCGCTTG CCGACAGCGA CCCGTTCTAC
301 GAATTTTTC AAGCGCTCGT CCCGAACATG CCCGAAATCC CCAAGAAGA
351 AGCAGATGAC GNGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGCTATAT TCTGACCAAT ACGCACGTCG TTACCGGCAT GGCAGTATC
451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTT
501 GGATGTCCAA TCCGATGTCT CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCCGCCA TCGCGCGGCC CTTCGGCTTC GACAACAGCG TGACCGCCGG
651 CNTCGTGTCC GCCAAAGGCA GAAGCTGCC CAACGAAAGC TACACACCTT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
801 CAGCGCGGGA TTATGAGGCA TTTCTTTCGC CATCCCGATT GACGTTGCCA
851 TGAATGTGCG CGAACAGCTG AAAACACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATCAAGA AGTATCCTAC GGTTCGGCAC AATCGTTCGG
951 TTTGGACAAA GCCGCGCGCG CACTGATTGC CAAATCCTG CCCGGCAGCC
1001 CCGCAGAACG TGCCGGCCTG CGGGCGGGCG ACATCGTCCT CAGCCTCGAC
1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
1101 TACGCCGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAA GGCGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTCGAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTTCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCGG TCAATGACGA
1401 AGCCGTTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAC CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2972; ORF 986.a>:

```

a986.pep
1  VFKKYQYLAL AALCAASLAG CDKAGSFFGA DKKEASFVER IKHTKDDGSV
51  SMLLPDFVQL VQSEGPVVN IQAAPAPRTQ NGSSNAETDS DPLADSDPFY
101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKDGYYLTN THVVTGMGSI
151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGXVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ

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1393

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301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL RAGDIVLSLD
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
401 SKTDEAPYTE QSGTFSVES AGITLQHTD SSGHLVVVR VSDAAERAGL
451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

m986/a986 98.2% identity in 499 aa overlap

      10      20      30      40      50      60
m986.pep VFKKYQYLALAALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL
a986      VFKKYQYLALAALCAASLAGCDKAGSFFGADKKEASFVERIKHTKDDGSVSMLLPDFVQL
      10      20      30      40      50      60

      70      80      90     100     110     120
m986.pep VQSEGPVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPNMPEIPQEEADD
a986      VQSEGPVVNIQAAPAPRTQNGSSNAETDSDPLADSDPFYEFFKRLVPNMPEIPQEEADD
      70      80      90     100     110     120

      130     140     150     160     170     180
m986.pep GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA
a986      GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA
      130     140     150     160     170     180

      190     200     210     220     230     240
m986.pep TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTIVA
a986      TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGXVSAKGRSLPNESYTPFIQTIVA
      190     200     210     220     230     240

      250     260     270     280     290     300
m986.pep INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ
a986      INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ
      250     260     270     280     290     300

      310     320     330     340     350     360
m986.pep LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL
a986      LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLRAGDIVLSLDGGEIRSSGDL
      310     320     330     340     350     360

      370     380     390     400     410     420
m986.pep PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES
a986      PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES
      370     380     390     400     410     420

      430     440     450     460     470     480
m986.pep AGITLQHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN
a986      AGITLQHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN
      430     440     450     460     470     480

      490     500
m986.pep VPLLIMRRGNTLFIALNLQX
a986      VPLLIMRRGNTLFIALNLQX
      490     500

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2973>:

```

g987.seq
1  ATGAAACAC GCAGCCTCAT TTCCCTTTA TGCCTCCTC TCTGTTTCATG

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1394

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51  TTCTTCATGG TTGCCCCCAC TGGAAGAACG GACGGAAAGC CGTCATTTTA
101 ATACTTCCAA ACCTGTCTCT CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATAACA ACGGGCTATC CGACATCTAC CTGCTCGACG ACCCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATTTGG CGCAACGACA TTTCCGGCAG GCTGCTGTTC
301 AACCTCATGT ACCTTGCCCGC agaacgcGGC GTGCGCGTAC GCCTGCTGTt
351 ggacgacaAC AACAcgcgcg gcttgacga tctcctGCTC GCCCTCGACA
401 GCCATCCCAA TAtctaagtG CGCCTGTTCA ACCCCTtctg CCTACGCAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCGCCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTGACCGCG TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACATCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACGGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCCT GATCAGCGAC AGCCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCGG GAGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCTACA AAATCCGGCA
1001 CAGACGCACT GGCAAAACTG GTGCAGGACG GCATAGACGT TACCGTCTCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGTACGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGacg gCAAACGCAT
1251 CTTTCATCGG TCATTCAACC TCGACCCCCG TTCCGCACGG CTCAATACCG
1301 AAATGGGCGT CGTCATCGAA AGCCCCAAA TCGCAGAACA GATGGAGCGC
1351 AccctCGCG AtacCACACC CGAATACGCC TACCGCGTTA CCCTCGACAA
1401 ACACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TCGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2974; ORF 987.ng>:

```

g987.pep
1  MKTRSLISLL CLLLCS CSSW LPPLERTES RHFNTSKPVL LDNILQIRHT
51  PHNNGLSDIY LLDDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLMYLA AERG VRVRLLLDDN NTRGLDDLLL ALDSHPNI*V RLFNPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 LDDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD SPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
451 TLADTTPEYA YRVTLDKHNR LQWHD PATRK TYPNEPEAKL WKRIA AKILS
501 LLPIEGLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2975>:

```

m987.seq
1  ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCCAC TGGAAGAACG GACGGAAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCCGGCAG GCTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTT GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCGCCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GATTGGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTGACCGCG TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CGACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACAGGATG CATCGACTGG CAGAGCGTCC
851 GAACCCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC

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1395

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901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCCG
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTTCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTTCTG
1051 ACCAACTCGC TGCAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAAACCA GCCTGCACGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGGT TCGTTCAACC TCGACCCCGG TTCCGCGCGT CTCAACACCG
1301 AAATGGGCGT TGTTCATCGA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCACACC CGCCTACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCGCG CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TAGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2976; ORF 987>:

```

m987.pep
1  MKTRSLISLL CLLLCSCSSW LPPLERTES RHFNTPSKPVR LDNILQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAERG VRVRLLLDDN NTRGLDDLLL ALDSHPNIEV RLFNPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGDIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGCIDW QSVRTRLISD DPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
451 TLADTTPAYA YRVTLDRHNR LQWHDPATRK TYPNEPEAKL WKRIAANKILS
501 LLPIEGLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m987/g987 97.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLCLLLCSCSSWLPPLERTESRHFNTPSKPVRLDNILQIRHTPHTNGLSDIY					
g987	MKTRSLISLLCLLLCSCSSWLPPLERTESRHFNTPSKPVLLDNILQIRHTPHNGLSDIY					
	10	20	30	40	50	60
m987.pep	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNVLVYLAERGVVRVRLLLDDN					
g987	LLDDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAERGVVRVRLLLDDN					
	70	80	90	100	110	120
m987.pep	NTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
g987	NTRGLDDLLLALDSHPNIXVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
	130	140	150	160	170	180
m987.pep	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGDIG					
g987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG					
	190	200	210	220	230	240
m987.pep	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVRTRLISDDPAKGLDRDR					
g987	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDSPAKGLDRDR					
	250	260	270	280	290	300
m987.pep	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA					
g987	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA					
	310	320	330	340	350	360
m987.pep						
g987						

1396

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g987      |||
          RKPP|AGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGDIVTVLTNSLQATDVA
          310      320      330      340      350      360

          370      380      390      400      410      420
m987.pep  AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKRIFIG
          |||
g987      AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKRIFIG
          370      380      390      400      410      420

          430      440      450      460      470      480
m987.pep  SFNLDPRSARLNT|EMGVVIESPKIAEQMERTLADTT|PAYAYRVTLDRHNRLQWHD|PATRK
          |||
g987      SFNLDPRSARLNT|EMGVVIESPKIAEQMERTLADTT|PEYAYRVTLDKHNRLQWHD|PATRK
          430      440      450      460      470      480

          490      500      509
m987.pep  TYPNEPEAKLWKRIA|AAKILSLLPIEGLLX
          |||
g987      TYPNEPEAKLWKRIA|AAKILSLLPIEGLLX
          490      500

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2977>:

```

a987.seq
1  ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTCATG
51  TTCTTCATGG TTGCCCCCAC TGGAAGAACG GACGGAAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGCTATC CGATATCTAT CTGTTGAACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTCCCGGCCG ACTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCTGCTC GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCGCGCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GCCCTTGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCGAGCG CAACATCGGC AAGGCTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCTCTAC CAAAAAATAC AGACAGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCTTG
1051 ACCAACTCGC TACAGCGGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCT GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTCATCGGC TCATTCAACC TCGACCCCGG TTCGCGACGG CTAATACTG
1301 AAATGGGCGT TGTATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCTCACC CGAATACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TAGAAAGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 550; ORF 2978.a>:

```

a987.pep
1  MKTRS|LISLL C|LLLCSCSSW LPPLEERTES RHFNTSKPVR LDNILQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAERG VVRRL|LLDDN NTRGLDDLLL ALDSHPNIEV RLENPFVLRK
151 WRALGYLTD F|PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATG S|V VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLR Y|RETVEQSPLY QKIQTGRIDW QSVQTRLISD DPAKGLDRDR
301 RKPP|IAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGDIVTVL

```

1397

351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS  
 401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER  
 451 TLADTSPEYA YRVTLDRHNR LQWHDPATRK TYPNEPEAKL WKRIA AKILS  
 501 LLPIESLL\*

m987/a987 98.8% identity in 508 aa overlap

m987.pep	10	20	30	40	50	60
	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY					
a987						
	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY					
	10	20	30	40	50	60
m987.pep	70	80	90	100	110	120
	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
a987						
	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
	70	80	90	100	110	120
m987.pep	130	140	150	160	170	180
	NTRGLDDLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
a987						
	NTRGLDDLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
	130	140	150	160	170	180
m987.pep	190	200	210	220	230	240
	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGDIG					
a987						
	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG					
	190	200	210	220	230	240
m987.pep	250	260	270	280	290	300
	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVTRTLISDDPAKGLDRDR					
a987						
	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDDPAKGLDRDR					
	250	260	270	280	290	300
m987.pep	310	320	330	340	350	360
	RKPPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNLQATDVA					
a987						
	RKPPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNLQATDVA					
	310	320	330	340	350	360
m987.pep	370	380	390	400	410	420
	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
a987						
	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
	370	380	390	400	410	420
m987.pep	430	440	450	460	470	480
	SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPAYAYRVTLDRHNR LQWHDPATRK					
a987						
	SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTSPEYAYRVTLDRHNR LQWHDPATRK					
	430	440	450	460	470	480
m987.pep	490	500	509			
	TYPNEPEAKLWKRIA AKILSLLPIEGLLX					
a987						
	TYPNEPEAKLWKRIA AKILSLLPIESLLX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2979>:

g988.seq

1 ATGAATAAAA ATATTAAATC TTAAATTTA CGGAAAAAG ACCCGTTTTT



```

51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCCAGT CGGgaATGGA
101 TAATCGAATT GTTGGAGCGC AAAGGTGTGC CTTCAAAAAT CGAATCGCTT
151 GCACGCGAGC TGTGCGATTAC GGAAGacgag tATGTCTTTT TTGAACGCCG
201 TCTGAaggCG atgGCGCGGG AcggtCAGGT TTTAATCAAC CGCCgaggcg
251 CagtTTGCGc gGCGgacaag ctgGATTTGG TCAAATGccg Cgtcaggcg
301 catAAgGAcg gtttcggctt cgcCGTGCCG CTCATGCCGA TGGACGAAGG
351 GGATTTCTGT TTATACGAAC GCCAgatgcg tggTgtcatG CAcggcgaca
401 ccgttACCGT CCGTCTGCG ggtatggaCC GCAGGGGccg ccgcGAAagg
451 acgtttctGG ATATTGTGCG ACGCGCGCAA AGCAAAGTTG TCGGCCGTTT
501 CTATATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTGTTGGAA CCGGACGGCG TGGCGCGTTT CAAACCCGAA
601 TCCGGTCAGG TTATCGTCGG CAAAATTGAG GTTTATCCCG AGCAAAACCG
651 GCCTGCAGTG GCAAAAATCA TTGAAGTTTT GGGCGATTAT GCCGACAGCG
701 GGATGGAAAt cgAAATTGCC GTGCGCAAGC ATCATTGCC GCAccgaTTC
751 AGTGAagcgt gtGcCAAAATC CGcgaAAAAA ATtcccagacc ATGTACGCAA
801 AAGCGATTTC AAAGGCCGCG TCGATTGTG CGACCTTCCT TTGGTAACGA
851 TAGACGGCGA AACGGCGCG GATTTTCGACG ACGCGGTGTT TGCCGAAAAA
901 GTCGGACGCA ATTACGCCT GGTCTGGCG ATTGCGGATG TCAGCCATTA
951 TGTCCGCCCT GACGATGCGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
1001 GCGTGTATTT CCCGCGCCGT ATGATTCCGA TGCTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
1101 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTATC
1151 CCGCCGTGAT GCGCTCTCAT GCCCGCTGA CCTACAACCA AGTTTGGAAA
1201 TGGCTTTCAG ACGGCATCGG GAATCCGCAC AAAGCCCAA TCGACACGCT
1251 TTACAAGCTG TTTAAATTT TGCAGAAAAA ACGTCTGGCG CGCGGGGCGG
1301 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGACGA CAACGGCAAA
1351 ATCGAAAAAA TTGTCCCGT CGTCCGCAAC gatGCCACA AGCTGATTGA
1401 AGAATGTATG CTGGCGGCGA ATGTTTGCGC GCGGGATTTT CTGTTGAAAA
1451 ACAAACATAC GGCTTTGTTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1501 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1551 CGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GAACAATTCA
1601 AAGCAGGCC GGATGCGGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAGCAGGCGG TTTACGAACC GCATTGCGAA GGGCATTTCG GTTTGGCTTA
1701 TGAAGCATAC GCCCACTTTA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTCCACCG TGCCATCAAA GCCGTATTGA ACCGAAAAAC CTACACGCCA
1801 AACAAAAGCT GGCAGGCTTT GGGCGTGCAT ACTTCGTTT GCGAACGCCG
1851 TGCCGACGAT GCTGGCCGCG ATGTGGAAAA CTGGCTGAAA ACTTATTATA
1901 TGCGCGATAA GGTCGGTGAA ATATTTGAAG GcaaaatCtc ccggggtgtg
1951 gcaaaTtttg gaATATTGT CACTTTGGAC GATATccata tcgacggtct
2001 ggtacaTATC AGCGatttgg gcgaAGATTA TTTCaacttc cgccccgAAA
2051 TCATGGCAAT CGAAGCGGAA CGCAGCGGCA TCCGTTTCAA TATGGGGGAC
2101 AGGGTTGCCG TCCGGGTGCG CCGTGCCGAT TTGGATGATG GAAAAATCGA
2151 CTTTGTCTTA ATTGCCGAG AAAGCGGCAG GCGGCGGAAG GTCAAATTAT
2201 CCGCATCTGC CAAACCGGCA GGGGCGGCGG GGAAAGGGAA ATCGAAAACC
2251 ACCGCCGAGA AAAAAACAGC CCGATGCGGC AAAGTAAGGG GAAGGGGCGT
2301 GCCTGCCGTT GCCGAATCGG GGAAAAAGGC AAAGAAACCG GTTCCGATTA
2351 AGGTCAAAA ACAGAAAGGC AAATCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2980; ORF 988.ng>:

g988.pep

```

1  MNKNIKSLNL REKDPFLSRE KORYEHPLPS REWIIELLER KGVPSKIESL
51  ARELSITEDE YVFFERRLKA MARDGQVLIN RRGAVCAADK LDLVKCRVEA
101 HKDGFGFAPV LMPMDEGDFV LYERQMRGVM HGDTVTVRPA GMDRRGRREG
151 TFLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
201 SGQIVVGKIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPHRF
251 SEACAKSAKK IPDHVRKSDL KGRVLDCLDL LVTIDGETAR DFDDAVFAEK
301 VGRNYRLVVA IADVSHYVRP DDAIDADAQE RSTSVYFRR MIPMLPNLS
351 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPVMRSH ARLTYNQVWK
401 WLSDGIGNPH KAQIDTLYKL FKILQKKRLA RGAVEFESVE TQMI FDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LATLREQLGL LGLQLGGGDN PSPKDYAALA EQFKGRPDAE LLQVMMLRSM
551 QQAVYEPHCE GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNRKITYTP
601 NKSWQALGVH TSFCERRADD AGRDVENWLK TYMRDKVGE IFEGKISRGV
651 ANFGIFVTL DDIHIDGLVHI SDLGEDYFNF RPEIMAIEGE RSGIRFNMGD
701 RVAVRVARAD LDDGKIDFVL IAGESGRRRK VKLSASAKPA GAAGKGKSKT
751 TAEKKTARCG KVRGRGVPAV AESGKKAKKP VPIKVKRKG KS*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2981>:

```

m988.seq (partial)
1      ..ACAGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
51     CTATATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
101    ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
151    TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
201    GCCGGCAGTG GCAAAAATCA TCGAAGTTTT GGGCGATTAT GCCGACAGCG
251    GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
301    AGTGAAGCGT GTGCCAAAGC TGCAGAAAAA ATTCCCGTCC ATGTACGCAA
351    AAGCGATTTC AAAGGCCGCG TCGATTTGCG CGACCTGCCT TTGGTAACGA
401    TAGACGGCGA AACGGCGCGC GATTTGACG ACGCGGTGTT TGCCGAAAAA
451    GTCGGACGCA ATTACCGTCT GGTGCGGGCG ATTGCGGATG TCAGCCATTA
501    TGTCCGCCCT GACGATGTGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
551    GCGTATATTT CCCGCGCCGT GTGATTCCGA TGCTGCCGGA AAACCTGTCT
601    AACGGCATT TCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
651    CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTACC
701    CCGCCGTAAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGGAAA
751    TGGATTTTCA ACGGCATCGA CCATCCGTAC AAAGCCCAA TCGACACCCT
801    TTACAACTC TTCAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGCGCGG
851    TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGATGA CAACGGCAAA
901    ATCGAAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCACA AGCTGATTGA
951    AGAATGTATG CTGGCGGCGA ATGTTTGCGC AGCGGATTTT CTGTTGAAAA
1001   ACAAGCATA GCGCTTTGTT CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1051   CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGCCGG
1101   CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGTC GAACAATTCA
1151   AAGGCAGACC TGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1201   CAGCAGGCGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCTTA
1251   CGAAGCATA GCGCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1301   CCGTACACCG CGCCATCAA GCGGTGTTGA ATCAGCAAAC CTACACGCCA
1351   AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1401   TGCCGACGAC GCCAGCCGCG ACGTGGA AAA CTGGCTGAAA ACCTATTATA
1451   TGCGCGATAA GGTGCGCGAA GTATTCGAAG GTAAAATCTC CGGCATGACC
1501   AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
1551   GCATATCAGC GATTTGGGCG AAGACTATTT CAACTCCGC CCCGAAATCA
1601   TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTTCACAT GGGGGACAGG
1651   GTTGCCGTCC GGGTCGCCCC TGCCGATTG GATGACGGAA AAATCGATT
1701   TGTCTGATT GCCGGGGGGA GCGGCAGGG GCGGAAAGTT AAATCATCCG
1751   CGTCTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGGAAGCC GAAACCGGCC

```

1400

1801 GCCGAGAAAA AAACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC  
 1851 TGCCCGCCGA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAGG  
 1901 TAAAAAACG GAAAGGCAAA TCATAA

This corresponds to the amino acid sequence <SEQ ID 2982; ORF 988>:

m988.pep (partial)

1 ..TVLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE  
 51 SGQVIVGEIE VYPEQNRPAV AKIEVLGDY AD SGMEIEIA VRKHHLP HQF  
 101 SEACAKAAKK IPVHVRKSDL KGRVDLRDLP LVTIDGETAR DFDDAVFAEK  
 151 VGRNYRLVVA IADVSHYVRP DDVIDADAQE RSTSVYFPRR VIPMLPENLS  
 201 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK  
 251 WISDGIDHPY KAQIDTLYKL FKILQKKRFE RGAVEFESVE TQMIFDDNGK  
 301 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK  
 351 LATLREQLGL LGLQLGGGDN PSPKDYAALV EQFKGRPDAE LLQVMMLRSM  
 401 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQQTYP  
 451 KKSQALGVH TSFCERRADD ASRDVENWLK TYMRDKVGE VFEGKISGMT  
 501 SFGIFVTLTG IHIDGLVHIS DLGEDYFNFR PEIMAIEGER SGIRFNMGDR  
 551 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGKPKTA  
 601 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKRKGK S\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m988/g988 94.2% identity in 642 aa overlap

m988.pep				10	20	30
				TVLDIVERAQSKVVGRFYMDRGVAILEPED		
g988	LYERQMRGVMHGDVTVTVRPAGMDRRGRREGTFLDIVERAQSKVVGRFYMDRGVAILEPED					
	130	140	150	160	170	180
m988.pep		40	50	60	70	80
		KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA				
g988		KRLNQSIVLEPDGVARFKPESGQVIVGKIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA				
	190	200	210	220	230	240
m988.pep		100	110	120	130	140
		VRKHHLP HQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLP LVTIDGETARDFDDAVFAEK				
g988		VRKHHLP HRFSEACAKSAKKIPDHVRKSDLKGRVDLCDLPLVTIDGETARDFDDAVFAEK				
	250	260	270	280	290	300
m988.pep		160	170	180	190	200
		VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRR VIPMLPENLSNGICSLNPDV				
g988		VGRNYRLVVAIADVSHYVRPDDAIDADAQERSTSVYFPRRMIPMLPENLSNGICSLNPDV				
	310	320	330	340	350	360
m988.pep		220	230	240	250	260
		ERLCMVCDMV VTYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL				
g988		ERLCMVCDMV VTYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIGNPHKAQIDTLYKL				
	370	380	390	400	410	420
m988.pep		280	290	300	310	320
		FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF				
g988		FKILQKKRLARGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF				
	430	440	450	460	470	480
m988.pep		340	350	360	370	380
		LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALVEQFKGRPDAE				
g988		LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALAEQFKGRPDAE				

1401

	490	500	510	520	530	540
	400	410	420	430	440	450
m988.pep	LLQVMMLRSMQQAVYEPHCDGHFLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
g988	:     :     :     :     :     :					
	550	560	570	580	590	600
	460	470	480	490	500	509
m988.pep	KKSQWALGVHTSFCERRADDASRDVENWLKTYIMRDKVGEVFEGKIS-GMTSFGIFVTL					
g988	NKSQWALGVHTSFCERRADDAGRDVENWLKTYIMRDKVGEVFEGKISRGVANFGIFVTL					
	610	620	630	640	650	660
	510	520	530	540	550	569
m988.pep	GIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVL					
g988	DIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVL					
	670	680	690	700	710	720
	570	580	590	600	610	629
m988.pep	IAGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAESRKKAKKP					
g988	IAGESGRRRKVKLSASAKPAGAAGKGSKTAEKKTARCGKVRGRGVPAAVESGKKAKKP					
	730	740	750	760	770	780
	630	640				
m988.pep	VPIKVKRRKGKXS					
g988	VPIKVKRRKGKXS					
	790					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2983>:

```

a988.seq
1  ATGAATAAAA ATATTAAATC TTAAATTTA CGGGA AAAAG ACCCGTTTTT
51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CGGGAATGGA
101 TAATCGAGCT GCTTGAACGT AAAGGCGTAC CATCCAAGAT TGAAGCTTTG
151 GTACGCGAAT TGTCGATTAA GGAAGAAGAG TACGAATTTT TCGAACGTCG
201 TCTGAAGGCG ATGGCGCGGG ACGGTCAGGT TTTAATCAAC CGTCGGGGCG
251 CGGTTTGCGC GGCGGACAAA TTGGATTGCG TCAAATGCCG TGTCAAGGCG
301 CACAAAGACC GCTTCGGTTT CGCCGTGCCG CTCACGCCCG CCAAAGACGG
351 TGATTTTGTC TTGTACGAAC GCCAGATGCG CGGCATTATG CACGGCGATA
401 TTGTCACTGT TCGTCCTGCC GGCATGGACG GTAGGGGCCG CCGCGAAGGG
451 ACGGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
501 CTANATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
601 TCCGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
651 GCCGCGAGTG GCAAAAATCA TCGAAGTTT GGGCGATTAT GCCGACAGCG
701 GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTGACC GCACCAATTC
751 AGTGAAGCGT GTGCCAAAGC CGCGAAAAAA ATTCGCCGACC ATGTACGCAA
801 AAGCGATTTG AAAGGCCGCG TCGATTGCG CGACCTGCCT TTGGTAACGA
851 TAGACGGCGA AACGGCTCGA GATTTTGACG ATGCGGTGTT TGCCGAGAAA
901 ATCGGACGCA ATTACCGTCT GGTCTGGCG ATTGCCGATG TCAGCCATTA
951 TGTCCGCCCC GATGACGCTA TCGACACGGA CGCTCAGGAA CGCAGCACCA
1001 GTGTTTACTT CCCGCGCCGC GTGATTCCCA TGTTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCTCATGTC GAGCGTTTGT GTGTGGTGTG
1101 CGATATGGTT ATCACTTACG CGGGCAATAT CAAAGAATAC CGCTTCTACC
1151 CCGCGTGAT GCGCTCTCAT GCCCGCTGA CCTACAACCA AGTTTGAAAA
1201 TGGCTTTCAG GCGGCATCGA GCATCCGTT AAAACCCAAA TCGACACGCT
1251 TTACAAATC TTCAAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGGGCGG
1301 TGGAGTTTGA CAGCATCGAA ACCCAAATGC TTTTCGACGA CAACGGTAAA
1351 ATTGAAAAAA TCGTCCCGT TGTCCGCAAC GATGCCACCA AGCTGATTGA
1401 AGAATGTATG TTGGCGGCAA ACGTTTGCGC AGCGGATTTT CTGTTGAAAA
1451 ACAAGCATAC CGCATGTTC CGCAACCATT TGGGGCCAC GCCCGAAAAA
1501 CTCGCCGCT TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1551 CGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GGACAGTTCA

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a988.pcp

1	MNKNIKSLNL	REKDPFLSRE	KQRYEHPLPS	REWIIELLER	KGVPSKIEAL
51	VRELSIKEEE	YEFFERRLKA	MARDGQVLIN	RRGAVCAADK	LDLVKCRVK
101	HKDRFGFAVP	LTPAKDGDVF	LYERQMGRIM	HGDIVTVRPA	MDGGRGRREG
151	TVLDDIVERAQ	SKVVGFRFXM	RGVAILED	KRLNQSIVLE	PDMGARFKPE
201	SGQVIVGEIE	VYPEQNRPAV	AKIIEVLGDY	ADSGMEIETA	VRKHHLPHQF
251	SEACAKAAKK	IPDHVRKSDL	KGRVDLRDLP	LVTIDGETAR	DFDDAVFAEK
301	IGRNYRLVVA	IADVSHYVRP	DDAIDTDAQE	RSTSVYFPRR	VIPMLPENLS
351	NGICSLNPHV	ERLCVVCMDV	ITYAGNIKEY	RFYPVMRSH	ARLTYNQVWK
401	WLSGSGIEHPF	KTQIDTLYKL	FKILQKKRFE	RGAVEFDSIE	TQMLFDDNKG
451	IEKIVPVVRN	DAHKLIEECM	LAANVCAADF	LLKNKHTALF	RNHLGPTPEK
501	LAALREQGLGL	LGLQLGGGDN	PSPKDYAALA	GQFKGRPDAE	LLQVMMLRSM
551	QQAVYEPHCD	GHFGLAYEAY	AHFTSPIRRY	PDLTVHRAIK	AVLNQQTYTP
601	KKSQWALGVH	TSCERRADD	ASRDVENWLK	TYYMRDKVGE	VFEGKISGMT
651	SFGIFVTLDG	IHDGLVHIS	DLGEDYFNFR	PEIMAEIEGR	SGIRFNMGDR
701	VAVRVARADL	DDGKIDFVLI	AGGSGRGRKV	KSSASAKPAG	TAGKGPKPTA
751	AEKKTARGGK	VRGRGASAAA	ESRKAKKPV	PIKVKKRKGK	S*

m988/a988 97.0% identity in 641 aa overlap

				10	20	30
m988.pep				TVLDIVERAQSKVVG	RFYMDRGVAILEPED	
a988	LYERQMRGIMHGDI	VTVRPAGMDGRGR	REGTVLDIVERAQSKVVG	RFXMDRGVAILEPED		
	130	140	150	160	170	180
	40	50	60	70	80	90
m988.pep	KRLNQSIVLEPDG	VARFKPESGQVIV	GEIEVYPEQNRPA	VAKIIIEVLGDY	ADSGMEIEIA	
a988	KRLNQSIVLEPDG	VARFKPESGQVIV	GEIEVYPEQNRPA	VAKIIIEVLGDY	ADSGMEIEIA	
	190	200	210	220	230	240
	100	110	120	130	140	150
m988.pep	VRKHHLPHQFSE	ACAKAAKKIPVH	VRKSDLKGRVDL	RDLPLVTIDGET	ARDFDDAVFAEK	
a988	VRKHHLPHQFSE	ACAKAAKKIPD	HVRKSDLKGRVDL	RDLPLVTIDGET	ARDFDDAVFAEK	
	250	260	270	280	290	300
	160	170	180	190	200	210
m988.pep	VGRNYRLVVAI	ADVSHYVRPDD	VIDADAQERSTSV	YFPRRVIPLMP	ENLSNGICSLNP	PDV
	:	:	:	:	:	:
a988	IGRNYRLVVAI	ADVSHYVRPDD	AIDTDAQERSTSV	YFPRRVIPLMP	ENLSNGICSLNP	PHV
	310	320	330	340	350	360
	220	230	240	250	260	270
m988.pep	ERLCMVCDMVV	TYAGNIKEYRFY	PAVMRSHARLT	YNQVWKWISD	GIDHPYKAQID	TLYKL
a988	ERLCVVC	DMVITYAGNI	KEYRFYPAVMR	SHARLTYNQV	WKWISGGIEH	PFKTOIDTLYKL

1403

	370	380	390	400	410	420
	280	290	300	310	320	330
m988.pep	FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
a988	FKILQKKRFERGAVEFDSIETQMLFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
	430	440	450	460	470	480
	340	350	360	370	380	390
m988.pep	LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGDNPSPKDYAALVEQFKGRPDAE					
a988	LLKNKHTALFRNHLGPTPEKLAALREQLGLLGLQLGGDNPSPKDYAALAGQFKGRPDAE					
	490	500	510	520	530	540
	400	410	420	430	440	450
m988.pep	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
a988	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
	550	560	570	580	590	600
	460	470	480	490	500	510
m988.pep	KKSQWALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKISGMTSFGIFVTLDG					
a988	KKSQWALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKISGMTSFGIFVTLDG					
	610	620	630	640	650	660
	520	530	540	550	560	570
m988.pep	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
a988	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
	670	680	690	700	710	720
	580	590	600	610	620	630
m988.pep	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKKAKKPV					
a988	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKKAKKPV					
	730	740	750	760	770	780
	640					
m988.pep	PIKVKKRKGSX					
a988	PIKVKKRKGSX					
	790					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2985>:

```

g989.seq
1   ATGACCCCTT TCACACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
51  TGCCGCCGCA TCTGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCACGGCA AATGCCGCCG ACGCGTCGAC CATCTTCTAC
151 AATCCCGCCG GCCTGACCAA ACTCGACAGC AGCCAGATTT CCGTCAACGC
201 CAACATCGTG CTGCCCAGCA TTCATTATGA AGCAGATTCC GCCACCGACT
251 TTACCGGGCT TCCCGTCCAA GGTTCATAAA ACGGCAAAAT CACCAAAACC
301 ACGGTGCGAC CCCACATTTA CGGCGCATAC AAAGTCAACG ACAATCTGAC
351 CGTGGGCTTG GGCGTGACG TCCCCTTCGG CTCTGCCACC GAATACGAAA
401 AAGATTCGCT GTTGCGCCAC AACATCAACA AACTCGGTCT GACCAGCATC
451 GCCGTCGAAC CTGTCGCCGC GTGGAAGCTC AACGAACGCC ATTCCTTCGG
501 CGCAGGCATC ATCGCCCAAC ATAATTCCGC CGAACTGCGC AAATATGCCG
551 ACTGAGGAAT CCCAAAAAAA GCGCAAATGC TGCAAGCAAC ACCTTCTAAT
601 CCTACTGCCG CTGCTCAAAT CAAGGCCGAC GGACACGCCG ATGTCAAAGG
651 CACGATTGGG GGCGTCGGCT ACCAACTGGC GTGGATGTGG GACATCAACG
701 ACCGCGCGCG CGTGGGCGTG AACTACCGTT CCAAAGTTTC ACACACGCTC
751 AAAGGCGATG CCGAATGGGC GGCAGACGGC GCGGCGGCGA AACAACAGTG
801 GAATGACAAT ATGCTCACAC CGCTCGGTTA CACGGCGAAT GAAAAAGCCA
851 GTGTCAAAAT CGTAACGCCT GAGTCTTTGT CCGTACACGG CATGTACAAA

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1404

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901 GTGTCCGACA AAGCCGACCT GTTCGGCGAC GTAACCTGGA CGCGCCACAG
951 CCGCTTCAAT AAGGCGGAAC TGTTTTTTGA AAAAGAAAAA AATATTGCTA
1001 ATGGCAAAAA ATCCGACCGC ACCACCATCA CCCCCAACTG GCGCAACACC
1051 TACAAAGTCG GCTTGGGCGG TTCTTATCAA ATCAGCGAAC CGCTGCAACT
1101 GCGCGTCGGC ATCGCTTTTG ACAAACCGCC TGTCCGCAAC GCCGACTacC
1151 GCATGAACAG CCTGCCCCGAC GGCAACCGCA TCTGGTTCTC CGCCGGCATG
1201 AAATACCATA TCGGCAAAAA CCACGTCGTC GATGCCGCCT ACACCCACAT
1251 CCACATCAAC GACACCAGCT ACCGCACGGC GAAGGCAAGC GGCAACGATG
1301 TGGACAGCAA AGGTGCGTCT TGCGCACGTT TCAAAAACCA CGCCGACATC
1351 ATCGGCCTGC AATACACCTA CAAATTCAAA TAA

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This corresponds to the amino acid sequence <SEQ ID 2986; ORF 989.ng>:

```

g989.pep
1  MTPFTLKKTV LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAADASTIFY
51  NPAGLTKLDS SQISVNANIV LPSIHYEADS ATDFTGLPVQ GSKNGKITKT
101 TVAPHIYGAY KVNNDLTVGL GVVVPFGSAT EYEKDSVLRH NINKLGLTSI
151 AVEPVAAWKL NERHSFGAGI IAQHNSAELR KYAD*GIPPK AQMLQATPSN
201 PTAAAIKAD GHADVKGSDW GVGYQLAWMW DINDRARVGV NYRSKVSHTL
251 KGDAEWAADG AAAKQQWNDN MLTPLGYTAN EKASVKIVTP ESLSVHGMKY
301 VSDKADLFGD VTWTRHSRFN KAELEFEKEK NIANGKKS DR TTITPNWRNT
351 YKVLGGSYQ ISEPLQLRVG IAFDKPPVRN ADYRMSLPD GNRIWFSAAGM
401 KYHIGKNHVV DAAYTHIHIN DTSYRTAKAS GNDVDSKGAS CARFKNHADI
451 IGLQYTYKFK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2987>:

```

m989.seq
1  ATGACCCCTT CCGCACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
51  TGCCGCCGCA TCCGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCACGGCA AATGCCGCCG CCGCAGAAGC CGCCGACGCA
151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA
201 GATTTCGTC AACGCCAACA TCGTGCTGCC CAGCATTCAT TATGAGGCGG
251 ATTCCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGGTTC GAAAAGCGGC
301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTGG GCTTGGGCGT GTACGTCCCC TTCGGCTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 CCGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAAC
551 TGCGCAAATA TGCCGACTGG GGGATTAAGA GTAAAGCAGA GATATTGACG
601 GCAAAACCGC CCAAACCTAA CGGTGTAGCC GAAGCTGCAA AAATTCAGGC
651 CGACGGACAC GCCGATGTCA AAGGCAGCGA TTGGGGCTTC GGCTACCAAC
701 TGGCGTGGAT GTGGGACATC AACGACCGTG CGCGCGTGGG CGTGAACCTAC
751 CGTTCCAAAG TCTCGCACAC GCTCAAAGGC GATGCCGAAT GGGCGGCAGA
801 CGGCGCGGCG GCGAAAGCAA TGTGGAGTAC GATGCTTGCA GCAAACGGCT
851 ACACGCGGAA TGAAAAAGCC CGCGTTAAAA TCGTTACGCC TGAGTCTTTG
901 TCCGTACACG GTATGTACAA AGTGTCCGAT AAAGCCGACC TGTTCCGCGA
951 CGTAACTTGG ACGCGCCACA GCCGCTTCGA TAAGGCGGAA CTGGTTTTTG
1001 AAAAAGAAAA AACCCTCGTC AAAGGCAAAAT CCGACCGCAC CACCATCACC
1051 CCAACTGGC GCAACACCTA CAAAGTCGGC TTCGGCGGTT CTTATCAAAT
1101 CAGCGAACCG CTGCAACTGC GCGCCGGCAT CGCTTTTGAC AAATCGCCCG
1151 TCCGCAACGC CGACTACCGC ATGAACAGCC TACCCGACGG CAACCGCATC
1201 TGGTCTCCG CCGGTATGAA ATACCATATC GGTAAAAACC ACGTCGTCGA
1251 TGCCGCCTAC ACCACATCC ACATCAACGA CACCAGCTAC CGCACGGCGA
1301 AGGCAAGCGG CAACGATGTG GACAGCAAAG GCGCGTCTTC CGCACGTTTC
1351 AAAAACCACG CCGACATCAT CGGTCTGCAA TACACCTACA AATTCAAATA
1401 A

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This corresponds to the amino acid sequence <SEQ ID 2988; ORF 989>:

```

m989.pep
1  MTPSALKKTV LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAAAAEADA
51  STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVDN LTVGLGVYVP FGSATEYEK SVLRHNINKL
151 GLTSIAVEPV AAWKLNDRHS FGAGIIAQHT SAELRKYADW GIKSKAEILT
201 AKPPKPNGVA EAAKIQADGH ADVKGSWDGF GYQLAWMWDI NDRARVGVNY
251 RSKVSHTLKG DAEWAADGAA AKAMWSTMLA ANGYTANEKA RVKIVTPESL
301 SVHGMKYKSD KADLFGDVTW TRHSRFDKAE LVFEKEKTVV KGKSDRTTIT

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1405

351 PNWRNTYKVG FGGSYQISEP LQLRAGIAFD KSPVRNADYR MNSLPDGNRI  
 401 WFSAGMKYHI GKNHVVDAA YTHIHINDTSY RTAKASGNDV DSKGASSARF  
 451 KNHADIIGLQ YTYKFK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

**g989/m989** 90.0% identity in 468 aa overlap

	10	20	30	40	50
g989.pep	MTPFTLKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAA-----DASTIFYNPAGL				
m989	MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL				
	10	20	30	40	50
	60	70	80	90	100
g989.pep	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNGKITKTTVAPHIYGAYKVNDN				
m989	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN				
	70	80	90	100	110
	120	130	140	150	160
g989.pep	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHN				
m989	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNRHSFGAGIIAQHT				
	130	140	150	160	170
	180	190	200	210	220
g989.pep	SAELRKYADXGIPKKAQMLQATPSNPTA---AAQIKADGHADVKGSDWGVGYQLAWMWDI				
m989	SAELRKYADWGIKSKAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWGFYQLAWMWDI				
	190	200	210	220	230
	240	250	260	270	280
g989.pep	NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKQQWNDNMLTPLGYTANEKASVKIVTPES				
m989	NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKAMWS-TMLAANGYTANEKARVKIVTPES				
	250	260	270	280	290
	300	310	320	330	340
g989.pep	LSVHGMVKVSDKADLFGDVTWTRHSRFNKAELFFEKEKNIANGKKSDRTTITPNWRNTYK				
m989	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAEVFEKEKTVVKGK-SDRTTITPNWRNTYK				
	300	310	320	330	340
	360	370	380	390	400
g989.pep	VGLGGSYQISEPLQLRVGIAFDKPPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA				
m989	VGFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA				
	360	370	380	390	400
	420	430	440	450	460
g989.pep	AYTHIHINDTSYRTAKASGNDVDSKGASCARFKNHADIIGLQYTYKFKX				
m989	AYTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX				
	420	430	440	450	460

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2989>:

a989.seq  
 1 ATGACCCCTT CCGCACTGAA AAAAACCGTC CTACTGCTCG GCACTGCCTT  
 51 TGCCGCCGCA TCCGCACAAG CCTCCGGCTA CCACTTCGGC ACACAGTCGG  
 101 TCAACGCGCA AAGCACGGCA AATGCCGCCG CCGCAGAAGC CGCCGACGCA  
 151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA  
 201 GATTTCCGTC AACGCCAACA TCGTGCTGCC CAGCATTCAT TATGAGGCGG  
 251 ATTCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGGTTC GAAAAGCGGC



1406

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301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTAG GCTTGGGCGT GTACGTCCCC TTCGGTTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 ACGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAGC
551 TGCGCAAATA TGCCGACTGG GGGATTATGG AAAAAGCGAA AGCACTAAAA
601 GAAACACCCC CCAATCCAAC TAAAGCCGCC CAAATCAAAG CCGACGGACA
651 CGCCGATGTC AAAGGCAGCG ATTGGGGCTT CGGCTACCAA CTGGCGTGGA
701 TGTGGGACAT CAACGACCGT GCGCGCGTGG GCGTGAAC TA CCGTTCCAAA
751 GTCTCACACA CGCTCAAAGG CGATGCCGAA TGGGCGGCAG ACGACGCAAT
801 GGCGAAACAG TTATGGGATG CAAACAAACT CGCACTGCTC GGCTACACGC
851 CAAGCGAAAA AGCCCGCGTT AAAATCGTTA CGCCCGAGTC TTTGTCCGTA
901 CACGGTATGT ACAAAGTGTC CGACAAAGCC GACCTGTTCG GCGACGTAAC
951 TTGGACGCGC CACAGCCGCT TCGATAAGGC GGAAGTGGTT TTTGAAAAAG
1001 AAAAAACCAT CGTCAACGGC AAATCCGACC GCACCACCAT CACCCCCAAC
1051 TGGCGCAACA CCTACAAAGT CGGCTTCGGC GGTTCCTATC AAATCAGCGA
1101 ACCGCTGCAA CTGCGCGCCG GCATCGCTTT TGACAAATCG CCCGTCCGCA
1151 ACGCCGACTA CCGCATGAAC AGCCTGCCCG ACGGCAACCG CATCTGGTTC
1201 TCCGCCGGCA TGAAATACCA TATCGGCAAA AACCACGTCG TCGATGCCGC
1251 CTACACCCAC ATCCACATCA ACGACACCAG CTACCGCACG GCGAAGGCAA
1301 GCGGCAACGA TGTGGACAGC AAAGGCGCGT CTTCCGCACG TTTCAAAAC
1351 CACGCCGACA TCATCGGCCT GCAATACACC TACAAATTCA AATAA

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This corresponds to the amino acid sequence <SEQ ID 2990; ORF 989.a>:

```

a989.pep
  1 MTPSALKKTV LLLGTAFAAA SAQASGYHFG TQSVNAQSTA NAAAAEAADA
 51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYK VNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNERHS FGAGIIAQHT SAELRKYADW GIMEKAKALK
201 ETPPNPTKAA QIKADGHADV KGS DWGFGYQ LAWMWDINDR ARVG VNYRSK
251 VSHTLKGDAE WAADDAMAKQ LWDANKLALL GYTPSEKARV KIVTPESLSV
301 HGMVKVSDKA DLFGDVTWTR HSRFDKAE LV FEKEKTIVNG KSDRTTITPN
351 WRNTYKVGFG GSYQISEPLQ LRAGIAFDKS PVRNADYRMN SLPDGNRIWF
401 SAGMKYHIGK NHVVDAAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN
451 HADIIGLQYT YKFK*

m989/a989 93.1% identity in 467 aa overlap

      10      20      30      40      50      60
m989.pep MTPSALKKTVLLLGTAF AAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL
a989      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      10      20      30      40      50      60
m989.pep TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
a989      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      70      80      90      100     110     120
m989.pep TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
a989      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      70      80      90      100     110     120
m989.pep LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSGAGIIAQHT
a989      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      130     140     150     160     170     180
m989.pep LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHT
a989      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      130     140     150     160     170     180
m989.pep SAELRKYADWGIKSKAEILTA KPPKNGVAEAAKI QADGHADV KGS DWGFGYQLAWMWDI
a989      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      190     200     210     220     230
m989.pep SAELRKYADWGIKSKAEILTA KPPKNGVAEAAKI QADGHADV KGS DWGFGYQLAWMWDI
a989      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      190     200     210     220     230
m989.pep NDRARVG VNYRSKVSHTLKGDAEWAADGAAAKAMW-STMLAANGYTANEKARVKIVTPES
a989      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      250     260     270     280     290     299
m989.pep NDRARVG VNYRSKVSHTLKGDAEWAADGAAAKAMW-STMLAANGYTANEKARVKIVTPES
a989      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      250     260     270     280     290     299
m989.pep NDRARVG VNYRSKVSHTLKGDAEWAADGAAAKAMW-STMLAANGYTANEKARVKIVTPES
a989      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      250     260     270     280     290     299

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1407

	240	250	260	270	280	290
m989.pep	300	310	320	330	340	350
	LSVHGMKVS DKA DLF G D V T W T R H S R F D K A E L V F E K E K T V V K G K S D R T T I T P N W R N T Y K V					
a989	300	310	320	330	340	350
	LSVHGMKVS DKA DLF G D V T W T R H S R F D K A E L V F E K E K T I V N G K S D R T T I T P N W R N T Y K V					
m989.pep	360	370	380	390	400	410
	G F G G S Y Q I S E P L Q L R A G I A F D K S P V R N A D Y R M N S L P D G N R I W F S A G M K Y H I G K N H V V D A A					
a989	360	370	380	390	400	410
	G F G G S Y Q I S E P L Q L R A G I A F D K S P V R N A D Y R M N S L P D G N R I W F S A G M K Y H I G K N H V V D A A					
m989.pep	420	430	440	450	460	
	Y T H I H I N D T S Y R T A K A S G N D V D S K G A S S A R F K N H A D I I G L Q Y T Y K F K X					
a989	420	430	440	450	460	
	Y T H I H I N D T S Y R T A K A S G N D V D S K G A S S A R F K N H A D I I G L Q Y T Y K F K X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2991>:

```

m990.seq
1  ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCGA
51  CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCAG CCGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAATTACAAT AGCGGCATCC TCGCCGTCGA
201 TAATATGCCC GTTGTCAAAA AATATATTAC AGAGAAGTAT GGGGCTGATT
251 TAAAGCAGGC GGTAAAAGT CAATTACAGG ATTTATACAA AACAGACCG
301 GAAGCTTGGG CAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGCACA
351 GTTTGGAACA AAATTTAGTA CGCTCAAACA GACGATGCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCCAC GTCGCCGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATCCCTT TTGGGAACCG CGCCGCCATT CCGACATCCA TACGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAACTGAC
651 CGTCCATAAG GATTATGCGG GCGGCGCGGA TTTCTGTTT GGCTACGACG
701 TGCGGGAGTC GGACGAACCC GCCCTGACCT TTGAAGACAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTGGGA ACGCCGGCCG GAAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CAAAACGGC GGATTCCGGT TCGTTTGCCT
851 TTAAACAAA TTACCGGCAG GGAATGTACG AATTATTGCT CAAGCAATGC
901 GAAGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAAATACT TTGTTTGGGC
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCGT
1051 CAAAATTGTT GGCTGCGCTT CATCGGCGGC CGGTCGCATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GGTGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GACTGGCAAT CGGCTGATG
1201 GGCGGCAGGG CCGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTGAT TTGTATGGTT ATGGCGGGGG TGTATTATGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GTGCGGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGTACAA
1401 AACCAGAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGGCAT TGTCGAAAAA GGCAATAATG TGCGGTTTTA CCTACAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GGCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGGCAA AGCCGCGCCG
1601 GCATTGCGGC AAAAACCCGT TTTGCTTTGC GTAACGGGTG CAATCTTCA
1651 CCTTTGCGG CTTTAAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGG
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCA CTCGAAGGGC
1751 GGTTCGGTAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TATGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTTGA

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This corresponds to the amino acid sequence <SEQ ID 2992; ORF 990>:

m990.pep

1408

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1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGNKYN SGILAVDNMP VVKKYITEKY GADLKQAVKS QLQDLYKTRP
101 EAWAENKKRT EEAYIAQFGT KFSTLKQTMP DINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK DYAGGADFLF GYDVRESDEP ALTFEDKVSQ
251 QSGVVLERRP ENLKTLDGRK LIAAKTADSG SFAFKQNYRQ GLYELLKQK
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGWRKGVQ IGGEVFVRQN EGSRLAIGVM
401 GGRAGQHASV NGKGAAGSD LYGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGIVGK GNNVRFYLPQ
501 QAQFTYLGVN GGFTDSEGTA VGLLGSQWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2993>:

a990.seq

```

1 ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCGA
51 CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCCAG CGGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AACTACAAT AGCGGCATAC TCGCCGTCGA
201 TAATATGCCC GTTGTTAAGA AATATATTAC AGATACTTAC GGGGATAATT
251 TAAAGGATGC GGTAAAGAAG CAATTACAGG ATTTATACAA AACAAGACCC
301 GAAGCTTGGG AAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGACA
351 GCTTGGACCA AAATTTAGTA TACTCAAACA GAAAAACCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTC AAATCGAAAA
501 CAAATCCAC GTCCGCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TATGCTGGA
601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAAGTAC
651 CGTCCATAAA GCGTATCAGG GCGGTGCGGA TTTCTGTTC GGCTACGACG
701 TGCGGGAGTC GGACAAACCC GCCCTGACCT TTGAAGAAAA AGTCAGCGGA
751 CAATCCGGCG TGTTTTGGA ACGCCGGCCG GAAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CGGAAAAGGC AGACTCTAAT TCGTTGCGCT
851 TTAAACAAAA TTACCGGCAG GGACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAAATACT TTGTTCCGGC
1001 TGCGTGCCGC CGACAGGGTC GACGACGTGT ATGCCGCGCA TCCGTCCCGT
1051 CAAAATTTGT GGCTGCGCTT CATCGGCGGC CGGTGCGATC AAAATAACG
1101 GGGCGGCGCG GCTGCGGACG GCGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GGCTGGCAAT CCGCGTGATG
1201 GGCGGCAGGG CTGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTTAT TTGCATGGT ATGGCGGGG TGTATTGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGCTACAA
1401 AACCAGAGGT TGGACGGCTT CTGTGGAAGG CCGCTACAAC GCGCTTGTGG
1451 CGGAAGGCGT TGTCGAAAAA GGCAATAATG TGCGGTTTTA CCTGCAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGGAAC AGCCGCGCGC
1601 GCATTCCGGC AAAAACCCTT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCG CTTTTAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCG CTCGAAGGGC
1751 GGTTCGGCAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TACGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2994; ORF 990.a>:

a990.pep

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGNKYN SGILAVDNMP VVKKYITDLY GDNLKDAVKK QLQDLYKTRP
101 EAWAENKKRT EEAYIEQLGP KFSILKQKNP DINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK AYQGGADFLF GYDVRESDEP ALTFEEDKVSQ
251 QSGVVLERRP ENLKTLDGRK LIAAEKADSN SFAFKQNYRQ GLYELLKQK
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGRRKGVQ IGGEVFVRQN EGSRLAIGVM

```

1409

401 GGRAGQHASV NGKGGAGSY LHGYGGGVYA AWHQLRDKQT GAYLDGWLQY  
 451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGVVGK GNNVRFYLPQ  
 501 QAQFTYLGVN GGFTDSEGT VLLGSGQWQ SRAGIRAKTR FALRNGVNLQ  
 551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG  
 601 YGKRTDGDKE AALSLKWLF\*

m990/a990 96.0% identity in 619 aa overlap

	10	20	30	40	50	60
m990.pep	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNYN					
a990	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNYN					
	10	20	30	40	50	60
m990.pep	70	80	90	100	110	120
a990	SGILAVDNMPVVKYITEKYGADLKQAVKSQLQDLYKTRPEAWAENKKRTEEAYIAQFGT					
	70	80	90	100	110	120
m990.pep	SGILAVDNMPVVKYITDTYGDNLKDAVKKQLQDLYKTRPEAWAENKKRTEEAYIEQLGP					
a990	SGILAVDNMPVVKYITDTYGDNLKDAVKKQLQDLYKTRPEAWAENKKRTEEAYIEQLGP					
	70	80	90	100	110	120
m990.pep	130	140	150	160	170	180
a990	KFSTLKQTMPTDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
	130	140	150	160	170	180
m990.pep	KFSTLKQTMPTDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
a990	KFSTLKQTMPTDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
	130	140	150	160	170	180
m990.pep	190	200	210	220	230	240
a990	MTLKDSLWEPRRHSDIHTLETSDNARIRLNTKDEKLTVHKDYAGGADFLFGYDVRESDEP					
	190	200	210	220	230	240
m990.pep	MTLKDSLWEPRRHSDIHMLETSDNARIRLNTKDEKLTVHKAYQGGADFLFGYDVRESDEP					
a990	MTLKDSLWEPRRHSDIHMLETSDNARIRLNTKDEKLTVHKAYQGGADFLFGYDVRESDEP					
	190	200	210	220	230	240
m990.pep	250	260	270	280	290	300
a990	ALTFEDKVSQSGVVLERRPENLKTLDGRKLIAAKTADSGSFAFKQNYRQGLYELLKQC					
	250	260	270	280	290	300
m990.pep	ALTFEEKVSQSGVVLERRPENLKTLDGRKLIAAEKADSNSFAFKQNYRQGLYELLKQC					
a990	ALTFEEKVSQSGVVLERRPENLKTLDGRKLIAAEKADSNSFAFKQNYRQGLYELLKQC					
	250	260	270	280	290	300
m990.pep	310	320	330	340	350	360
a990	EGGFCLGVQRLAIPAEAVLYAQQAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
	310	320	330	340	350	360
m990.pep	EGGFCLGVQRLAIPAEAVLYAQQAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
a990	EGGFCLGVQRLAIPAEAVLYAQQAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
	310	320	330	340	350	360
m990.pep	370	380	390	400	410	420
a990	RSHQNIRGGAAADGWRKGVQIGGEVFRQNEGSRLAIGVMGGRAGQHASVNGKGAAGSD					
	370	380	390	400	410	420
m990.pep	RSHQNIRGGAAADGRRKGVQIGGEVFRQNEGSRLAIGVMGGRAGQHASVNGKGAAGSY					
a990	RSHQNIRGGAAADGRRKGVQIGGEVFRQNEGSRLAIGVMGGRAGQHASVNGKGAAGSY					
	370	380	390	400	410	420
m990.pep	430	440	450	460	470	480
a990	LYGYGGGVYAASHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
	430	440	450	460	470	480
m990.pep	LYGYGGGVYAASHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
a990	LYGYGGGVYAASHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
	430	440	450	460	470	480
m990.pep	490	500	510	520	530	540
a990	ALVAEGIVGKGNNVRFYLPQAQFTYLGVNNGGFTDSEGTAVGLLGSQWQSRAGIRAKTR					
	490	500	510	520	530	540
m990.pep	ALVAEGIVGKGNNVRFYLPQAQFTYLGVNNGGFTDSEGTAVGLLGSQWQSRAGIRAKTR					
a990	ALVAEGIVGKGNNVRFYLPQAQFTYLGVNNGGFTDSEGTAVGLLGSQWQSRAGIRAKTR					
	490	500	510	520	530	540
m990.pep	550	560	570	580	590	600
a990	FALRNGVNLQPFAAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					
	550	560	570	580	590	600
m990.pep	FALRNGVNLQPFAAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					
a990	FALRNGVNLQPFAAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					

1410

	550	560	570	580	590	600
	610	620				
m990.pep	YGKRTDGDKEAALSLKWLFX					
a990	YGKRTDGDKEAALSLKWLFX					
	610	620				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2995>:

g992.seq

```

1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCC  TGTCGCTTTT  GGGCGCGTTG  GGTATACGG
101 GATATGACAG  TGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGCACGTCAG  GGGACGTGGG  TTTCGACGCG  CCCGTTTCGC  GACGGGCATC
201 GGCAGAAATCC  GGCCACAGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGATACCCT  TCACGTCATC  GACGGCGACG  GCGCGAAACA  TAAAAATCGG
301 ATGGCGTATA  TCGACGCACC  GGAGATGAAA  CAGGCTTACG  GTACACGTTT
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAGGG  TAGGAAAGTC  AGTGTACGTG
401 TGTTTGAAAC  CGACCGCTAT  CAGCGCGAAG  TGGCGCAGGT  ATCCGCCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATTG
501 TAAAGATTAT  GCTAAAGAAC  AGCAGGATAA  GGCGGATTTT  GCCGACTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGAAAGCT
601 AAAAAATCCG  AAGCGCCGTG  GCGGTACCGC  CGGGCAGGCA  GGAGCGCGCG
651 GGGCAATAAG  GATTGGATGG  ATTCCGTGGG  CGAATGGTTG  GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2996 ORF 992.ng>:

g992.pep

```

1  MFRHRHLKN  MQIKKIMKWL  PVALSLLGAL  GYTGVDSEAV  RTAVAVLDVL
51  GTAGDVGFDA  PVRRRASAKS  GHSYTGTVSK  VYDGDTHLVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFETDRY  QREVAQVSAG
151 KTDNLMLQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDSVGEWL  GIW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2997>:

m992.seq

```

1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCC  TGTCGCTTTT  GGGTGCCTTG  GGTATACGG
101 GGTACGGCAG  CGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GCGCGGCGAG  GGGACGCGGG  TTCCGACGCG  CCCGCCCGCC  GCCGAGCATC
201 GGCAGAAATCC  GGCCACCGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGACACCCT  TCACGTTATC  GACGGCGACG  GCGCGAAACA  CAAAATCCGG
301 ATGGCGTATA  TCGACGCGCC  GGAGATGAAA  CAGGCTTACG  GCACGCGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAAGG  CAGGAAAGTC  AGCGTGCGCG
401 TGTTTCGATC  CGACCGCTAC  CAGCGCGAAG  TGGCGCAGGT  TTCTGTCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATTG
501 TAAAGATTAT  GCTAAAGAAC  AGCAGGATAA  GGCGGATTTT  GCCGATTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGAAAGCT
601 AAAAAATCCG  AAGCGCCGTG  GCGGTACCGC  CGAGCAGGCA  GGAGCGCGCG
651 GGGCAATAAG  GATTGGATGG  ATGCCGTGGG  CGAATGGTTG  GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2998; ORF 992>:

m992.pep

```

1  MFRHRHLKN  MQIKKIMKWL  PVALSLLGAL  GYTGYGSEAV  RTAVAVLDVL
51  GAAGDAGSDA  PARRRASAKS  GHRYTGTVSK  VYDGDTHLVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFETDRY  QREVAQVSAG
151 KTDNLMLQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDAVGEWL  GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 992 shows 96.1% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. gonorrhoeae*

m992/g992      96.1% identity in 233 aa overlap

1411

```

      10      20      30      40      50      60
m992.pep  MFRRHRHLKKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA
          |||||
g992      MFRRHRHLKKNMQIKKIMKWL PVALSLLGALGYTGYDSEAVRTAVAVLDVLGTAGDVGFDA
          10      20      30      40      50      60

      70      80      90      100     110     120
m992.pep  PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN
          |||||
g992      PVRRRASAKSGHSYTGTVSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN
          70      80      90      100     110     120

      130     140     150     160     170     180
m992.pep  LRAAAEGRKVSVRVFD TDRYQREVAQVSVGKTD LNLMQVQDGA AAWHYKSYAKEQQDKADF
          |||||
g992      LRAAAEGRKVSVRVFETDRYQREVAQV SAGKTD LNLMQVQDGA AAWHYKSYAKEQQDKADF
          130     140     150     160     170     180

      190     200     210     220     230
m992.pep  ADYADAQIQAE RERKGLWKAKNPQAPWAYRRAGRS GGGNKDWM DAVGEWLGIWX
          |||||
g992      ADYADAQIQAE RERKGLWKAKNPQAPWAYRRAGRS GGGNKDWM DSVGEWLGIWX
          190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2999>:

```

a992.seq
1  ATGTT CAGAC GGCATCGGCA TTGAAAAAT ATGCAGATTA AAAAAATCAT
51  GAAATGGCTT CCCGTCGCCT TGTCGCTTTT GGGTGCCTTG GGTATACGG
101 GGTACGGCAG CGAGGCGGTG CGGACGGCGG TTGCCGTACT CGACGTACTC
151 GCGCGGCAG GGGACGCGGG TTCCGACGCG CCCGCCGCC GCGGAGCATC
201 GCGCAATCC GGCCACCGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
251 GCGACACCTT TCACGTTATC GACGGCGACG GCGCGAAACA CAAAATCCGG
301 ATGGCGTATA TCGACGCGCC GGAGATGAAA CAGGCTTACG GCACGCGTTC
351 GCGCGACAAC CTGCGCGCGG CGGCGGAAGG CAGGAAAGTC AGCGTCCGCG
401 TGTTTCGACAC CGACCGCTAC CAGCGCGAAG TGGCGCAGGT TTCTGTCCGC
451 AAAACCGATT TGAACCTGAT GCAGGTGCAG GACGGGGCGG CGTGGCATT
501 TAAAAGTTAT GCTAAAGAAC AGCAGGATAA GGCGGATTTT GCCGATTATG
551 CCGACGCTCA AATTCAGGCG GAAAGGGAAC GCAAAGGATT GTGGAAAGCT
601 AAAAATCCGC AAGCGCCGTG GGCGTACGCG CGGGCAGGCA GGAGCGGCGG
651 GGGCAATAAG GATTGGATGG ATGCCGTGGG CGAATGGTTG GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 3000; ORF 992.a>:

```

a992.pep
1  MFRRHRHLKN MQIKKIMKWL PVALSLLGAL GYTGYGSEAV RTAVAVLDVL
51  GAAGDAGSDA PARRRASAKS GHRYTGT VSK VYDGD TLHVI DGDGAKHKIR
101 MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFD TDRY QREVAQVSVG
151 KTD LNLMQVQ DGA AAWHYKSY AKEQQDKADF ADYADAQIQ A ERERKGLWKA
201 KNPQAPWAYR RAGRS GGGNK DWM DAVGEWL GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 992 shows 100.0% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. meningitidis*

a992/m992 100.0% identity in 233 aa overlap

```

      10      20      30      40      50      60
a992.pep  MFRRHRHLKKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA
          |||||
m992      MFRRHRHLKKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA
          10      20      30      40      50      60

      70      80      90      100     110     120
a992.pep  PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN
          |||||
m992      PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN
          70      80      90      100     110     120

      130     140     150     160     170     180

```

1412

```

a992.pep      LRAAAEGRKVSVRVFDTDYQREVAQVSVGKTDNLNMQVQDGAAWHYKSYAKEQQDKADF
m992          |||
              130      140      150      160      170      180
              190      200      210      220      230
a992.pep      ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDAVGEWLGIWX
m992          |||
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3001>:

```

g993.seq
1   CTGAAAGTCG TATTGGGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
51  CCTTATCCGC AAGCAGAACA TCGATGTTCT CGATATCCGC ATGGTGGAAA
101 TTACCGGGCA GTATCTGCAC TATATTGCC AAATGGAAGC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCG GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAGGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGTCTGC TTGCCTACGA GCAAATGAAA
301 CTGGCGGCGC AGGGTTTGGG CGCGCTGCCG CGTGCGGGAC GGGATTTCGC
351 GTGGGCTTAC CTGCCGCTGG AAATTGCAGC CGAGACGAAG CTGCCCAGAG
401 TTTACATCGC CGATTTGATG CAGGCATGGT TGGGCATTCT TTCTCGGGCA
451 AAACATACGC GCAGCCACGA AGTAATCCAA GAAACCCTTT CCGTGCGCGC
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CGAACACGGG ATATGCAGGT
551 TTCACGCCCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GATCGTCAAC
601 TTCATCGCCC TGTGGAGCT TGCCAAAGAA GGATTGGTCG GAATCGTACA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTTCGGC ACACGGGGCG GCGCGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3002 ORF 993.ng>:

```

g993.pep
1   LKVVLSFGQ PLDLLLYLIR KQIDVLDIP MVEITGQYLH YIAQMEAYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTEAVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAETK LPEVYIADLM QAWLGILSRA
151 KHTRSHEVIQ ETLSVRAQMT AILRRLNEHG ICRFHALFNP EQGAAYVIVN
201 FIALLELAKE GLVGIVQEDG FGEIRISLNH EGAHSDGIFG TRGGRDVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3003>:

```

m993.seq
1   TTGAAAGTCG TATTGGGCAG CTCCAAGGC CCTTTGGATC TACTGCTGTA
51  TCTGATCCGC AAACAGAATA TCGACGTACT GGATATCCG ATGGTGAAGA
101 TTACCGAGCA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAAC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCTGCG TGCTTACGA ACAGATGAAG
301 CTGGCGGCGC AGGGTTTGGG CGCGCTGCCG CGAGCCGGAC GGGATTTCGC
351 GTGGGCTTAC CTGCCGCTGG AAATTGCCGT CGAAGCCAAG CTGCCCAGAG
401 TCTATATTAC CGACTTGACG CAAGCGTGGC TGGGTATTT GTCTCGGGCA
451 AAACACACGC GCAGCCACGA AGTAATCAA GAAACCATCT CCGTGCGCGC
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CGGACACGGA ATATGCAGGT
551 TTCACGACCT GTTCAATCCC AAACAGGGCG CGGCTTACGT GGTCGTCAAC
601 TTCATCGCAC TGTGGAGCT TGCCAAAGAA GGATTGGTCA GAATCGTGCA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTCCGGC ACACGAGGCG GCGCGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3004; ORF 993>:

```

m993.pep
1   LKVVLSFGQ PLDLLLYLIR KQIDVLDIP MVKITEQYLH YIAQIETYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTETVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLGILSRA
151 KHTRSHEVIK ETISVRAQMT AILRRLNGHG ICRFHDLFNP KQGAAYVVVN
201 FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 993 shows 93.1% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. gonorrhoeae*

1413

m993/g993 93.1% identity in 248 aa overlap

	10	20	30	40	50	60
m993.pep	LKVVLGSFQGPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQ	IETYQFDLAAEYLLMA			
g993	LKVVLGSFQGPLDLLLYLIRKQ	NIDVLDIPMVEITGQYLHYIAQ	MEAYQFDLAAEYLLMA			
	70	80	90	100	110	120
m993.pep	AMLIEIKSRLLLPRTETVEDEE	ADPRAELVRRLLAYEQMKLAAQ	GLDALPRGRDFAWAY			
g993	AMLIEIKSRLLLPRTETVEDEE	ADPRAELVRRLLAYEQMKLAAQ	GLDALPRGRDFAWAY			
	130	140	150	160	170	180
m993.pep	LPLEIAVEAKLPEVYITDLTQ	AWLGILSRKHTRSHEVIKETIS	SVRAQMTAILRRLNGHG			
g993	LPLEIAAETKLPEVYIADLMQ	AWLGILSRKHTRSHEVIQETLS	SVRAQMTAILRRLNEHG			
	190	200	210	220	230	240
m993.pep	ICRFHDLFNPQGAAAYVVVNF	IALLELAKEGLVRIVQEDGFGE	IRISLNHEGAHSDGISG			
g993	ICRFHALFNPQGAAYVIVNF	IALLELAKEGLVGIVQEDGFGE	IRISLNHEGAHSDGIFG			
	249					
m993.pep	TRGGRDVF					
g993	TRGGRDVF					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3005>:

a993.seq

```

1  CTGAAAGTCG TATTGAGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
51  CCTTATCCGC AAGCAGAACA TCGATGTCT CGATATCCG ATGGTGAAGA
101 TTACCGAACA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151 GATTTGCGCG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAAC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCCTGC TGGCTTACGA GCAGATGAAG
301 CTGGCGGCAC AAGGGTTGGA TGCCTTCCT CGTGGCGGCC GGGATTTCGC
351 ATGGGCATAC CTGCCACTGG AAATTGCCGT CGAAGCCAAG CTGCCCCAAG
401 TCTATATTAC CGACTTGACG CAGGCGTGGC TGAGTATTTT GTCTCGGGCA
451 AAACATACGC GCAGCCACGA AGTTATCAA GAAACCATCT CCGTGCGCGC
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CAAACACGGG ATATGCAGGT
551 TTCACGACCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GGTCTGTAAC
601 TTCATCGCAC TGTGGAGCT TGCCAAAGAA GGTTGGTTCG GAATCGTACA
651 GGAAGTCGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTCCGGC ACACGGGGCG GCGCGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3006; ORF 993.a>:

a993.pep

```

1  LKVVLSFQGPLDLLLYLIRKQ NIDVLDIPMVKITEQYLHYIAQIETYQF
51  DLAAEYLLMA AMLIEIKSRL LPRTETVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLSILSRA
151 KHTRSHEVIK ETISVRAQMT AILRRLNKHG ICRFHDLPNP EQGAAYVVVN
201 FIALLELAKE GLVGIVQEVG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 993 shows 97.6% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. meningitidis*

a993/m993 97.6% identity in 248 aa overlap

	10	20	30	40	50	60
a993.pep	LKVVLSSFGGPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQ	IETYQFDLAAEYLLMA			
m993	LKVVLGSFQGPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQ	IETYQFDLAAEYLLMA			



1414

	10	20	30	40	50	60
a993.pep	70	80	90	100	110	120
m993	70	80	90	100	110	120
a993.pep	130	140	150	160	170	180
m993	130	140	150	160	170	180
a993.pep	190	200	210	220	230	240
m993	190	200	210	220	230	240
a993.pep	249					
m993	249					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3007>:

**g996.seq**

```

1 ATGAACAGAA GAACCTTCCT CCTCGGCGCA GGCGCGTTGC TTCTTACCGC
51 CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATTTCC GAAGGAAGCA
101 CCGTGCTTGC CTTGGGCGAT TCGCTCACCT TCGGCTACGG AGCAAACCCC
151 GGCGAATCCT ACCCGCGCA ACTGCAAAAA CTGACGGGTT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACGTCCGC GCAAGCCCTA TCGCGCCTGC
251 CCGCGCTGTT GGCACGCAAA CCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TCGCAAAGT TCCCGAGGAG CAGACCCGCG CCAATATCGC
351 GAAAATCATC GAAACCGTGC AAAAGGAAAA CATTCCCGCC GTCCTCGTCG
401 GCGTGCCGCA CATCACACTG GGCGCGTTGT TCGGGCATT GAGCGACCAT
451 CCGCTGTATG AGGATTGTG CGAGGAATAC GGCATTCCGT TGTTCGGCGG
501 CCGGTGGGCG GAAATTTTGG GCAATAATAA TCTGAAATCC GACCAATCC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTCG CCGAAAATTT GAATCAATTT
601 TTGAGAAAAC ATGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3008 ORF 996.ng>:

**g996.pep**

```

1 MNRRTFLLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51 GESYPAQLQK LTGWNIVNGG VSGD TSAQAL SRLPALLARK PKLVIVGIGG
101 NDFLRKVPPE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
151 PLYEDLSEY GIPFLGGAWA EILGNLNLKS DQIHANGKGY RKFAENLNQF
201 LRKHGFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3009>:

**m996.seq**

```

1 ATGAACAGAA GAACCTTCCT CCTCGGCGCA GGCGCGTTGC TGCTTACCGC
51 CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATTTCC GAAGGAAGCA
101 CCGTACTTGC CTTGGGCGAT TCGCTTACCT TCGGCTACGG CGCAAACCCCT
151 GGCGAATCCT ACCCGCGCA ACTGCAAAAA CTGACGGGTT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACATCTGC CCAAGCCCTG TCGCGCCTGC
251 CCGCGCTGTT GGCACGCAAA CCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TCGCAAAGT TCCCAAGGAG CAGACCCGCG CCAATATCGC
351 GAAAATCATC GAAACCGTGC AGAAGGAAAA CATCCCGGCC GTCCTCGTCG
401 GCGTGCCGCA CATCACACTG GGTGCGTTGT TCGGGCATT GAGCGATCAT
451 CCGCTGTATG AGGATTGTG CGAGGAATAC GGCATTCCGT TGTTCGGCGG
501 CCGGTGGGCG GAAATTTTGG GCGATAATAA TCTGAAATCC GACCAATCC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTTG CCGAAGATTT GAATCAATTT
601 TTGAGAAAAC AGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3010; ORF 996>:

**m996.pep**

```

1 MNRRTFLLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51 GESYPAQLQK LTGWNIVNGG VSGD TSAQAL SRLPALLARK PKLVIVGIGG

```

1415

101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH  
 151 PLYEDLSEY GIPLFGGAWA EILGDNNLKS DQIHANGKGY RKFAEDLNQF  
 201 LRKQGFR

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 996 shows 98.1% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. gonorrhoeae*

m996/g996 98.1% identity in 207 aa overlap

	10	20	30	40	50	60
m996.pep	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQLOK					
g996	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQLOK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m996.pep	LTGWNIVNGGVSGDTSQAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII					
g996	LTGWNIVNGGVSGDTSQAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII					
	70	80	90	100	110	120
	130	140	150	160	170	180
m996.pep	ETVQKENIPAVLVGVPHITLALFGHLSHDHPLYEDLSEYGIPLFGGAWAEILGDNNLKS					
g996	ETVQKENIPAVLVGVPHITLALFGHLSHDHPLYEDLSEYGIPLFGGAWAEILGNNLKS					
	130	140	150	160	170	180
	190	200				
m996.pep	DQIHANGKGYRKFAEDLNQFLRKQGFR					
g996	DQIHANGKGYRKFAENLNQFLRKHGFRX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3011>:

a996.seq

1	ATGAACAGAA	GAACCTTCCT	CCTCGGCGCA	GGCGCGTTGC	TCCTTACCGC
51	CTGCGGCAGA	AAATCCGCCC	GAACCCACGC	CAAAATTCCC	GAAGGAAGCA
101	CCGTACTTGC	CTTGGGCGAT	TCGCTTACCT	TCGGCTACGG	CGCAAACCCC
151	GGCGAATCCT	ACCCCGCGCA	ACTGCAAAAA	CTGACGGGTT	GGAATATTGT
201	CAACGGCGGC	GTATCGGGCG	ATACATCCGC	CCAAGCCCTG	TCGCGCCTGC
251	CCGCGCTGTT	GGCACGCAAA	CCCAAGCTTG	TGATTGTCGG	CATAGGCGGC
301	AACGACTTTC	TGCGCAAAAGT	TCCCAAGGAG	CAGACCCGCG	CCAATATCGC
351	GAAAATCATC	GAACCGTGC	AGAAGGAAAA	CATCCCGGCC	GTCCTCGTCG
401	GCGTGCCGCA	CATTACCTTG	GGCGCGTTGT	TCGGGCATTT	GAGCGATCAT
451	CCGCTGTATG	AGGATTGTGC	CGAGGAATAC	GGCATTCCGC	TGTTCCGGCGG
501	CGCGTGGCGG	GAAATTTTGG	GCGATAATAA	TCTGAAATCC	GACCAATATCC
551	ACGCCAACGG	CAAAGGCTAT	CGGAAATTG	CCGAAGATT	GAATCAATTT
601	TTGAGAAAAC	AGGGGTTTAG	ATAA		

This corresponds to the amino acid sequence <SEQ ID 3012; ORF 996.a>:

a996.pep

1	MNRRTFLLGA	GALLLTACGR	KSARTHAKIP	EGSTVLALGD	SLTFGYGANP
51	GESYPAQLQK	LTGWNIVNGG	VSGDTSQAAL	SRLPALLARK	PKLVIVGIGG
101	NDFLRKVPKE	QTRANIAKII	ETVQKENIPA	VLVGVPHITL	GALFGHLSDH
151	PLYEDLSEY	GIPLFGGAWA	EILGDNNLKS	DQIHANGKGY	RKFAEDLNQF
201	LRKQGFR*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 996 shows 100.0% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. meningitidis*

a996/m996 100.0% identity in 207 aa overlap

	10	20	30	40	50	60
a996.pep	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQLOK					

1416

```

|||||
m996      MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFYGANPGESYPAQLQK
              10      20      30      40      50      60

              70      80      90      100     110     120
a996.pep   LTGWNIVNGGVSGDTSQAQALSRLPALLARKPKLVIVIGGNDFLRKVPKEQTRANIAKII
|||||
m996      LTGWNIVNGGVSGDTSQAQALSRLPALLARKPKLVIVIGGNDFLRKVPKEQTRANIAKII
              70      80      90      100     110     120

              130     140     150     160     170     180
a996.pep   ETVQKENIPAVLVGVPHITLGALFGHLSDHPLYEDLSEYGIPLFGGAWAEILGDNNLKS
|||||
m996      ETVQKENIPAVLVGVPHITLGALFGHLSDHPLYEDLSEYGIPLFGGAWAEILGDNNLKS
              130     140     150     160     170     180

              190     200
a996.pep   DQIHANGKGYRKFAEDLNQFLRKQGFRX
|||||
m996      DQIHANGKGYRKFAEDLNQFLRKQGFR
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3013>:

```

g997.seq (partial)
1  ATGATGAACA CGCCGCATCC GCGCCCCGAAA ATCGCCGTCA TEGGCGCAGG
51 CTGGGCCGCGC TTGTCCGCCG CCGTCACCTT GGCGCGGCAC GCCGACGTTA
101 CCTGTGTTTGA AGCCGGCCCG CAGGCGGGCG GAAGGGCGCG CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGCGGTGT TCGCCTGAT GAAAACCATC GGTTCCAGACC
251 CCCGTGCCGC CTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCGCCCGCG CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATCAAAGCC AAAGTCTTG
401 CCGATATGTC CGATTTCAG AAGTCCGCAC GCCTCGGACA GCGCGACACG
451 ACAGTTGCAC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTGG CAGCCCTTGG TCTGGGCGCG GCTCAACACG CCTTTGGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG CGACGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCGGAA CCGCCCTTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCTCCCGGA CGGAAAAGTC
751 CTCGTCAACG GGAAGCCTT CGATGCCGCC ATACTTGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CTTTCGCTAC CACGCCATCA CCACCGCTA TCTGCGCTAC
901 GCCGAACCCG TCCGcCTGcc CGCCCCGCTG AccGGCAttg CCGAcggcAC
951 ggcaCaatgG CTGCTTTgcc cgGGGcAGGC tccggactgc CcccaaAacg
1001 aagTCTCCGC cGTCattagc GTTTCGAcG GCGtcgGcgG Gtttgcaaac
1051 cga...

```

This corresponds to the amino acid sequence <SEQ ID 3014 ORF 997.ng>:

```

g997.pep (partial)
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51 GNTDGFGLD NGQHILLGAY RGVLRMLMTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPSAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSDGVL
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA ILATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGIADGTAQW LLCPGQAPDC PQNEVSAVIS VSDRVGAFAN
351 R....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3015>:

```

m997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCCGAAA ATCGCCGTCA TCGGCGCAGG
51 CTGGGCCAGGA CTGTCCGCCG CCGTCACCTT GGCGCGGCAC GCCGACGTTA
101 CCTGTGTTTGA AGCCGGCCCG CAGGCGGGCG GCAGGGCGCG CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGCGGTGT TCGCCTGAT GAAAACCATC GGTTCCGATC
251 CCCGTGCCGC CTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCGCCCGCG CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGTG CACCGACTGC ATCAAAGCC AAAGTCTTG
401 CCGATATGTC CGATTTCAG AAGTCCGCAC GCCTCGGACA GCGCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTGAT
501 GCAGTTTGG CAGCCCTTGG TTTGGGCGCG GCTCAACACG CCTTTGGAAA

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1417

```

551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAGCAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCCTTGG CGGATCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCCTCCCGGA CGGGAAAGTG
751 CTCGTCAACG GCGAAGCTTT CGATGCCGCC GTCCCCGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGCTGCGC CGCCCCGCTG ACCGGCCTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCAGGCT CGGACTGCCT GAAAACGAAG
1001 TGTCCGCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAAGCCCA CGCCGACCTC AAACGCATCC TTCCGCATTT
1101 GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCCGCCCGG GACTTGTCTG GGTGACCG GCACCGCATC
1201 TTCCCCGCCG GCGACTACCT CCACCCGGAC TACCCGCCA CGCTCGAAGC
1251 CCGCGTACAA TCAGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 3016; ORF 997>:

```

m997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51  GNTDGFGLD NGQHILGAY RGVRLRMKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRAPTAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVLT
201 KKSQSDYLLP KQDLGAIVAE PALADLQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTQWV LLCRGRGLP ENEVSAVISV SDRVGAFANR
351 AWADKAHADL KRILPHLGEP EAVRVITEKR ATTAADAPPD DLSWLHRHRI
401 FPAGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 997 shows 96.0% identity over a 351 aa overlap with a predicted ORF (ORF 997) from *N. gonorrhoeae*

g997/m997 96.0% identity in 351 aa overlap

```

g997.pep      10      20      30      40      50      60
MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD
|||||
m997          10      20      30      40      50      60
MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD

g997.pep      70      80      90      100     110     120
NGQHILGAYRGVRLRMKTIGSDPRAAFLRVPLHWHMHGGGLQFRALPLPAPLHILGGVLL
|||||
m997          70      80      90      100     110     120
NGQHILGAYRGVRLRMKTIGSDPRAAFLRVPLHWHMHGGGLQFRALPLPAPLHILGGVLL

g997.pep     130     140     150     160     170     180
ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT
|||||
m997         130     140     150     160     170     180
ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT

g997.pep     190     200     210     220     230     240
PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPAELQRLGADIRLETRVC
|||||
m997         190     200     210     220     230     240
PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPAELQRLGADIRLETRVC

g997.pep     250     260     270     280     290     300
RLNTLPDGKVLVNGEAFDAAAILATAPYHAAALLPEGTPEHVQTAQNRYHAITTVYLRY
|||||
m997         250     260     270     280     290     300
RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAQNRYHAITTVYLRY

g997.pep     310     320     330     340     350
AEPVRLPAPLTGIADGTAQWLLCPGQAPDCPQNEVSAVISVSDRVGAFANR
|||||
m997         310     320     330     340     350
AEPVRLPAPLTGLADGTQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKAHAD

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3017>:

```
a997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTC A TCGGCGCAGG
51  CTGGGCGCGG TTGTCCGCGG CCGTTACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCGCG CAGGCGGGCG GCAGGGCGCG CGCACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ATATTTTACT
201 CGGCGCATAC CGGGGCGTGT TGCAGCTGAT GAAAACCATC GGTTCAGACC
251 CCCATGCCGC CTTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CTTGCCCGCG CCCCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAAGTGTCTG
401 CCGATATGTC CGATTTGCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTGGC CAGCCCTTGG TTTGGGCGCG GCTCAACACG CCTTTGGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCGGAA CCCGCCTTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCATATGC CGTCTGAACA CCCTCCCGGA CGGGAAGTG
751 CTCGTCAACG GCGAACCTTT CGATGCCGCC GTCCCCGCCA CCGCGCCCTA
801 CCACGCGGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAT CACGCCATCA CCACCGTCTA TCTGCGCTAT
901 GCCGAACCCG TCCGCTTGCC TGCCCCGCTG ACCGGACTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCGAGGT CGGACTGCCT GAAAACGAAG
1001 TGTCCGCGGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAAGTCA CGCCGACCTC AAACGCATCC TTCCGCATTT
1101 GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCCGCCGCG GATTTGTCGT GGTTCACCG GCACCGCATC
1201 TTCCCCGCGG GCGACTACCT CCACCCAGAC TACCCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA
```

This corresponds to the amino acid sequence <SEQ ID 3018; ORF 997.a>:

```
a997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARALA
51  GNTDGFGLD NGQHILLGAY RGVRLRMKTI GSDPHAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPSAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVNQFW QPLVWGALNT PLETASLRVL CNVLSGVLT
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRIC RLNTLPDGKV
251 LVNGEPFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTQVQW LLCRGRGLP ENEVSAVISV SDRVGAFAFR
351 AWADKVHADL KRILPHLGEP EAVRVITEKR ATTAADAPPP DLSWLHRHRI
401 FPGADYLHPD YPATLEAAVO SGFASAEACL QSLSDAV*
```

Computer analysis of this amino acid sequence gave the following results:

#### Homology with a predicted ORF from *N. meningitidis*

ORF 997 shows 98.2% identity over a 437 aa overlap with a predicted ORF (ORF 997) from *N. meningitidis*

a997/m997 98.2% identity in 437 aa overlap

	10	20	30	40	50	60
a997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARALAGNTDGFGLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
a997.pep	NGQHILLGAYRGVRLRMKTIGSDPHAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
m997	NGQHILLGAYRGVRLRMKTIGSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
a997.pep	ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
a997.pep	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPALELQRLGADIRLETRIC					
m997	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPALELQRLGADIRLETRIC					
	190	200	210	220	230	240
a997.pep	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPALELQRLGADIRLETRIC					
m997	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPALELQRLGADIRLETRIC					

1419

```

m997      PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALADLQRLGADIRLETRVC
           190      200      210      220      230      240

a997.pep      250      260      270      280      290      300
RLNTLPDGKVLVNGEPFDAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
|||||
m997      RLNTLPDGKVLVNGEAFDAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
           250      260      270      280      290      300

a997.pep      310      320      330      340      350      360
AEPVRLPAPLTGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKVHADL
|||||
m997      AEPVRLPAPLTGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKAHADL
           310      320      330      340      350      360

a997.pep      370      380      390      400      410      420
KRILPHLGEPEAVRVITEKRATTAADAPPPDLSSLHRHRIFPAGDYLHPDYPATLEAAVQ
|||||
m997      KRILPHLGEPEAVRVITEKRATTAADAPPPDLSSLHRHRIFPAGDYLHPDYPATLEAAVQ
           370      380      390      400      410      420

a997.pep      430
SGFASAEACLQSLSDAVX
|||||
m997      SGFASAEACLQSLSDAVX
           430

```

g999.seq Not found yet

g999.pep Not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3019>:

```

m999.seq
1  ATGAATATGA  AAAAAATTGAT  TTCCGCAATT  TGTGTTTCAA  TTGTTTTATC
51  AGCCTGCAAC  CAACAATCAA  AAACGGCACA  AGCCGAAGAA  CCTGTCCAAA
101  GTATCCAGGC  TGCTGATTGT  ACCGCCCCAA  TGGACATCAC  AGTTGAACAA
151  TATCTCATCA  ATTTGGAGCA  AGCATTAAAA  ACTCAGAACG  TCTCAACAAA
201  AATCCATAAT  AAAAAATTG  TCAAGACCGA  TTGTGTTTAT  GACCTTACTT
251  TGGTAATGGA  TTTTGGGGCG  ATTGCGCTCA  AACTGGACGA  GCAGCAAAAA
301  ATTAGAGCTA  TCTCAGTAGG  CTACATTTTA  AAAACCGACG  GAGAGAAAGG
351  ACAAATCTA  GTCAATAATG  CCATAAATGG  ATTACACAGT  ATTCAGGCAG
401  TTCTGTCTTT  AACTACCACA  GACAAATTGG  GCGAATCGGA  AGCAGGAAAA
451  CAACTTTTAA  CAGCTTTAAC  CGAAGTCGTC  AAAGAATCCA  ATCAGACAGG
501  AGCAACAGCG  CAAAAAGACG  TTCCGGCAGA  TGGTATTTTA  TATAGCGTTG
551  TTTTGAATA  AGAAACAAAC  ACCATTGCAA  TAATCGGCAG  AAAACAACCC
601  TAA

```

This corresponds to the amino acid sequence <SEQ ID 3020; ORF 999>:

```

m999.pep
1  MNMKKLISAI  CVSIVLSACN  QSKTAQAE  PVQSIQAADC  TAPMDITVEQ
51  YLINLEQAFK  TQNVSTKIHN  KNIVKTD  DCGY  DLTLMDFGA  IALKLDEQQK
101  IRAISVGYIL  KTDGEKGQNL  VNNAINGL  HS  IQAVLSITTT  DKLGESEAGK
151  QLFTALTEVV  KESNQTGATA  QKDVPADG  IL  YSVVFEKETN  TIAIIGRKQP

```

a999.seq Not found yet

a999.pep Not found yet

The foregoing examples are intended to illustrate but not to limit the invention.

## CLAIMS

1. A protein comprising a fragment of an amino acid sequence from SEQ ID 2790 wherein said fragment comprises at least 7 amino acids from said sequence.
2. A protein comprising an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020.
3. A protein having 50% or greater homology to a protein according to claim 1.
4. A protein comprising a fragment of an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020, wherein said fragment comprises 7 or more consecutive amino acids from said sequence.
5. An antibody which binds to a protein according to any one of claims 1 to 3.
6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.
7. A nucleic acid molecule according to claim 5, comprising a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019.
8. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019, wherein said fragment comprises 10 or more consecutive nucleotides from said sequence.
9. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 5.
10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 6.
11. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 7.
12. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
13. A composition according to claim 11 being a vaccine composition or a diagnostic composition.
14. A composition according to claim 11 for use as a pharmaceutical.
15. The use of a composition according to claim 11 in the manufacture of a medicament for the treatment or prevention of infection due to Neisserial bacteria.

16. A composition comprising a protein of claim 1 wherein said composition is immunogenic.

17. A composition comprising a protein of claim 2 wherein said composition is immunogenic.

18. A composition comprising a protein of claim 3 wherein said composition is immunogenic.

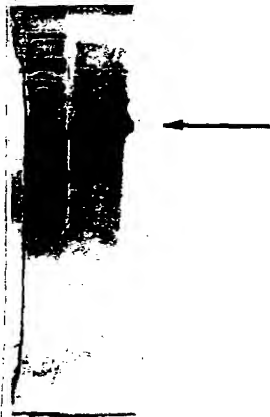


*FIG. 1A*

919 (46 kDa)

PURIFICATION

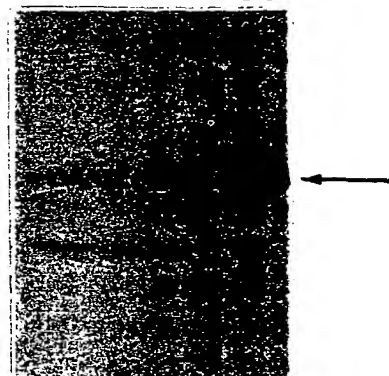
M1 919

*FIG. 1B*

919 (46 kDa)

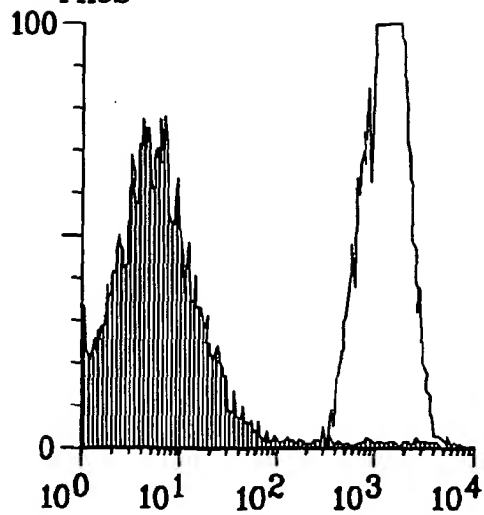
WESTERN BLOT

OMV TP PP

*FIG. 1C*

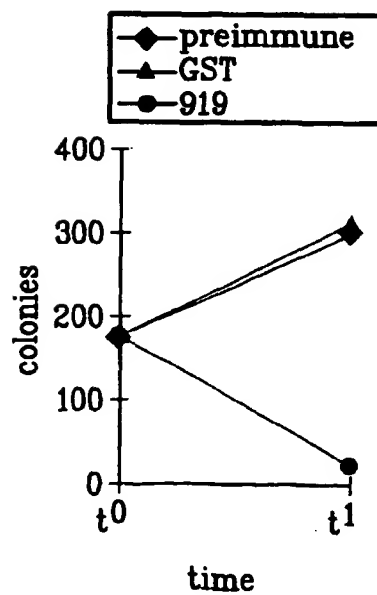
919 (46 kDa)

FACS

*FIG. 1D*

919 (46 kDa)

BACTERICIDAL ASSAY

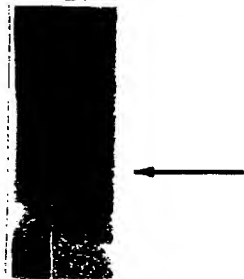
*FIG. 1E*

919 (46 kDa)

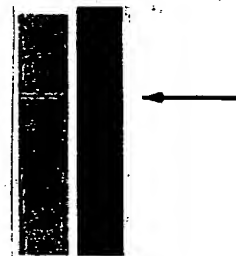
ELISA assay: positive

*FIG. 2A*

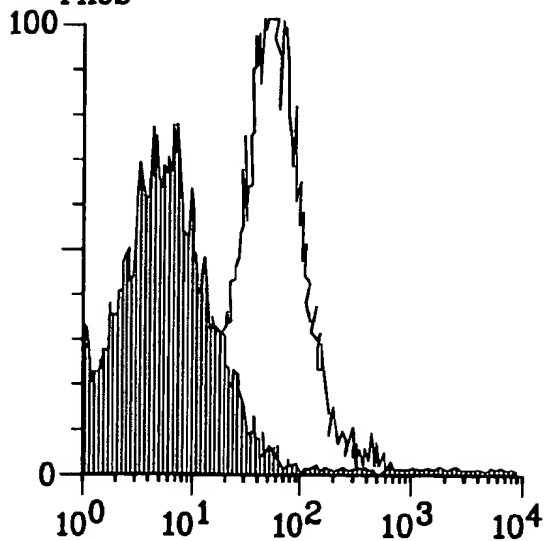
279 (10.5 kDa)  
PURIFICATION  
M1 279

*FIG. 2B*

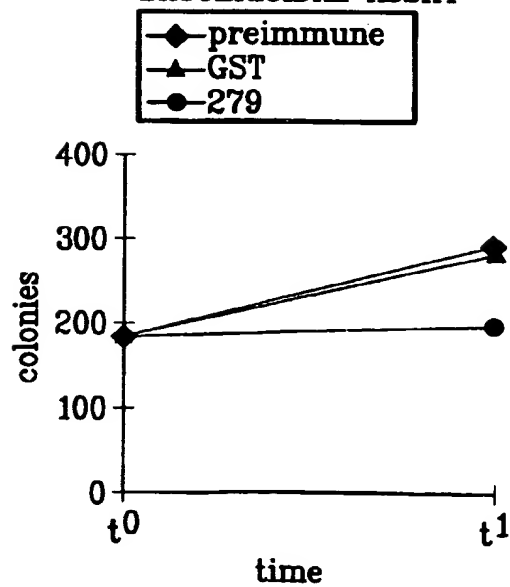
279 (10.5 kDa)  
WESTERN BLOT  
TP OMV

*FIG. 2C*

279 (10.5 kDa)  
FACS

*FIG. 2D*

279 (10.5 kDa)  
BACTERICIDAL ASSAY

*FIG. 2E*

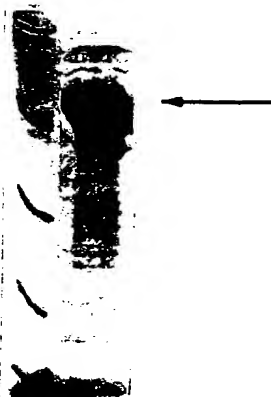
279 (10.5 kDa)  
ELISA assay: positive

*FIG. 3A*

576 (27.8 kDa)

PURIFICATION

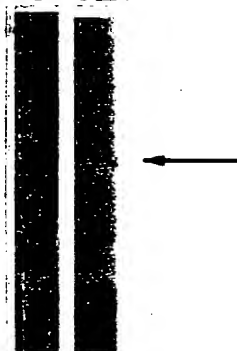
M1 576

*FIG. 3B*

576 (27.8 kDa)

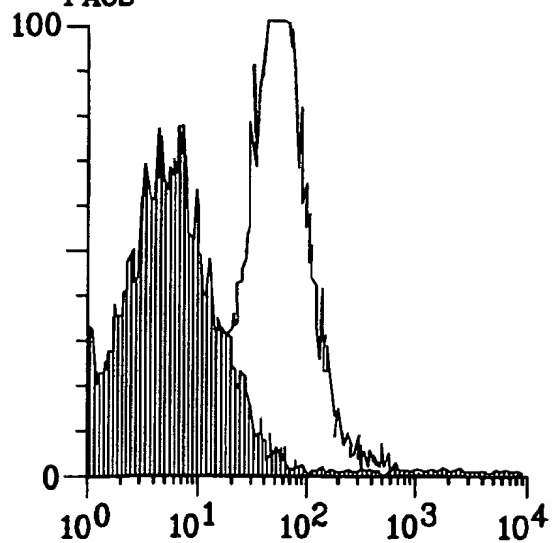
WESTERN BLOT

TP OMV

*FIG. 3C*

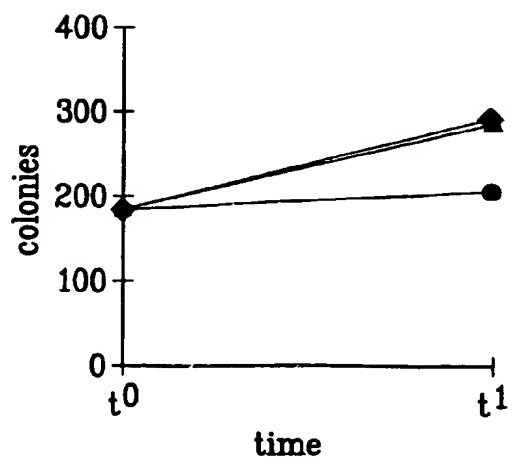
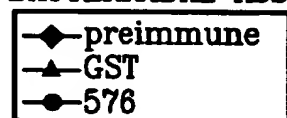
576 (27.8 kDa)

FACS

*FIG. 3D*

576 (27.8 kDa)

BACTERICIDAL ASSAY

*FIG. 3E*

576 (27.8 kDa)

ELISA assay: positive

*FIG. 4A*

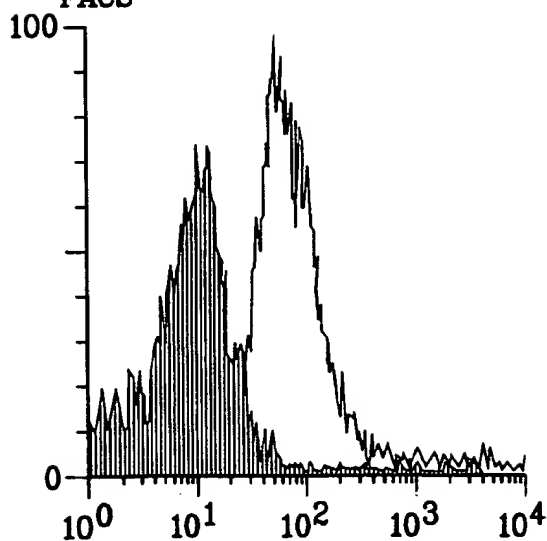
519 (33 kDa)  
PURIFICATION  
M1 519

*FIG. 4B*

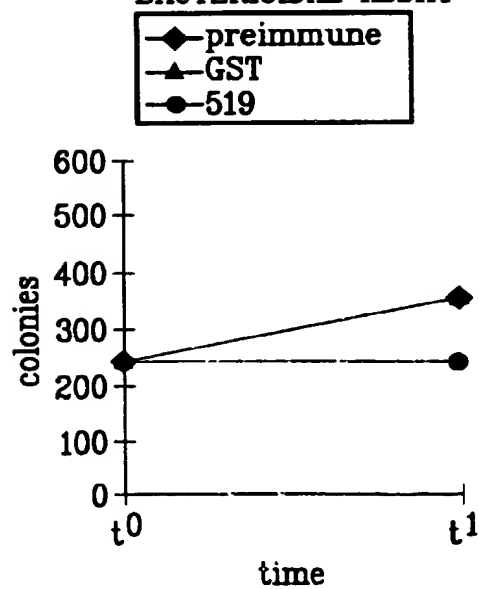
519 (33 kDa)  
WESTERN BLOT  
TP OMV

*FIG. 4C*

519 (33 kDa)  
FACS

*FIG. 4D*

519 (33 kDa)  
BACTERICIDAL ASSAY

*FIG. 4E*

519 (33 kDa)  
ELISA assay: positive

*FIG. 5A*

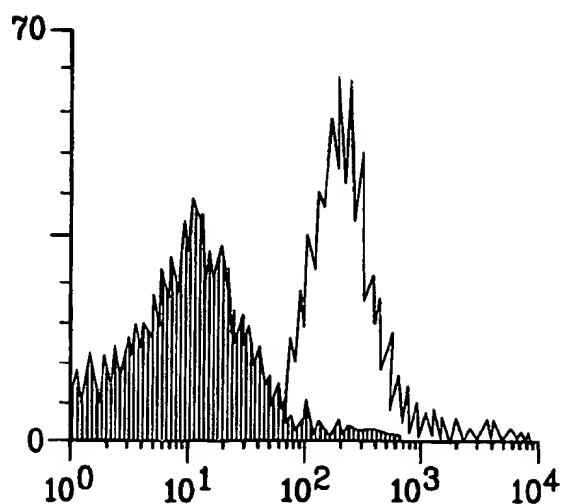
121 (40 kDa)  
PURIFICATION  
M1 121

*FIG. 5B*

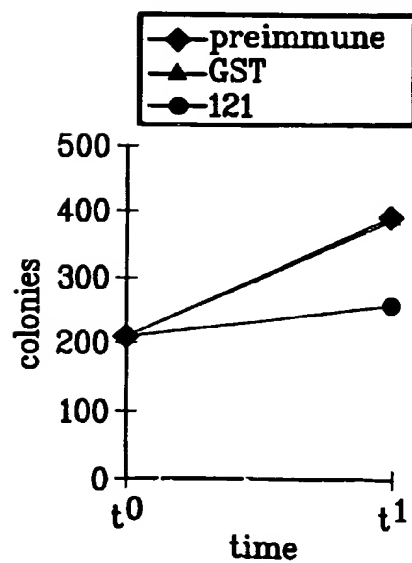
121 (40 kDa)  
WESTERN BLOT  
TP OMV

*FIG. 5C*

121 (40 kDa)  
FACS

*FIG. 5D*

121 (40 kDa)  
BACTERICIDAL ASSAY

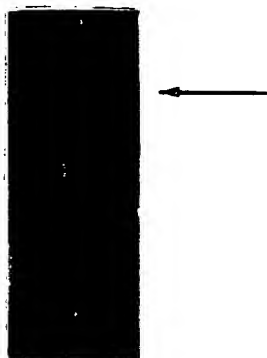
*FIG. 5E*

121 (40 kDa)

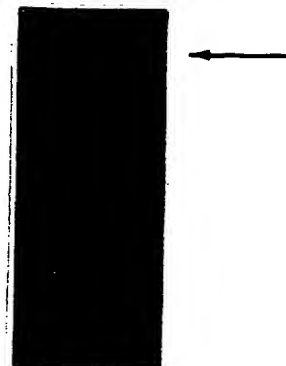
ELISA assay: positive

*FIG. 6A*

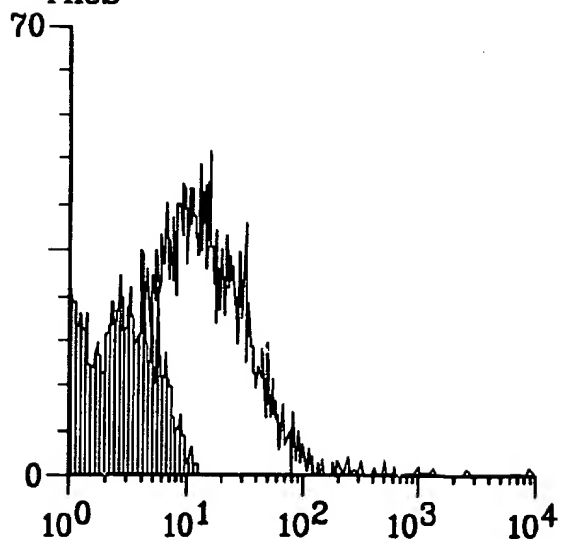
128 (101 kDa)  
PURIFICATION  
M1 128

*FIG. 6B*

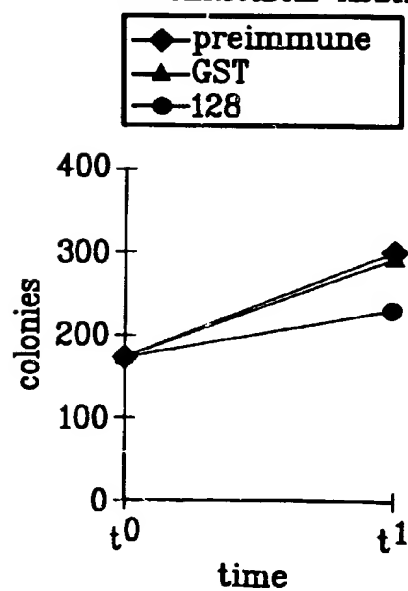
128 (101 kDa)  
WESTERN BLOT  
TP OMV

*FIG. 6C*

128 (101 kDa)  
FACS

*FIG. 6D*

128 (101 kDa)  
BACTERICIDAL ASSAY

*FIG. 6E*

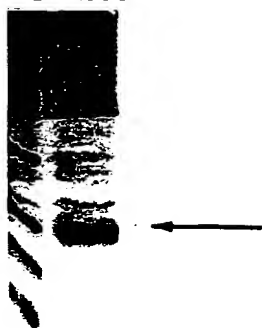
128 (101 kDa)  
ELISA assay: positive

*FIG. 7A*

206 (17 kDa)

PURIFICATION

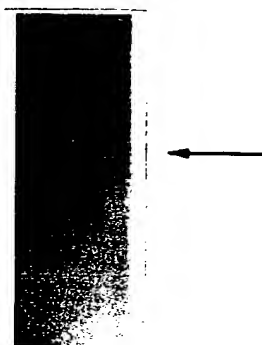
M1 206

*FIG. 7B*

206 (17 kDa)

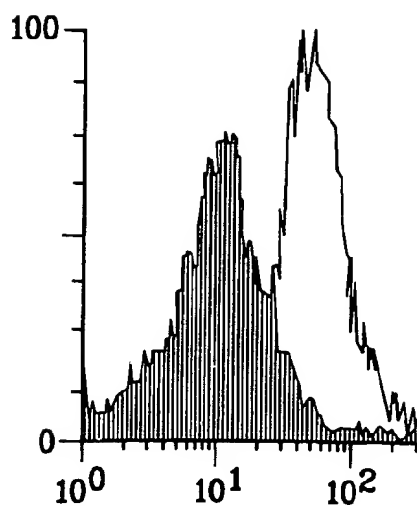
WESTERN BLOT

TP OMV

*FIG. 7C*

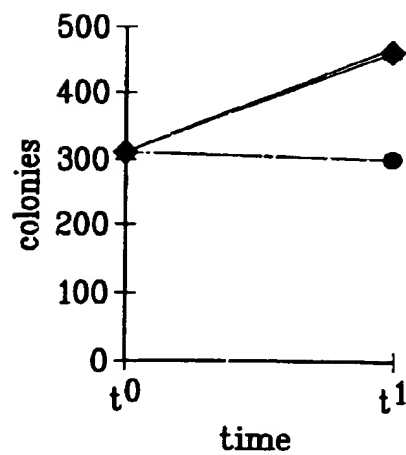
206 (17 kDa)

FACS

*FIG. 7D*

206 (17 kDa)

BACTERICIDAL ASSAY

*FIG. 7E*

206 (17 kDa)

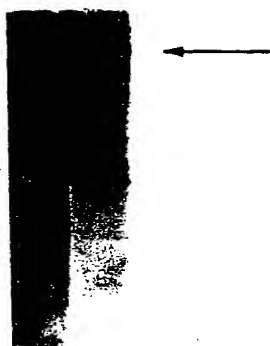
ELISA assay: positive

*FIG. 8A*

287 (78 kDa)

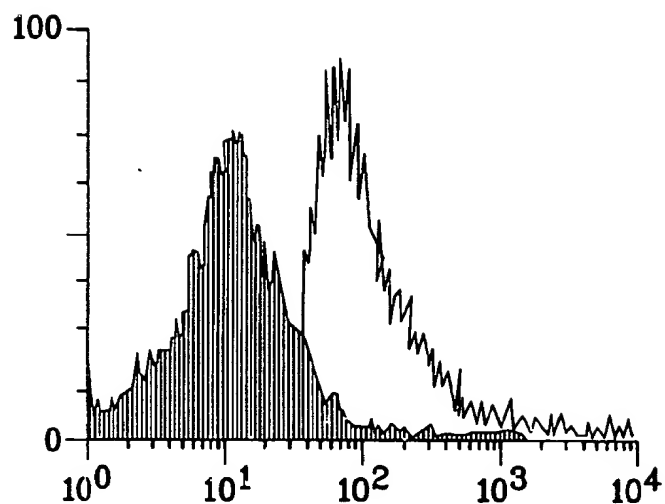
PURIFICATION

M1 287

*FIG. 8B*

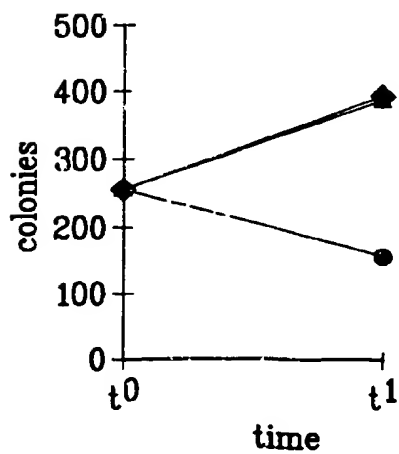
287 (78 kDa)

FACS

*FIG. 8C*

287 (78 kDa)

BACTERICIDAL ASSAY

*FIG. 8D*

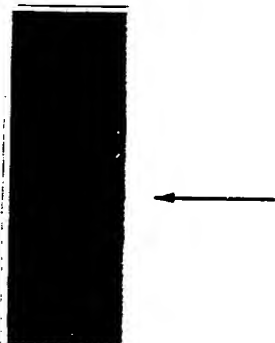
287 (78 kDa)

ELISA assay: positive



*FIG. 9A*

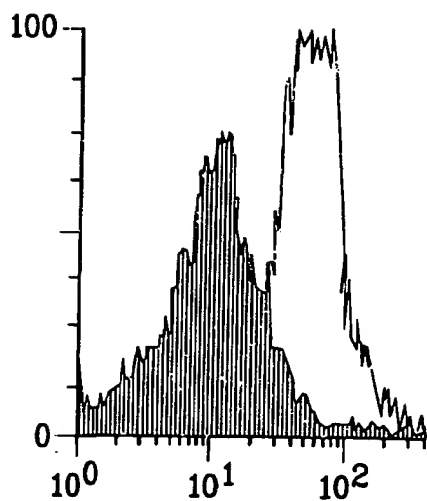
406 (33 kDa)  
PURIFICATION  
M1 406

*FIG. 9B*

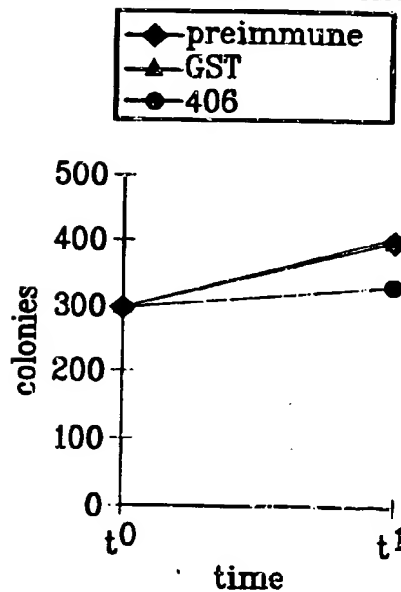
406 (33 kDa)  
WESTERN BLOT  
TP OMV

*FIG. 9C*

406 (33 kDa)  
FACS

*FIG. 9D*

406 (33 kDa)  
BACTERICIDAL ASSAY

*FIG. 9E*

406 (33 kDa)  
ELISA assay: positive

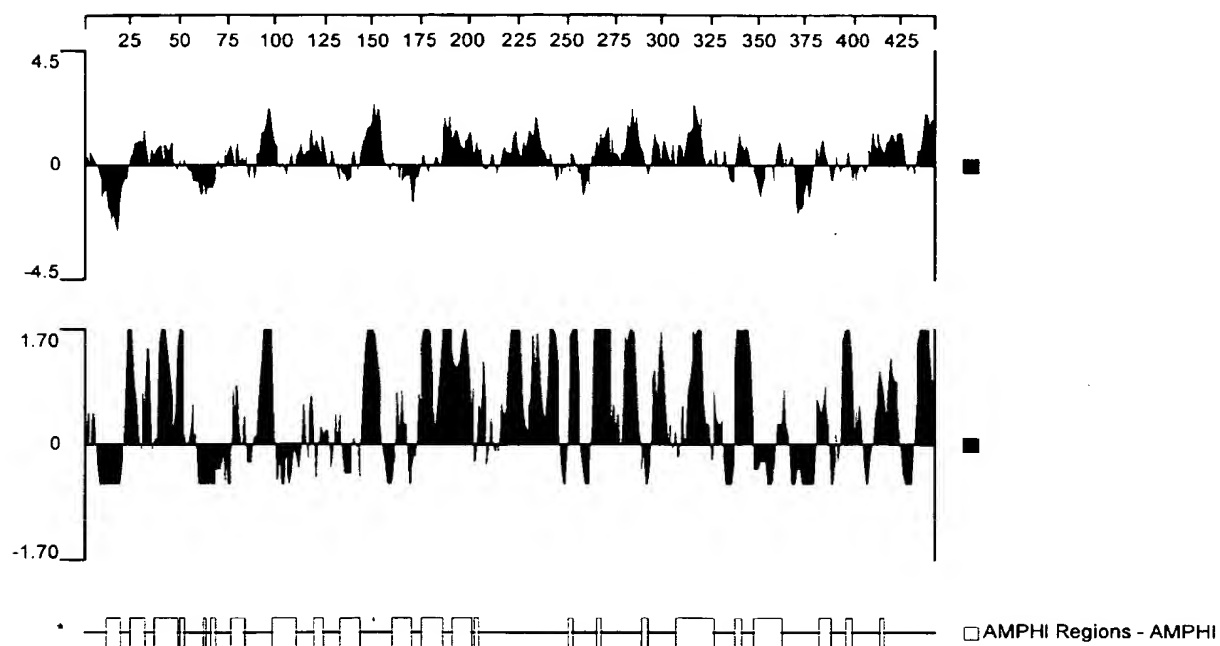
919Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 10